

**Advancing microbial risk management through strategic integration
of risk assessment and water supply operations**

by

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Author's Declaration

This thesis consists of material all of which I authored or co-authored: see Statement of Contributions included in the thesis. This is a true copy of the thesis, including any required final revisions, as accepted by my examiners.

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Statement of Contributions

Dafne de Brito Cruz was the primary author for all chapters of this thesis. This thesis consists of five manuscripts written for publication. Exceptions to sole authorship of material are described below.

Chapter 2 is based on the following journal article:

de Brito Cruz, D., Schmidt, P. J., Kundert, K. L., Ruecker, N. J., & Emelko, M. B. (2025). Particulate contaminants and treatment decision-making: maximizing the value of raw water pathogen monitoring for drinking water safety. *J Water Health*, 23 (6): 764–779. <https://doi.org/10.2166/wh.2025.020>

This research was conducted by Dafne de Brito Cruz under the supervision of Dr. Monica Emelko and Dr. Philip Schmidt. Dafne de Brito Cruz prepared the original draft manuscript and analyzed the data. Dr. Philip Schmidt and Dr. Monica Emelko conceptualized the study and contributed to review and editing. Dr. Norma Ruecker and Kelsey Kundert reviewed the manuscript and supported the contextualization of the research. The City of Calgary contributed to the collection of microbial water quality data presented in this work.

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Abstract

Controlling risks posed by microbial contaminants is a key focus for the provision of safe drinking water. Increasing threats to water supply systems—such as rapid water quality changes associated with climate-shocks (e.g., wildfires, heavy precipitation, etc) as well as infrastructure failures and treatment deficiencies—increasingly challenge microbial risk management and underscore the need for resilience in safe water supply. The goal of this research was to advance drinking water microbial risk management through integration of risk assessment approaches and real-world water supply treatment operations scenarios. Quantitative and qualitative risk-based frameworks were developed to address gaps in knowledge and practice related to monitoring, treatment decision-making, risk assessment and treatment operations.

Routine pathogen monitoring programs and the use of monitoring data in risk assessment for treatment decision making were addressed using data from a full-scale water treatment plant. Practical guidance was provided about monitoring and associated risk-based treatment requirements including methods for choosing sampling locations and frequency. Policy contributions involved definition of treatment sufficiency compliance rules and evidence for inclusion of *Giardia* in protozoa monitoring programs. This work underscored that data collection should be tailored to best represent water entering treatment plants so their use in risk assessment can best inform treatment decisions and maximize return on investment. While this may seem obvious, how to best represent system-specific attributes in monitoring design and implementation is often far from obvious. To shift from routine operations to extreme events, a scenario-based quantitative microbial risk assessment (QMRA) framework was applied in a case study involving a wastewater spill upstream of a drinking water intake, in which urgent risk-informed treatment decisions were needed. Conducting comprehensive and mathematically complex QMRA is not practical when time-sensitive decisions are needed. Thus, the simplified framework developed here demonstrated how preliminary risk assessment can be conducted for short-term, rapid source water quality degradation events and used to inform operational decisions and improve drinking water system response to adverse events.

Filtration plays a central role in microbial risk management during drinking water treatment. Although filtration plants include multiple filters, risk is typically evaluated based on individual filter performance. A model was developed to evaluate how dynamic, concurrent operation of multiple filters affects plant-scale filtration performance and thus microbial risk. It was demonstrated that operational

response strategies should prioritize improving performance when it is “low” rather than maximizing performance when it is already “high” because microbial treatment performance is typically expressed on a logarithmic scale. Practical implications of several design or operational decisions for microbial risk management such as the number of filters in operation, backwash staggering schedules and filter-to-waste operation were presented. Plant-scale risk assessment is essential to microbial risk management because risk is driven by the collective and dynamic operation of multiple treatment units. Yet, current practice and regulatory guidance do not always acknowledge plant scale considerations. Linking several aspects of water supply integrally related to risk, the effect of dependence between model inputs in drinking water QMRA was then evaluated. Hypothetical scenarios and data from a full-scale water treatment plant were used to demonstrate that ignoring dependence can over- or underestimate risk, sometimes substantially (e.g., more than an order of magnitude), and mislead decision-making. A framework was developed for characterizing the potential for biased interpretation of risk when assumed independence that is typical in QMRA practice is not valid.

Finally, the themes and insights described above were connected to more broadly highlight the inextricable linkage between microbial risk assessment and resilience in safe drinking water supply. The concept of operational resilience was defined as a water supply system’s capacity to limit the risk consequences of insufficient treatment performance when adverse events perturb it. Then, hypothetical case studies were used to demonstrate that resilience description must explicitly reflect risk to be an actionable tool. These foundations can be used to develop tools to operationalize resilience in the future. In addition to contributions to advancing risk and resilience sciences and drinking water policies, this research provides actionable knowledge to water utilities for improving decision-making during challenging conditions, assessing microbial risks more accurately and increasing the resilience of treatment operations.

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Dedication

To Matheus, my life partner, for making everything in my life happier and lighter.

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List of Abbreviations

AEP	Alberta Environment and Parks
AWWA	American Water Works Association
CDF	Cumulative Density Function
CEDAE	Companhia Estadual de Águas e Esgotos do Rio de Janeiro
CF-VP	Constant Flow-Variable Production
CT	Product of residual free chlorine concentration and contact time
DALY	Disability-Adjusted Life Years
FMEA	Failure Mode and Effects Analysis
IMS	Immunomagnetic separation
IPCC	Intergovernmental Panel on Climate Change
LIMS	Laboratory Information Management System
LT2ESWTR	Long Term 2 Enhanced Surface Water Treatment Rule
MAC	Maximum Acceptable Concentration
NHMRC	National Health and Medical Research Council
NR	Not reported
NRMMC	National Resource Management Ministerial Council
NTU	Nephelometric Turbidity Units
O. Reg.	Ontario regulation
PFAS	Per- and polyfluoroalkyl substances
PCR	Polymerase chain reaction
QMRA	Quantitative Microbial Risk Assessment
qPCR	Quantitative polymerase chain reaction

RT-PCR	Reverse transcription polymerase chain reaction
RT-qPCR	Reverse transcription quantitative polymerase chain reaction
SWRCB	State Water Resources Control Board
U.S. EPA	United States Environmental Protection Agency
U.S.	United States
UV	Ultraviolet
VF-CP	Variable Flow-Constant Production
WHO	World Health Organization
WTP	Water Treatment Plant

Chapter 1

Introduction

1.1 Background

The provision of microbiologically safe drinking water is a cornerstone of public health protection. The connections between water and public health engineering have a history that date back to the 19th century, when a sanitary revolution accelerated efforts to provide safe drinking water and improve sanitation and hygiene conditions (Tulchinsky & Varavikova, 2014). This turning point in the history of water engineering drastically reduced the number of infectious diseases and mortality rates in several countries. Although substantial scientific and technological progress has been made over the last two centuries, waterborne outbreaks associated with drinking water remain a problem both in high- and low-income countries (Moreira & Bondelind, 2017). For example, it has been estimated that waterborne pathogens caused 7.15 million illnesses and 6630 deaths annually in the United States between 2000 and 2015 (Collier et al., 2021).

Drinking water supply systems are increasingly challenged by extreme climate-related events affecting source water quality (e.g., floods, droughts, erosion, wildfires) and accidents caused by aging infrastructure (e.g., spills) that are sometimes unexpected and require rapid decisions for ensuring public health protection. Extreme rainfall events have been associated with fecal pollution and increased concentrations of microbial contaminants, and even with waterborne outbreaks (Charron et al., 2004; Jofre et al., 2010; Wu et al., 2016; Graydon et al., 2022). Wastewater contamination caused by infrastructure failures (Preisner, 2020) and combined sewer overflows after extreme precipitation (Jagai et al., 2015) can also impact water quality and potentially, downstream drinking water treatment. Other apparently unrelated water quality changes that do not increase microbial contaminant concentrations can nonetheless affect pathogen treatment. For example, increases in natural organic matter can affect coagulation, an important physico-chemical process that enables pathogen removal and inactivation in downstream treatment processes (Emelko et al., 2011). While water regulations have focused on providing guidance for sufficient water treatment under typical conditions, there is also a need for better support of treatment decisions during unexpected adverse events. The assumption of stationarity

(i.e., the idea that natural systems fluctuate within fixed patterns of variability) has historically been relied upon for design, operations and risk management of water systems. However, climate change is undermining this assumption (Milly et al., 2008). In situations where knowledge about the past should be used with caution to determine present and future decisions, treatment processes must be especially resilient to reliably control microbial risks under changing environmental conditions.

Water treatment is a set of multi-objective processes in which different types of contaminants—chemical, physical, microbiological, radiological—can pose health risks (WHO, 2022). Pathogens were ranked as the second greatest water contaminant concern by respondents of the 2025 State of the Water Industry report, which reflects the status of the water sector in Canada and in the United States (AWWA, 2025). A substantial focus of media and regulatory attention, PFAS (per- and polyfluoroalkyl substances) were the top-ranked contaminant concern in this survey. However, PFAS mostly pose health risks from long-term exposure. The period between exposure and observation of effects differentiates acute and chronic risks. Although both pathogens and chemicals can produce acute and chronic risks, microbial contaminants are generally known for posing acute risks from short-term exposure (hours/days), while most chemicals present chronic risk from longer-term exposure periods (years). When compared with other contaminants of emerging concern (e.g., PFAS, microplastics), pathogenic microorganisms are especially concerning because they are associated with acute risks and generally require faster interventions for risk management.

Reducing risks to “zero” (i.e., the idea of sterile water, completely free from microbial contaminants) is not practical because resources (e.g., financial, material, human) are limited in the water sector. Thus, the notion of acceptable risk grounds what is defined as safe drinking water. To reduce risks from water contaminants to an acceptable level, water supply managers rely on drinking water quality guidelines, established internationally (e.g., WHO, 2022) or nationally (e.g., Health Canada, 2019a), that can also be part of regulatory frameworks. Health-based targets for chemical substances are usually established in terms of water quality, sometimes presented as maximum acceptable concentrations (MAC). For example, the MAC for lead from Health Canada is 0.005 mg/L (Health Canada, 2019b).

To control risk from microbial contaminants, most guidance globally aligns with approaches similar to the suite of U.S. Surface Water Treatment Rules (U.S. EPA 1989, 1998, 2002, 2006a) that are based on indirect indicators of treatment performance such as turbidity, disinfectant concentration and contact time. Unlike MACs for chemicals, treatment-technique-based criteria are established for microbial contaminants because it is impractical to ensure microbial safety of treated water using a threshold-based approach, which would require analysis of extraordinarily large water volumes (on the order of 10^5 – 10^6 L) due to low pathogen concentrations (Regli et al., 1991). Non-detects occur when microorganisms cannot successfully be detected in the sample analyzed, even if the concentration is not actually zero, and they are common when practical volumes of treated drinking water are analyzed. Non-detects are difficult to interpret, and depending on how they are handled, concentration

and risk estimates can be biased (Chik et al., 2018). Thus, microbial risks in drinking water typically need to be assessed via evaluation of raw water concentrations and treatment performance (Haas et al., 1996). However, monitoring pathogen concentrations directly can be an expensive and time-consuming procedure that cannot be done as frequently as the measurement of indirect indicators. Therefore, credits awarded to “well-operated” treatment technologies are usually established in drinking water regulations. For example, a minimum 3-log (i.e., 99.9%) treatment credit for *Cryptosporidium* removal is awarded to conventional filtration systems whose 95th percentile of combined filter effluent turbidity is below 0.3 NTU (Nephelometric Turbidity Units) (U.S. EPA, 2006a; Health Canada, 2019a). It is generally believed that conventional filtration can provide at least 3 log of treatment when the turbidity target is met. Treatment requirements, on the other hand, are generally determined considering pre-defined health-based risk targets given a known (or assumed) raw water pathogen concentration and using Quantitative Microbial Risk Assessment (QMRA), a widely applied framework for microbial risk analysis in drinking water treatment.

In addition to risk assessment frameworks, resilience has been an extensively discussed topic in many areas, including in water treatment engineering (e.g., Quitana et al., 2020; Blackburn et al., 2023). Several studies have sought to evaluate the role of treatment technologies or infrastructure in building resilience in the water sector (Pamidimukkala et al., 2021). However, the implementation of treatment redundancies and advanced treatment technologies results in extra treatment costs that cannot be affordable in every place. Moreover, as indicated by the occurrence of waterborne outbreaks in developed regions, the existence of adequate infrastructure is not always enough (Hrudey et al., 2006), which highlights the need for operational guidance on optimal use of these technologies. Ensuring the microbial safety of drinking water is an old but persistent concern that has been exacerbated by new water challenges. Health risks posed by waterborne pathogens must not be overlooked and sufficient drinking water treatment should never be taken for granted, which underscores opportunities to advance practice and policy of microbial risk management and operational resilience in drinking water treatment.

To confirm treatment needs pre-established using risk-based criteria, it is important to characterize pathogen concentrations in the source water; however, monitoring pathogen concentrations is not a typical regulatory requirement for informing water treatment decisions. Two national pathogen monitoring rounds were mandated in the United States since the Long Term 2 Enhanced Surface Water Treatment Rule in 2006 (U.S. EPA, 2006a). In Canada, pathogen monitoring is not required by federal

regulations but can be required at a provincial or local level. Although national guidelines recommend treatment requirements for some reference pathogens and use of QMRA to determine extra treatment needs when applicable (Health Canada, 2019a), there is no guidance on how to collect and analyze monitoring data for this purpose. In Brazil, *Escherichia coli* is occasionally monitored as an indicator of fecal contamination in source water to signal further need for monitoring (Brasil, 2021), and turbidity thresholds are used to indicate sufficient microbial water quality of treated water. In the Netherlands, on the other hand, monitoring of reference pathogens in source water and risk assessment are required every three years (Schijven et al., 2011). Notably, relying only on indirect measures of microbial safety undermines detailed and system-specific knowledge of microbial threats and pathogen treatment performance in drinking water supply systems. Water regulations tend to prescribe generic rules that can be followed by most systems. However, one-size-fits-all policies might overlook potentially risky situations, being ineffective in some circumstances. For instance, the turbidity rule that is globally applied to indicate acceptable pathogen removal by filtration has proved to be insufficient in high quality source water systems like in Toronto, where source water turbidity can often be below the 0.3 NTU threshold (Ballantyne et al., 2024). Thus, the lack of informative monitoring can lead to insufficient treatment when it is needed. Conversely, excessive and costly treatment infrastructure might be implemented when it is not necessary. Without any monitoring, the need for extra treatment beyond the minimum established in water guidelines can also be overlooked in systems that experience long-term increases in contaminant concentrations in their water sources. Monitoring of microbial contaminants is important and guidelines are limited for when it is recommended or required, thus it is critical to improve guidance on how to collect monitoring data (e.g., sampling location and frequencies) and use them to assess the sufficiency of treatment or determine additional treatment needs to better support policy and treatment decision-making (**Research Gap 1**).

To link collection of monitoring data with appropriate treatment decisions, it is important that the risks associated with pathogenic microorganisms in water are evaluated. Formally established in the 1990s (Regli et al., 1991; Haas et al., 2014), QMRA enables evaluation of risks from sources of hazards to the individual or system affected, contributing to better decisions and control. In drinking water QMRA, factors integrally linked to risk such as concentrations of pathogens in water and treatment efficiency are typically used to assess risk. This framework can also be applied in what is known as “reverse QMRA” to determine the level of treatment required to reduce known pathogen concentrations to an acceptable level, defined by a risk threshold. The most common risk reference values used in

QMRA are the annual probability of 10^{-4} infections per person-year and the annual burden of disease of 10^{-6} DALYs (disability-adjusted life years) per person-year (Owens et al., 2020). Daily thresholds based on these annual limits (e.g., probability of infection of 2.74×10^{-7} per person-day) have also been reported in risk assessments (Signor & Ashbolt, 2009; Taghipour et al., 2019), especially for risks related to short-term events in which a smaller timeframe for a risk reference is more consistent with the event duration and could better help to control risks. However, these daily references are overly restrictive when compared to annual metrics because their derivations assume this daily risk reference is sustained year-round, allowing no risk fluctuations throughout a year. Thus, drinking water QMRA is generally reliant on an annualized, long-term timeframe for risk evaluation (Hamilton et al., 2026). In contrast, water systems have been increasingly challenged by potentially concerning short-term events such as sudden water quality variations caused by climate-change-related disturbances as well as treatment deficiencies and infrastructure failures. In the context of acute risks, instances of short-term high-magnitude disturbances especially require time-sensitive decisions that are often confronted with the lack of case-specific data to enable risk assessment. Practical guidance on the use of QMRA to support treatment decisions in such situations has become of increasingly recognized importance (**Research Gap 2**).

In drinking water treatment, filtration and disinfection are the two treatment processes usually required to control risks from pathogens, especially in systems sourcing from surface water or groundwater under the influence of surface water (U.S. EPA, 2006a). Despite the high efficiency of different disinfection processes to inactivate pathogens, filtration remains critical to control microbial risks because it can effectively remove pathogens prior to disinfection and the improved water quality contributes to disinfection efficiency. For example, UV is known for its ability to inactivate several types of pathogens, including ones that are resistant to the common chlorine-based disinfectants used in water treatment (Clancy et al., 1998); however, this performance can be undermined by the presence of particles in water that were not removed earlier in the treatment train (Mamane, 2008). Among the various types of filtration, conventional granular media filtration is probably the most commonly applied process in drinking water treatment because it is effective, fast and relatively inexpensive. However, this process exhibits inherent variations in performance over time within each filter, both regularly (e.g., ripening, stable operation) and occasionally (e.g., sub-optimal coagulation, onset of breakthrough) (Emelko et al., 2005; Nilsen et al., 2019). Moreover, treatment optimization studies have focused on maximizing pathogen removal by individual filters and applying those values in QMRA;

however, plant-scale treatment usually involves the asynchronous operation of multiple filters in parallel (instead of a single filter) that do not always have concurrently maximal performance. Management of microbial risks in water utilities depends on the impact of these variations on plant-scale performance, which in turn can be influenced by different design and operational strategies. Notably, the lack of tools to describe the dynamic and combined nature of the filtration process and the impact of filtration operation on plant-scale microbial risk hinder identification of potential opportunities for and barriers to risk management (**Research Gap 3**).

Like filtration, the whole drinking water treatment system is comprised of individual smaller processes that are combined to ensure the provision of safe drinking water. On a larger scale, this notion of combining multiple systems for achievement of pre-defined goals is also reflected in the multi-barrier approach for safe drinking water that includes elements such as source water protection, water treatment and distribution of treated water to consumers (Canadian Council of Ministers of the Environment, 2002). Synergies and conflicts among individual elements are characteristic of complex systems like these and, depending on how the individual elements are combined, relationships between them can impact risk. In QMRA, a potential issue that is often overlooked is the dependence among model inputs such as raw water pathogen concentration, treatment efficiency and volume of water consumed. Although this issue has been explored theoretically and in other fields of risk analysis (e.g., Smith et al., 1992; Haas, 1999; Botai et al., 2020), its implications on drinking water microbial risk have not been discussed. For example, if high contaminant concentrations happen to be more prevalent during periods of lower treatment efficiency, then pathogen concentrations and treatment efficiency are dependent in a way that increases risk because their co-occurrence is likely. Dependence can be illustrated by the Walkerton outbreak in Canada in 2000: a flooding event caused both well contamination including *E. coli* O157:H7 and failure to maintain chlorine residuals needed to inactivate them (Hrudey et al., 2003). This association between high pathogen concentration and low treatment efficiency resulted in a high-risk situation, contributing to 2300 illnesses and seven deaths. Nonetheless, dependence between variables in QMRA has not generally been considered—or even reflected as an assumption or an issue—when evaluating risk, potentially leading to bias in probabilistic risk assessment (**Research Gap 4**).

Atypical conditions, as exemplified by occasional dependencies or extreme short-term events, underscore the vulnerability of water systems when facing unexpected adverse events. As discussed above, reliance on generic rules based on typical and stable conditions has been proven to be insufficient

to ensure the protection of public health in these contexts, which illustrates the need for more specific guidance as well as advances to how microbial risks are managed. Risk assessment frameworks that support risk management can be undermined in contexts of high variability because characterization of perturbations (e.g., probability of occurrence of extreme events, assessment of concentrations) becomes more difficult (Milly et al., 2008). Water systems are increasingly required to persist through, adapt to or recover from disruptions caused by known or unknown adverse events (i.e., events that can be well characterized or not). The word resilience has been used in the water sector to refer to these capacities (e.g., Rodina, 2019; Quitana et al., 2020), but advances are needed to transform conceptual frameworks into practical tools that can be used to improve risk management (Johannessen & Wamsler, 2017). In drinking water systems, the role of treatment technologies and infrastructure in increasing resilience (e.g., Luh et al., 2017; Pamidimukkala et al., 2021) has been more intensively studied in comparison to treatment operations. Notably, the existence of infrastructure alone does not ensure resilience because operations can have variations in performance over time, and these variations have been exacerbated by events causing sudden changes in water quality or treatment failures. Operational resilience has not been defined in drinking water treatment and, while the contributions of resilience to risk management are acknowledged, better resilience descriptions are needed to turn resilience into an actionable tool for risk management (**Research Gap 5**).

1.2 Objectives

The goal of this research is to advance drinking water microbial risk management through integration of risk assessment approaches and real-world water supply treatment operations scenarios. To address this overall goal, the five research gaps identified in Section 1.1 are respectively related to the following research objectives:

- 1) Provide guidance for monitoring pathogens in source water and integrating such data in risk assessment and drinking water treatment decision-making;
- 2) Develop a framework for evaluating microbial risk caused by short-term, high-magnitude events in drinking water treatment;

- 3) Assess how performance variations during a filter cycle and the collective operation of multiple filters impact plant-scale filtration performance and identify design and/or operational implications for treatment resilience and microbial risk management;
- 4) Evaluate the effects of dependence between model inputs in drinking water risk assessment and develop a framework for characterizing the potential for assuming independence to bias interpretation when it is not valid; and
- 5) Develop a framework for describing the resilience of drinking water treatment operations.

1.3 Thesis organization and research approach

This thesis is composed of seven chapters. Following the Introduction (Chapter 1), Chapters 2–6 address research objectives 1–5, respectively, and Chapter 7 presents a summary of the main conclusions and contributions of this research for practice. The objectives of this research were addressed through development of quantitative and qualitative risk-based frameworks using data from full-scale water treatment plants and the scientific literature as well as hypothetical scenarios. Figure 1.1 illustrates how these objectives fit together in a simplified overview of the general context of this research from source to tap. Source water and treatment are important elements of a water supply system in which risk prevention and management strategies are implemented in the multiple barrier approach for safe drinking water and public health protection (Canadian Council of Ministers of the Environment, 2002; U.S. EPA, 2006b). These elements are also important parts of exposure assessment within drinking water QMRA, as they can contribute to pathogen reduction in treated drinking water.

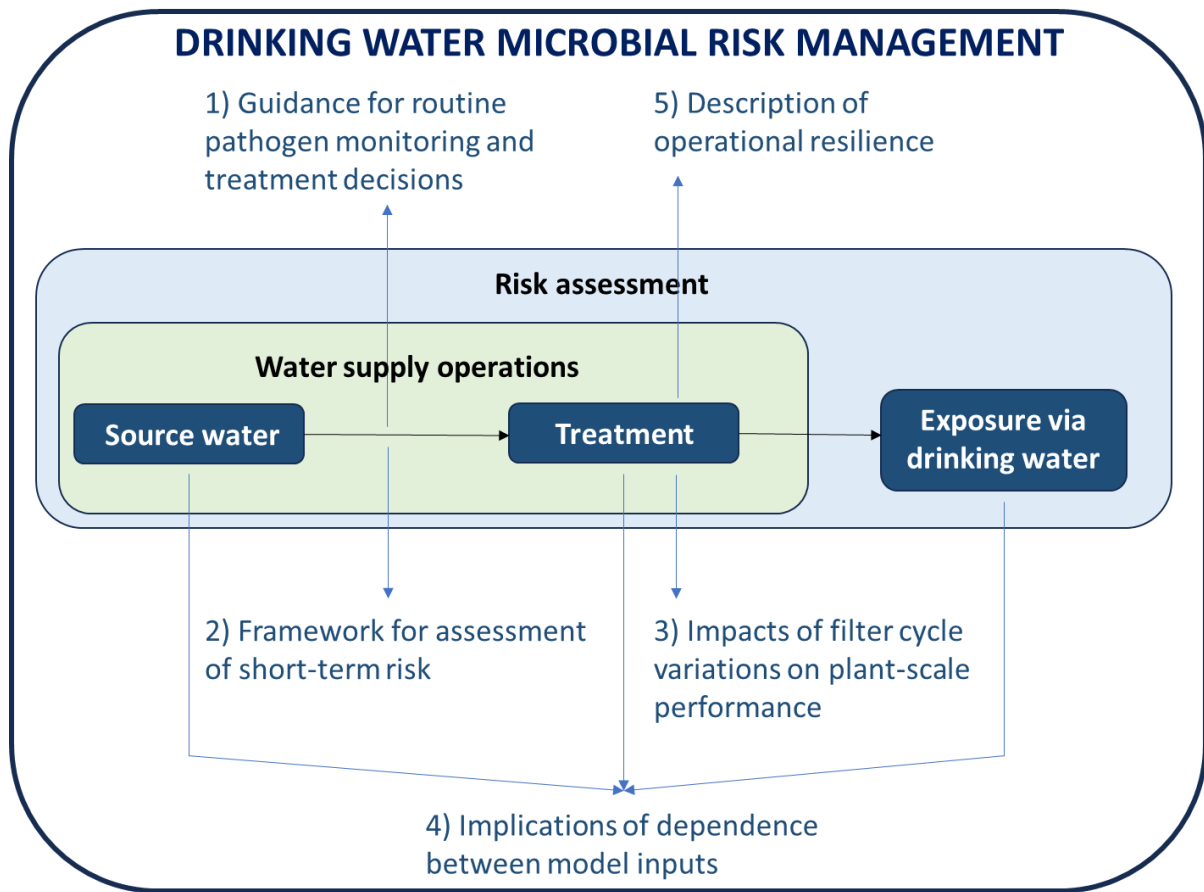


Figure 1.1: Overview of research topic and objectives addressed

Overall, to achieve a goal of advancing risk management using risk assessment, it is important to have clearly defined assessment goals and ensure that the context studied is well represented in the analysis and data used to inform it. Based on these principles, specific gaps in knowledge and practice were addressed by critically analyzing the current state of the art of drinking water microbial risk management.

To investigate risk from source water contamination and its implications for treatment decisions, it is important for source water quality monitoring data used in risk assessment to be tailored to inform the treatment decision of interest. While it is common practice to use literature values or whatever data are available in QMRA, Chapter 2 focuses on the development of specific guidance for implementation of routine pathogen monitoring programs from collection of data to their use in risk assessment. This was done by critically reviewing an established monitoring program along with seven years of monitoring data and considering the local and international regulatory background.

During short-term adverse events, it might not be possible to collect case-specific data to inform treatment decisions. Scenario-based QMRA can still provide valuable information for decision making as long as event durations are appropriately reflected and reasonable assumptions are considered in the absence of informative data. Although impactful short-term events are of great concern, motivating the need for resilient systems, guidance for developing risk-based approaches to support treatment decisions in such situations is not broadly available. Chapter 3 addresses the impacts of short-term events on drinking water safety that are not limited to water contamination but can also be caused by treatment failures. A framework was developed for assessment of risk from short-term events based on a case study involving a wastewater spill upstream of a drinking water intake in 2023, in which urgent risk-informed treatment decisions were needed.

Treatment must also be appropriately described in risk models. Pathogen reduction during treatment is usually represented in QMRA by one value (or probability distributions) describing peak performances of individual treatment units, though microbial risks are driven by the collective operation of multiple treatment units in parallel and/or in series at plant scale. Chapter 4 investigates opportunities for enhanced plant-scale filtration performance and associated implications for microbial risk management. A model was developed to assess the effects of dynamic operation of multiple filters on plant-scale filtration performance. Literature data were used for illustrative purposes, but the model can also be used for case-specific assessment.

Good descriptions of source water quality and treatment as isolated systems do not ensure that their collective effect on pathogen presence in drinking water is always accurately represented in risk models because there may be associations between them that can impact risk. Chapter 5 focuses on the modelling aspect of QMRA to address the potential bias introduced to risk estimates by the typically implicit assumption of independence among model inputs (e.g., source water quality, treatment efficiency and broader behavioural factors such as water consumption). To evaluate the risk implications of dependence, both hypothetical scenarios of relevance for drinking water QMRA and a case study using data from a full-scale water treatment plant were analyzed.

The last research chapter connects the previous research topics to reconcile risk and resilience. While resilience has been increasingly discussed in the water sector, it is sometimes used as a trendy word with unclear meaning and some resilience metrics do not assess the value of resilience for risk management. In Chapter 6, a framework is developed to describe the resilience of drinking water

treatment operations using illustrative hypothetical case studies that explore operational resilience in drinking water treatment and its contribution to microbial risk management.

Chapter 2

Particulate contaminants and treatment decision-making: maximizing the value of raw water pathogen monitoring for drinking water safety

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de Brito Cruz, D., Schmidt, P. J., Kundert, K. L., Ruecker, N. J., & Emelko, M. B. (2025). Particulate contaminants and treatment decision-making: maximizing the value of raw water pathogen monitoring for drinking water safety. *J Water Health*, 23 (6): 764–779. <https://doi.org/10.2166/wh.2025.020>

2.1 Summary

Periodic evaluation of particulate contaminants in raw/untreated water is integral to assessing risk, establishing treatment requirements, and ensuring drinking water safety. However, pathogenic microorganisms and other discrete particles (e.g., microplastics) are not typically monitored with any regularity. When monitoring is required, recommended, or proactively used to evaluate the adequacy of treatment or assess treatment needs, there is a need for guidance on how to collect data and use them to maximize return on investment. The potentially increasing variability in source water quality associated with climate change emphasizes the importance of knowing contaminant concentrations to effectively manage risks. This work presents a framework to guide the development of monitoring protocols for particulate contaminants in water and the integration of monitoring data and quantitative microbial risk assessment into treatment decisions. The protozoa monitoring and risk-based compliance approach of a drinking water utility in Canada is presented along with seven years of data. Guidance for determining sampling frequencies and locations is provided. It is shown that *Cryptosporidium* monitoring may be insufficient to inform treatment needs when *Giardia* cysts are more abundant in source water. This work underscores the importance of revisiting and enhancing monitoring practices for effective treatment and public health protection.

2.2 Introduction

Over the past decades, contaminants of emerging concern in drinking water—such as per- and polyfluorinated substances, microplastics, and cyanotoxins—have received international focus, while revisiting regulatory frameworks for managing microbial contamination has received little attention. Nonetheless, management of acute risks caused by waterborne pathogens is still the paramount objective of drinking water treatment. Critically, little guidance exists to determine whether treatment requirements prescribed in drinking water regulations are sufficient or how to evaluate additional treatment needs. For example, growing evidence underscores that turbidity monitoring is not enough to ensure the sufficiency of treatment in all systems (Ballantyne et al., 2024). Moreover, risks from microbial and other particulate contaminants are exacerbated in a changing climate. Extreme rainfall events increase erosion and particulate contaminant runoff from the landscape (Emelko et al., 2024); they are recognized as a factor leading to fecal pollution, increased concentrations of microbial contaminants, and even outbreaks of waterborne disease (Charron et al., 2004; Wu et al., 2016; Graydon

et al., 2022). Treatment disturbances caused by other climate-related events like wildfires can also affect pathogen and other particulate contaminant removal in drinking water treatment by affecting coagulation (Emelko et al., 2011). Additionally, climate change undermines assumptions of stationarity (i.e., the idea that natural systems fluctuate within fixed patterns of variability) that have historically facilitated the management of water demand, supply, and risk (Milly et al., 2008). Thus, landscape disturbances such as wildfires and floods (Emelko et al., 2024) as well as changes in water use such as widespread implementation of *de facto* potable reuse (Rice et al., 2015) also contribute to unpredictability in source water quality. Accordingly, the incorporation of recent contaminant concentration data into treatment decisions becomes more critical in a more variable and/or non-stationary context, which emphasizes the need to critically revisit common practices to enhance particulate contaminant risk management in the provision of safe drinking water. While health endpoints for particulate contaminants such as microplastics are still evolving and risk management approaches for treatment (such as the “Threshold Microplastics Concentration”) are limited by data availability (Chowdhury et al., 2024), approaches for management of acute risks from pathogens in drinking water are well established.

To control microbial risks in drinking water, the United States Environmental Protection Agency implemented a series of regulations starting in the late eighties (U.S. EPA, 1989, 1998, 2002). These regulations culminated in the Long Term 2 Enhanced Surface Water Treatment Rule (LT2ESWTR) in 2006 (U.S. EPA, 2006a), which inspired regulatory guidance in several other jurisdictions worldwide (e.g., NHMRC & NRMCC, 2011; Brasil, 2021). Filtration (or equivalent technology) and disinfection are the two treatment processes usually required to control risks from pathogens in systems depending on or influenced by surface water. In the LT2ESWTR and subsequent international analogues, a treatment-technique-based approach that awards treatment credits for “well-operated” technologies is used to ensure sufficient treatment performance.

For example, a minimum 3-log treatment credit for *Cryptosporidium* removal is given to conventional filtration systems whose 95th percentile of combined filter effluent turbidity is below 0.3 Nephelometric Turbidity Unit (NTU). Besides this treatment-based approach, monitoring of pathogen concentrations can be used to assess treatment needs more accurately than using generic indicators such as filter effluent turbidity. Nevertheless, monitoring is not a typical regulatory requirement for informing water treatment decisions.

To establish treatment requirements under the LT2ESWTR, the United States mandated two national monitoring rounds since 2006, and utilities were classified in bins requiring specific levels of treatment based on their *Cryptosporidium* oocyst concentrations. Notably, this implicitly assumes that risks from *Giardia* are appropriately controlled if sufficient treatment is provided for *Cryptosporidium*. In the Netherlands, water utilities must monitor source water and conduct a quantitative microbial risk assessment (QMRA) every three years for enterovirus, *Campylobacter*, *Cryptosporidium*, and *Giardia* to ensure sufficient microbial water quality (Schijven et al., 2011). In Canada, provinces and territories establish their own regulatory requirements, and these may be informed by national guidelines for drinking water quality. Health Canada guidelines recommend a minimum 3 log of removal and/or inactivation of *Cryptosporidium* and *Giardia* as well as use of QMRA to determine the level of treatment needed to meet health-based targets (Health Canada, 2019); however, practical advice on how to collect and analyze monitoring data for this purpose is lacking. In general, little guidance exists to determine whether a 3-log minimum treatment requirement is sufficient or how to evaluate additional treatment needs.

This study investigates the integration of QMRA and monitoring data into drinking water treatment decisions using the monitoring experience of a water utility in Canada as an example. The City of Calgary has conducted routine monitoring for protozoa following provincial requirements since 1999. In 2010, an agreement with the province of Alberta specified a set of rules for protozoa treatment requirements and associated monitoring as well as measuring and reporting of raw water protozoa concentration values. These rules have a bin classification approach (Alberta, 2012) based on the LT2ESWTR for *Cryptosporidium* and apply a similar approach for *Giardia* using limits based on a study summarized in U.S. EPA (1991). A more contemporary risk-based approach to managing protozoan risks in drinking water, such as that reflected in the Guidelines for Canadian Drinking Water Quality for enteric protozoa (Health Canada, 2019), became attractive for evaluation of treatment needs, especially during winter months when disinfection credits for *Giardia* declined due to lower water temperatures. Practices to monitor and control protozoan risk in Calgary were reviewed to develop an implementation plan that merges treatment criteria from the Health Canada guidelines into the existing regulatory approaches. The framework applied by the City of Calgary since 2021 is presented here to support the implementation of monitoring programs in drinking water treatment plants and offer additional recommendations to systems that apply QMRA as a risk management approach in water treatment. While protozoa were the focus of the Calgary framework, statistical tools reflecting their

discrete nature (Emelko et al., 2010) are the same that would be applied to other particulate contaminants in water such as other pathogens and microplastics (Chowdhury et al., 2024; Zhu et al., 2024). Using the example of protozoa, this study aims to provide guidance for (1) monitoring particulate contaminants in the water sources of treatment plants to ensure the representativeness of the water entering the plant and (2) using monitoring data to assess the sufficiency of treatment to meet health-based targets. The need for periodic review of monitoring programs is also discussed along with the reassessment of the framework after 2 years of its implementation.

2.3 Methodology

2.3.1 Calgary's water supply system

The city of Calgary has two water treatment plants, Bearspaw and Glenmore, that collectively provide drinking water to approximately 1.5 million people. Figure 2.1 depicts the main elements of Calgary's water supply system. The Bearspaw treatment plant draws water from the Bow River watershed, which provides nearly 60% of the total water supply. At this plant, water is principally drawn from an intake at the Bearspaw Dam with automated flow control. Another intake that is in the river a short distance downstream provides a manually controlled supplementary or alternative water source. The remaining 40% of the water supply is sourced from the Elbow River watershed, with the Glenmore water treatment plant's intake situated in the Glenmore reservoir. Both plants apply a high-rate sand-ballasted flocculation clarification system followed by rapid filtration. Sand and polymer are added during flocculation to create denser flocs and increase sedimentation rates. The high quality of the source and clarified water enables chlorine addition before filtration to ensure sufficient contact time for disinfection of *Giardia*; it is added again after filtration to ensure sufficient residual.

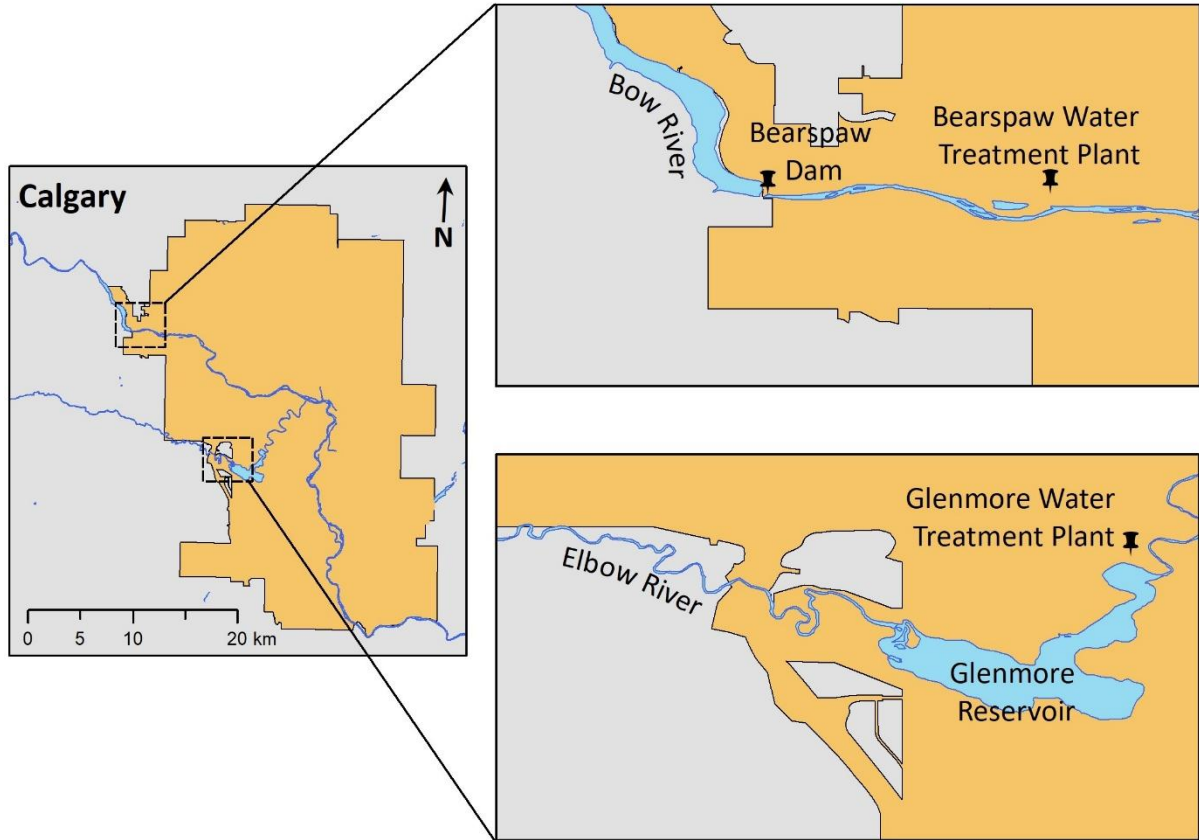


Figure 2.1: Location of water treatment plants in Calgary

2.3.2 Framework development

An implementation plan was developed to merge treatment criteria from the Health Canada guidelines (i.e., a 3-log minimum treatment requirement with additional treatment as needed depending on source water quality) into the existing regulatory approaches followed by the City of Calgary. Additional treatment requirements are evaluated using a QMRA model applied in reverse, which determines a minimum health-based treatment goal to limit risk to a reference level. This model uses exponential dose–response relationships for both *Cryptosporidium* and *Giardia*, which can be approximated by a linear relationship between a log-transformed average source water concentration and log-reduction for the acceptable risk reference levels usually applied in drinking water treatment. The log-reduction required (LR_{req}) may be calculated using Equation 2.1, with values below the 3-log minimum raised to 3-log, given the average source water (oo)cyst concentration (C_{raw}) in (oo)cysts/100 L, parameter of the dose–response model (A), daily volume of unboiled tap water consumed in litres (B), fraction of

infections leading to illness (C), disability-adjusted life years (DALYs) per illness (D), and maximum acceptable risk (E). The derivation of this equation is presented in Appendix A Section A.1. Health Canada recommends the following values for these parameters: A is 0.0199 for *Giardia* and 0.018 for *Cryptosporidium*, B is 1 L, C is 0.4 for *Giardia* and 0.7 for *Cryptosporidium*, D is 1.67×10^{-3} for both pathogens, and E is 10^{-6} DALYs/person/year. Here, an increased consumption volume of 1.45 L based on Pintar et al. (2009) was used to better represent local water use in Calgary. Calculation of the required log-reduction can be simplified using Equation 2.2 for *Giardia* cysts and Equation 2.3 for *Cryptosporidium* oocysts.

$$LR_{req} = \log(365 \times C_{raw}) + \log(A) + \log\left(\frac{B}{100}\right) + \log(C) + \log(D) - \log(E) \quad (2.1)$$

$$Giardia: LR_{req} = \max(3, \log(C_{raw}) + 1.85) \quad (2.2)$$

$$Cryptosporidium: LR_{req} = \max(3, \log(C_{raw}) + 2.05) \quad (2.3)$$

Critically, it is inappropriate to input a concentration value that is only representative of a single day or month into this model because the maximum acceptable risk is defined on an annual level—doing so determines what the required log-reduction would be if the concentration value were sustained year round. This misalignment between how model inputs and risk are evaluated directly contradicts the current philosophy of “acceptable risk” in microbial risk management. The annual time frame allows for periods of higher and lower risk that average out over the course of a year to an “acceptable” level. Although this metric may not be sufficient for the evaluation of short-term and high-magnitude risks (Signor & Ashbolt, 2009), it is widely applied for the determination of treatment requirements (WHO, 2022). In QMRA, variation in pathogen concentrations over time is often incorporated in the form of a distribution rather than just using a mean concentration value. Such variation does not need to be considered here because the mean annual risk is the same regardless of whether daily variation in concentration is incorporated or simply represented by the mean. This is a mathematical property of the type of dose–response model used, together with the assumed maximum acceptable risk as well as the constant water consumption and treatment level, as demonstrated in Appendix A Section A.1. Thus, collecting sufficient data to obtain a suitably accurate estimate of the mean concentration is the principal monitoring objective from a risk assessment perspective. The effect of dependence between concentration and treatment efficiency on risk was explored by de Brito Cruz et al. (2024) (Chapter 5)

and it was determined to be minimal in the present case. As such, mean concentration values can be used to estimate average treatment needs in a year.

Here, a mean concentration value is calculated every month and a one-year rolling average concentration is used to update the required log-reduction. Using a rolling average rather than calendar years of data allows timelier treatment responses to changes in pathogen concentrations. A one-year period is preferable to the two-year period suggested in the provincial guidelines for municipal waterworks (Alberta, 2012) because it will be more rapidly responsive to increases in (oo)cyst concentrations and will be more conservative in that the peaks will be higher. It also does not allow a one-year period with high risk to be averaged out with a preceding year of lower risk.

A range of statistical approaches to estimate average concentrations while incorporating analytical recovery were considered (Schmidt et al., 2013). For this application, it is recommended to use simple expressions providing a point estimate of concentration for each sample. This choice results in an uncomplicated and operationally sustainable approach to be carried out every month that does not require substantial mathematical expertise. Equation 2.4 shows the estimation of pathogen concentration from each sample (i.e., the count divided by the analyzed volume and estimated recovery), where C_i represents the concentration value for sampling occasion i in (oo)cysts per 100 L, X_i is the number of indigenous (oo)cysts observed, and V_i is the volume of water analyzed in L. An estimate of the sample-specific analytical recovery is represented in this formula by the ratio Y_i/N_i , where Y_i is the number of seeded (oo)cysts observed and N_i is the number of (oo)cysts seeded. In these calculations, non-detects are seamlessly incorporated as counts of zero rather than manipulated values that introduce bias to estimated calculations (Chik et al., 2018). Resampling is recommended when no seeded (oo)cysts are observed ($Y_i = 0$), as further discussed in Section 2.4.1.3. Given n_m sampling occasions per month, the monthly concentration (C_m) is computed using the average of the individual sampling concentrations, according to Equation 2.5. Similarly, the average of monthly concentration values over a particular 1-year period (Equation 2.6) gives the yearly concentration (C_y) assigning equal weight to all monthly average concentrations, for simplicity. The use of yearly average concentrations to estimate treatment assumes that drinking water consumption is constant throughout the year.

$$C_i = 100 \times \frac{X_i}{V_i \times \frac{Y_i}{N_i}} \quad (2.4)$$

$$C_m = \frac{\sum_{i=1}^{n_m} C_i}{n_m} \quad (2.5)$$

$$C_y = \frac{\sum_{i=1}^{12} C_m}{12} \quad (2.6)$$

In the risk-based approach proposed by Health Canada, the concentration of pathogens in the source water is an important model input to determine treatment needs. Hence, it is critical that the concentrations evaluated during the monitoring program accurately reflect the water entering the treatment plant to avoid introducing bias to the estimated treatment needs. Fitting how data are collected to the purpose of monitoring leads to more informative results for decision-making. Once monitoring data are collected, it is also important to ensure that data are appropriately used in the risk assessment to be consistent with model formulation and assumptions. To provide guidance for protozoa monitoring including planning, collection, and analysis of data, the framework resulting from the implementation plan is divided into two main parts: establishment of an updated protocol to collect and analyze raw water samples and use of the collected data to inform treatment decisions.

The monitoring protocol is bound by constraints from the provincial approval signed in 2010 and the use of Method 1623.1 for the detection of *Cryptosporidium* and *Giardia* (U.S. EPA, 2012). To ensure the representativeness of the raw water entering the treatment plant by the samples collected, the choice of sampling locations, number of samples per sampling location, sample frequency, and scheduling are important factors to consider. For example, when a treatment plant draws from two or more intakes, it is important to consider the contribution of each intake to the plant. Data from event-based monitoring should also be handled with care to avoid biasing treatment needs. Practical advice on general procedures for sample collection and analysis is also given to complement guidance from Method 1623.1 (Section 2.4.1.3).

The second part of the framework addresses the use of the monitoring data to inform treatment needs. This is also bound by constraints established in the provincial approval and Health Canada guidelines (Health Canada, 2019). Results from the developed approach to estimate monthly and annual average pathogen concentrations from collected data and to evaluate treatment needs using these concentrations are presented. Finally, approaches to evaluate the sufficiency of treatment are discussed based on Calgary's regulatory framework that assigns credits based on treatment conditions (e.g., filter effluent turbidity). The main goal is to provide guidance on how to assess the sufficiency of treatment given the

monitoring data and Health Canada guidelines rather than defining prescriptive rules of how to achieve a required treatment performance or criticizing pre-established treatment credits.

The framework to monitor protozoa and evaluate treatment sufficiency is composed of six main elements: the monitoring protocol includes (1) sampling location and representativeness of water entering the plant, (2) sample frequency and scheduling, and (3) general procedures for sample collection and analysis, while the analysis of treatment sufficiency includes (4) estimation of monthly and yearly average pathogen concentrations, (5) evaluation of treatment needs, and (6) use of treatment process monitoring data and credits to evaluate the sufficiency of treatment. Two years after the implementation of this framework in 2021, the monitoring program was reassessed to evaluate the impact of the proposed changes. Seven years of monitoring data are analyzed to discuss the main lessons learned from implementation of this framework.

2.4 Results and Discussion

2.4.1 Monitoring protocol

2.4.1.1 Sampling location and representativeness of water entering the plant

When conducting a risk assessment to establish treatment requirements, the choice of sampling locations should ensure that the samples collected represent the raw water entering the plant well. For example, if a plant has multiple raw water intakes, monitoring blended water entering the treatment system can provide an uncomplicated representation of raw water quality. However, it is useful to collect samples from each of these intakes to inform risk management strategies such as the implementation of specific source water protection measures. At Bearspaw, there is no sampling location with blended water, so each raw water intake must be sampled separately. The LT2ESWTR's source water monitoring guidance (U.S. EPA, 2006b) provides two options for water treatment plants that have multiple raw water intakes: a composite sample or a weighted average approach. In the composite sample option, the proportion of instantaneous flow contribution is reflected in the sample volume collected from each intake. The weighted average approach uses the instantaneous proportional flow contribution of each intake to weigh the averaging of concentrations estimated from samples analyzed independently. Two other options were considered to collect intake-specific information

based on their proportional flow contributions: randomizing which intake to sample or adjusting the number of samples at each intake. The advantages and disadvantages of these five methods for accurately representing the raw water entering a treatment system are presented in Table 2.1.

Data from January 2016 to October 2020 were analyzed to compare the use of each raw water intake at Bearspaw. This analysis indicated that approximately 63% of Bearspaw water was drawn from the dam intake with almost all the monitoring data corresponding to this intake. It was decided to adjust the number of samples collected at each intake in the protozoa monitoring framework implemented in Calgary in 2021. To better represent the blend of water from the two intakes (approximately 2/3 from the dam and 1/3 from the river), the sampling approach for Bearspaw was modified to include at least two dam intake samples per month with a total analyzed volume of approximately 100 L in addition to one or more river intake samples per month with a total analyzed volume of approximately 50 L. If an intake is out of service in a particular month, then at least two samples with a total analyzed volume of approximately 100 L are drawn from whichever intake is in service. This method was chosen because it would lead to an uncomplicated and consistent monitoring protocol with a lower number of samples when compared to the weighted average approach. The contribution of each intake to the treatment plant and the impact of this change in the monitoring program were reassessed 2 years after implementation, and the results are also presented in Appendix A Section A.2. At the Glenmore treatment plant, at least two samples with a total analyzed volume of 100 L are collected per month at the single raw water intake.

Table 2.1: Comparison of methods for representing the water entering a treatment plant with multiples intakes

Method	Description	Advantages	Disadvantages
Blended water sampling	Sampling is from a location with blended water from multiple intakes	- Simple, uncomplicated representation of raw water entering the treatment plant	- Does not provide intake-specific information
Compositing samples	Sample volume from each intake reflects the proportion ^{2a} of flow contribution	- Analysis of only one sample reduces costs	- Requires sampling every intake on every occasion, but does not provide intake-specific information - More complicated if instantaneous flow contribution is used (different volumes at each sampling occasion)
Weighted average concentration	Independent samples are collected at each intake and a weighted average concentration is calculated using the proportions ^{2a} of flow contribution	- Provides intake-specific information	- Requires sampling every intake on every sampling occasion - Increases processing costs and time to analyze each sample
Random intake selection	Only one intake is sampled per sampling occasion, selected randomly according to the proportions ^{2a} of flow contribution	- Provides intake-specific information - Does not require sampling at all intakes on every sampling occasion, reducing costs	- More complicated monitoring protocol (different sampling locations at each sampling occasion)
Adjusting the number of samples per intake	The number of samples at each intake is adjusted according to the proportion ^{2a} of flow contribution	- Provides intake-specific information - Depending on the proportions, this can lead to a lower number of samples per sampling occasion	- Unequal amounts of information about each intake - Imperfect proportional representation (numbers of samples must be integers)

^{2a} The proportion of flow contribution can be instantaneous or average. Using the instantaneous proportion results in a more accurate temporal representation of water entering the plant, but it is more complicated than using the average.

2.4.1.2 Sampling frequency and scheduling

When determining the frequency of sampling, it is important to consider that risk is generally assessed on an annual basis in drinking water QMRA. To characterize annual risk, factors influencing risk (e.g., pathogen concentrations and drinking water consumption) must be well characterized throughout a year. Consequently, monitoring should be strategically planned so that the average pathogen concentration through a year is well represented by the samples collected. If water consumption (i.e., ingestion) patterns also change substantially throughout a year, it is recommended to sample more frequently when the consumption is higher. Collecting many samples is not always feasible, so it is necessary to balance the better representation of temporal variations in microbial water quality of high-frequency sampling with the drawback of expending more human and financial resources.

To determine a suitable sampling frequency in Calgary, historical pathogen concentration data from January 2016 to June 2020 were analyzed assuming no temporal autocorrelation between sampling events and that these data could be informative of future pathogen concentrations. Five different numbers of samples collected during a year ($n = 4, 6, 12, 24, \text{ or } 48$) were considered and 10,000 simulations were conducted for each to compare the precision of estimated yearly treatment requirements. Because variability of the mean concentration is not practically relevant when the 3-log minimum treatment is not exceeded, precision was assessed in terms of treatment requirements rather than average concentrations. Precision can be described using 95% probability intervals so that a relatively wide interval indicates poor precision. However, the length of an interval does not provide sufficient information about over- and underestimation of required treatment if it is asymmetrical, and these have different practical implications for safety. Considering the treatment required using all historical data as the true required treatment, overestimation is measured by the difference between the 97.5th percentile of the 10,000 simulated treatment values and the true treatment required, and underestimation is represented by the difference between the true treatment required and 2.5th percentile of simulated values. Equations 2.2 and 2.3 were used to calculate the log-reduction required, in which C_{raw} represented the average of n samples. The results (Appendix A Section A.3, Table A.1) show that the sampling frequency of twice a month previously implemented in Calgary is sufficient to estimate treatment requirements with an error of 0.16 log (i.e., neither the 97.5th nor the 2.5th percentile of log-reduction required is more than 0.16 log away from the true required treatment value). This frequency was maintained in Calgary for continuity, but a lower frequency could be justified, especially if those concentrations were observed in systems that cannot afford this frequency of sampling. For example,

sampling once a month would be acceptable in Calgary so treatment is not under- or overestimated by more than 0.25 log.

While both the LT2ESWTR and monitoring requirements established in the Netherlands (Schijven et al., 2011) use the size of a system to determine the frequency of sampling, here it is recommended to consider the variability of previous pathogen concentrations observed in the source water. Although this approach may be limited when past concentrations cannot inform about the future, the site-specific variability in concentration is useful to determine sampling frequency because it is more directly linked to source water quality. For example, sampling costs can be saved if the variability of pathogen concentrations is low. It is a challenge to balance the benefits of a one-size-fits-all approach—which is easier to implement and possibly less expensive—with the advantages of tailoring monitoring practices (which can provide more information and reveal the specific needs of a particular system). Given a specified frequency of sampling that is deemed acceptable for a particular system, it is also important to consider when these samples are collected. To prevent bias in concentration data due to any possible systematic patterns in source water quality (e.g., greater wastewater discharges during a specific period of the day or day of the week, autocorrelation in pathogen concentrations), a random approach is suggested to choose dates and times for sample collection.

In addition to routine monitoring, it is also important to develop protocols for an event-based monitoring program given sudden water quality variations that can occur following extreme events. It is recommended, however, that such event-based monitoring and discretionary forms of exploratory monitoring should be excluded from routine analyses to determine the log-reduction required unless they are deemed to have an acceptable effect upon the result (e.g., not reducing the estimated average concentration or biasing it with substantial overrepresentation of short periods of time or rare conditions).

Overrepresentation of specific events is more impactful with lower numbers of samples contributing to the yearly average concentration. For example, a yearly average concentration of 8.9 oocysts/100 L requires 3-log reduction of *Cryptosporidium* in Calgary (Equation 2.3). When calculating a 1-year rolling average concentration, replacing one routine sample from an average value of 8.9 oocysts/100 L with a concentration of 1,000 oocysts/100 L measured after an extreme event increases the treatment requirement to 3.8 log if 24 samples compose the yearly average. On the other hand, if 6 samples compose the yearly average, the treatment required would be 4.3 log. In this example,

the new concentration of 1,000 oocysts/100 L practically represents 0.5 and 2 months given 24 or 6 samples per year, respectively. Thus, if a high concentration after an event does not last for this long, the treatment required is overestimated. Similarly, treatment needs might be underestimated if presumed events correspond to low concentrations or fail to capture periods with the highest concentrations. For example, peak *Giardia* concentrations at the Glenmore intake in Calgary have previously been associated with snowmelt runoff caused by chinooks rather than rain events (Sokurenko, 2014). If, in a hypothetical situation, all sampling after extreme events results in non-detects, incorporating these data in the routine monitoring program could decrease treatment requirements. It is important for sampling used in QMRA to be performed at random without biasing results by targeting specific events. Extremely high or low concentrations should not be excluded from data analysis if they were randomly observed (e.g., occurring in proportion to their relative frequency and not especially sought out).

Fixing a frequency for event-based sampling is not possible, but there should be protocols to determine when it should occur. For example, the baseline conditions of precipitation and flow can be characterized so that thresholds can be established to trigger sampling. Knowing the characteristics of a system can also guide assessment of the need for event-based sampling. For example, reservoirs may have a role in controlling pathogen loading after rainfall events (Signor et al., 2007).

2.4.1.3 Sample collection and analysis procedures

Method 1623.1 (U.S. EPA, 2012) is a common protocol to detect *Cryptosporidium* oocysts and *Giardia* cysts in water matrices. Adaptations of this method as well as other laboratory techniques such as membrane filtration, flocculation, and molecular methods have also been applied worldwide (Rosado-García et al., 2017). Despite being expensive and requiring both adequate infrastructure and technical expertise of laboratory staff, Method 1623.1 and previous similar versions have been applied since 1999 in Calgary. Specific details of how this method is implemented in Calgary are critically reviewed and some lessons are discussed to provide general guidance, particularly related to the evaluation of analytical recovery and (oo)cyst enumeration practices.

Regardless of the analytical method used to assess concentrations of protozoa in water, it is essential to incorporate knowledge of the losses associated with imperfect analytical recovery into description of raw water concentrations – ignoring the effect of these losses upon observed counts leads to underestimated concentrations. Calgary’s monitoring program typically follows the national guideline

recommendation to measure the recovery efficiency of each sample (Health Canada, 2019). Sample-specific analytical recovery is quantified using internal standards in every sample (or at least on every sampling occasion for a given source). Calgary's practice is to reject samples in which the internal standard recovery estimate is less than 33% for *Cryptosporidium* oocysts or less than 22% for *Giardia* cysts and to resample the associated source to ensure a minimum number of reliable samples that are not affected by significant matrix effects or other problems leading to unusually low recovery. These thresholds are based on the ongoing precision and recovery quality control acceptance criteria from Tables 3 and 4 of Method 1623.1. Although rejecting samples with low recovery is a good practice for quality control, it is worth mentioning that these acceptance criteria are for method validation of mean recovery in reagent water and are not a requirement for every sample analyzed using Method 1623.1.

Using an internal standard in every sample supports laboratory quality control (including resampling when achieved analytical recovery is low), enables evaluation of matrix effects or other shifts or trends in analytical recovery patterns, permits minor variations in methodology after seeding by ensuring corresponding evaluation of recovery, and improves the accuracy of individual concentration estimates (provided that the estimated recovery is not near zero). Despite being a good practice, using spiking suspensions for every sample can also be costly. Sporadic recovery analysis may be a feasible alternative in small systems.

Regarding sample volumes, the objective is to collect approximately 50 L per sampling occasion in Calgary. When multiple filters are needed to process the desired volume of water, the (oo)cyst counts and volumes of all filters are added and the sample-specific recovery information of one filter is applied to these cumulated data. To minimize variations of analytical recovery that might be caused by different sample volumes, similar volumes should be run through each filter in such circumstances. In some samples, the packed pellet may be too large for a single immunomagnetic separation (IMS). In Calgary, this sometimes happens during spring freshets when the full pellet is analyzed in several parts. Subjecting only a portion of the resuspended pellet to IMS reduces the effective analyzed volume of the sample and the precision of the analytical recovery estimate compared to analysis of the full pellet as not all seeded (oo)cysts are in the analyzed portion. To meet a monthly analyzed volume target and avoid compromising the value of internal standards added to every sample, the entire packed pellet of such samples should be analyzed in several portions. Statistically, the counts from the various portions may be added as though they were processed in a single IMS procedure. Referring to Equation 2.4, X_i

and V_i would be the sums of the counts and volumes, respectively, for all filters and/or IMS tubes utilized.

Finally, when using microscopy to enumerate (oo)cysts, care should be taken to count everything that exhibits morphological features and staining attributes like *Cryptosporidium* oocysts and *Giardia* cysts (e.g., without discrimination based on subtle variations in size or shape) rather than rigidly limiting counts to respective size ranges (e.g., 4–6 μm diameter for *Cryptosporidium* oocysts, 5–15 μm width and 8–18 μm length for *Giardia* cysts). Microscopy-based methods have the limitation of not accounting for pathogen viability (i.e., determining if the pathogen is alive or not) and infectivity (i.e., differentiating human pathogenic species from others), which can lead to overestimation of epidemiologically relevant pathogen concentrations in water. In the absence of practical methods to evaluate the viability of (oo)cysts and their potential to cause illness in humans for each monitoring sample, presuming that all observed (oo)cysts are infectious provides a substantial safety factor by overestimating risk or treatment required (Lapen et al., 2016).

2.4.2 Use of monitoring data for treatment decisions

2.4.2.1 Estimating pathogen concentrations

Following the approach described in Section 2.3.2, the protozoa monitoring data collected from January 2016 to April 2023 were used to calculate the concentrations reported herein. In Figure 2.2, monthly and 12-month rolling average concentrations of *Giardia* and *Cryptosporidium* are presented for the Bears paw and Glenmore water treatment plants. For both pathogens, monthly concentrations in Bears paw are generally higher than in Glenmore, as indicated by the vertical position of the red and blue lines in Figure 2.2. The difference in concentration between the two pathogens is also notable. The average of monthly *Giardia* concentrations is approximately 20 times higher than for *Cryptosporidium* in both treatment plants. Higher *Giardia* concentrations (compared to *Cryptosporidium*) have also been found in other studies (Briancesco & Bonadonna, 2005; Carmena et al., 2007). This result highlights the importance of including both protozoa in a monitoring program, as their occurrence will not necessarily follow the same patterns. The capacity to conduct such analysis also depends on the reliability and organization of stored data. Once pathogen concentrations are analyzed in the laboratory, ensuring that the collected data are appropriately recorded contributes to the quality control of the

monitoring program. Guidance to manage data (e.g., where to store them and which parameters are important to record) is briefly discussed in Appendix A Section A.4.

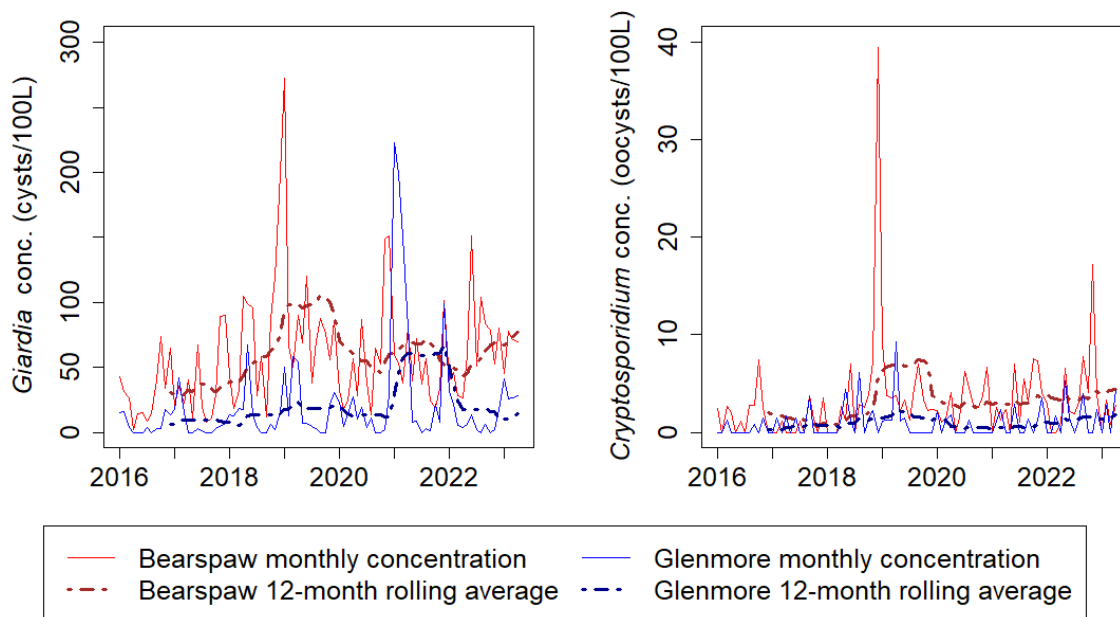


Figure 2.2: *Giardia* and *Cryptosporidium* concentrations in the raw water of Bears paw and Glenmore treatment plants from January 2016 to April 2023

2.4.2.2 Evaluating treatment needs

Using the 12-month rolling average pathogen concentrations, the corresponding log-reduction values required to meet 10^{-6} DALYs per person per year were calculated and results for *Cryptosporidium* and *Giardia* at both treatment plants are presented in Figure 2.3. Because *Cryptosporidium* concentrations are relatively low (below 10 oocysts/100 L) in both plants, the minimum 3 log level of treatment was required during the whole period analyzed. On the other hand, the comparatively higher *Giardia* concentrations make the treatment required exceed 3 log in certain periods at Glenmore and during the whole period analyzed at Bears paw. This result shows the implications of high *Giardia* concentrations for evaluating treatment needs, emphasizing the importance of considering *Giardia* in monitoring programs. When *Cryptosporidium* is selected as the reference protozoan for drinking water risk assessment, there is an underlying belief that treatment sufficient for *Cryptosporidium* will also be sufficient for *Giardia*, especially due to the additional treatment of *Giardia* that can be provided by chlorination. For example, the United States only requires monitoring for *Cryptosporidium* to

determine the level of treatment required for each water supply system (U.S. EPA, 2006a). However, these results show how *Cryptosporidium* analyses might not be enough to determine treatment requirements when *Giardia* cysts are much more abundant than *Cryptosporidium* oocysts.

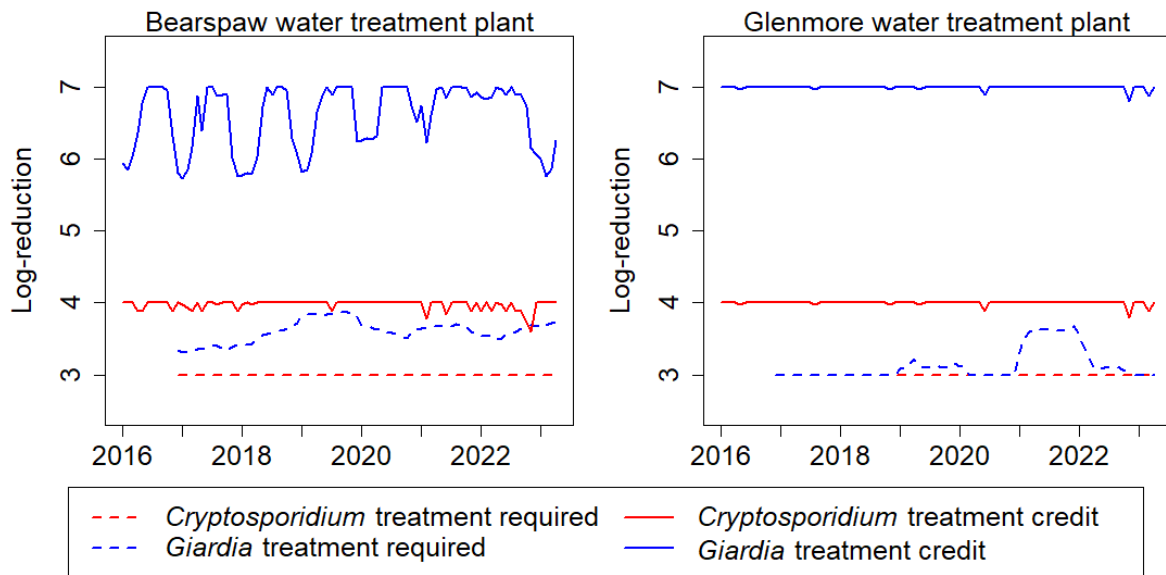


Figure 2.3: Treatment log reduction required and credited for *Cryptosporidium* and *Giardia* at Bears paw and Glenmore treatment plants from January 2016 to April 2023

The methodology presented herein to compute required log-reduction makes many assumptions due to limitations in the best available science (e.g., representativeness of dose–response models) or to facilitate uncomplicated data analysis approaches. Appendix A Section A.5 provides a summary of these assumptions and their likely effects on the computation of required log-reduction.

2.4.2.3 Evaluating the sufficiency of treatment

Treatment sufficiency is not usually determined empirically due to the difficulties of quantifying pathogen concentrations in treated water. Instead, treatment credits are often established in drinking water regulations according to design and operational conditions. This section discusses metrics to compare levels of treatment credited and required based on the Calgary monitoring and reporting experience. The accuracy of these credits with respect to actual treatment efficacy is beyond the scope of this study.

Log-reduction credits have been granted to the treatment system in accordance with the operating approval from the province of Alberta, which includes a 3-log basic credit for conventional filtration,

a 0.5-log or 1.0-log additional filtration credit assigned monthly based on filter effluent turbidity, and a further credit for chlorination (for *Giardia* only) assigned based on each day's minimum achieved CT (the product of residual free chlorine concentration and contact time). The turbidity-based filtration credit is awarded based on a calendar month of turbidity data. The 0.5-log credit is granted when at least 99% of combined effluent turbidity data are below 0.15 NTU, whereas the 1.0-log credit is given when 99% of individual filter effluent turbidity data are less than 0.1 NTU. Calgary computes the credit daily allowing a cumulative maximum of 15 min above the turbidity threshold. This daily time span is generally more stringent than the monthly criteria described above because it does not allow days with more frequent turbidity exceedances to be averaged out with days with less frequent turbidity exceedances over a month. The disinfection credit is evaluated once per minute based on CT data that depend on relatively variable parameters such as temperature and flow. The current approval specifies reporting and use of a minimum daily CT value, and the resulting credit is limited to a maximum 3 log.

Figure 2.3 presents the log-reduction required and credited for *Cryptosporidium* oocysts and *Giardia* cysts at both treatment plants in Calgary according to the rules established in the provincial approval. Treatment credits are equal to or higher than the required treatment during the whole period analyzed, complying with provincial requirements. In Bearspaw, an effect of seasonality on the treatment credit for *Giardia* cysts can be observed. This is explained by the reduction in chlorination efficiency due to low temperatures during the winter. Unlike at Glenmore, the size of the chlorination tanks and the water flow rate at the Bearspaw treatment plant do not allow for an increase in contact time, which results in lower CT values. Risk can increase if these periods of lower treatment are associated with high pathogen concentrations in water. De Brito Cruz et al. (2024) (Chapter 5) investigated the impact of the correlation between treatment and concentration data in Bearspaw, and no substantial impact on risk estimates was found.

The daily treatment credits are compared to monthly treatment requirements each day in Calgary. However, Figure 2.3 presents the monthly average of treatment credits calculated using the effective log-reduction approach given in Equation 2.7. This equation can be applied to average treatment efficacy over any period of time, including a 1-year moving average of treatment achieved, for example. It is inappropriate to average log-reductions or CT credits because an arithmetic average can overestimate treatment (Schmidt et al., 2020). In Calgary's compliance framework, an average value for each day is recommended to avoid underestimation of treatment achieved by using a minimum daily CT value. This average can be calculated using Equation 2.7, where $credit_t$ represents the disinfection

credit for a time step t , n represents the number of times steps and LR_{eff} is the effective log-reduction over n time steps.

$$LR_{eff} = -\log \left(\frac{1}{n} \sum_{t=1}^n 10^{-credit_t} \right) \quad (2.7)$$

In Calgary, achieved treatment is only allowed to fall below the required treatment once per month to a minimum of 90% of the required treatment. However, this metric is problematic because it gets more lenient when there is a greater need for treatment (90% of 3.0-log is 2.7-log, 90% of 4.0-log is 3.6-log, and so on). Rather than relying on unquantified conservatism to assure safety (which may be overly cautious in some cases and not safe enough in others), it is better to apply a well-reasoned and equitable safety factor. It is suggested to use a fixed 0.3-log difference (10% of the 3-log minimum) so that the achieved treatment is expected to exceed the required treatment daily with at most one day per month where the achieved treatment falls no more than 0.3-log short of the required treatment. The difference between achieved and required log-reduction and how it varies over time is a useful metric for operational targets and it is more meaningful in the drinking water industry than log-reduction ratios. Several levels could be set for different purposes to trigger responses, such as an alert level (e.g., requiring action by operators and utility managers), a notification level (e.g., requiring discussion with regulators), and a warning level (e.g., declaring that existing treatment may not have assured adequate safety of the treated water over a 1-year period).

2.4.3 Framework revision

Monitoring in an ongoing fashion rather than, for example, over a single one-year period accounts for possible changes in the watershed that could lead to non-stationarity (i.e., substantial shifts relative to historical patterns) and allows more timely treatment responses to high pathogen concentrations. However, ongoing monitoring requires revisions, especially if there are major changes in the watershed or operation of the treatment plant, as well as when there is a sustained shift in pathogen occurrence patterns. In the absence of those, periodic revisions are also suggested to reflect current practices and/or incorporate updates of the best available science. Two years after implementation, the monitoring program in Calgary was reassessed, particularly to consider new data from the river intake at Bearspaw. Moreover, the relative sampling frequency at the two intakes depends on their proportional contribution, which should be reassessed periodically. The impact of including an additional sampling point representing the river intake at the Bearspaw treatment plant is discussed in Appendix A Section

A.2. In Calgary, the water quality of the two intakes is not substantially different (the river intake is 4 km downstream of the dam intake) which allows less frequent analysis.

To reassess the frequency of sampling, the same type of analysis described in Section 2.4.1.2 was conducted with two different datasets: the first considers 2 years of data after the implementation of the framework (from May 2021 to April 2023) and the second uses the whole dataset available since January 2016. The results are presented in Appendix A Section A.3 (in Table A.2 and Table A.3, respectively). Similar to the results found in 2020, a sampling frequency of twice a month allows estimation of treatment needs with an error of no more than 0.14 log in Glenmore and 0.11 log in Bearspaw when the last 2 years of data are used. When the whole dataset is used, the same frequency results in a maximum error of 0.27 log in Glenmore and 0.15 log in Bearspaw. These two analyses were conducted to compare the effect of the two considered distributions of pathogen concentrations. When using all available data, there is an underlying assumption that they all represent samples from the same distribution. If it is believed that the distribution of pathogen concentrations is changing over time (i.e., the dataset shows non-stationarity), then it is important to use a timeframe that better describes the current pattern of concentrations observed to tailor monitoring practices and treatment needs accordingly. On the other hand, it is also critical to not respond to random noise as though it were a change in pattern. Because the frequency of sampling is influenced by the variability of concentration in these analyses, it is important that a few very extreme data points do not lead to an impractical sampling frequency.

2.4.4 Implementing risk-based monitoring and compliance programs

Managing microbial risks in drinking water involves the challenge of balancing generic assumptions taken to simplify modelling and regulations with site-specific considerations necessary to accurately represent the context studied. Historically, regulatory policies have focused on prescriptive rules that can cover as many situations as possible such as the designation of “well-operated” filtration systems or the use of system sizes when determining sampling frequencies. For simplification, one-size-fits-all approaches are frequently needed to develop global guidelines or national policies in populous or low-income countries. While this approach may work in most systems under stable conditions, it is important to acknowledge that water utilities are required more and more to operate under challenging conditions, which calls for more specific guidance. For example, changes in the magnitude and variability of microbial contamination caused by extreme events can rapidly disrupt water treatment

operations, compromising drinking water safety. In a changing climate, it is important to revisit knowledge about source water quality more frequently to meaningfully inform treatment decisions. Widespread implementation of *de facto* reuse also necessitates more guidance to ensure that water reaching drinking water treatment plants can be sufficiently treated. Moreover, the criteria to define good operation for one system might not be the same for another. Research has demonstrated how the current regulatory turbidity goal of 0.3 NTU might not ensure sufficient *Cryptosporidium* removal in systems relying on high-quality source water (Ballantyne et al., 2024). Little guidance is given for systems that need more than the 3-log minimum treatment requirement for *Cryptosporidium*. Furthermore, relying only on *Cryptosporidium* monitoring may not be sufficient to determine treatment requirements if *Giardia* cysts are more abundant in the source water. Hence, a one-size-fits-all approach can be under-protective in some cases if system-specific details are not considered.

Complementing general guidance provided in drinking water policies, the development of fit-for-purpose methods and models can contribute to decision-making regarding water safety. “Know your system” is an expression emphasized more and more in the water industry, which underscores the need for practical guidance. This work provides specific guidance for water utilities interested in implementing a monitoring protocol for protozoa with the purpose of informing drinking water treatment decisions. When water contaminants – which can be protozoa, other pathogens, or even microplastics – are the proverbial “needle in a haystack” (i.e., discrete and found in low concentrations in water), it is especially important that monitoring adequately represents the system being studied by designing protocols and analyzing data in a way that is fit-for-purpose for how risk is characterized. While it is common practice to implement monitoring as a one-size-fits-all approach, it is important to understand that monitoring the watershed to inform source water protection measures is different from monitoring the water entering the treatment plant to inform treatment decisions. A monitoring program that is designed to characterize average source water quality may not be informative enough to determine treatment decisions about the water entering the plant and to ensure the provision of safe drinking water not just on average but all the time. Peak raw water contaminant concentrations may not be captured by watershed monitoring or routine sampling at treatment plants. Although not addressed in this study, event-based monitoring can also help improve resilience during these episodic periods of deteriorated source water quality. With the exception of a few daily risk references in QMRA, guidance for short-term risk management in drinking water is still scant. In any case, it is critical to know when and where to collect data to serve the intended purpose and improve the return on investment of these

costly monitoring programs. Moreover, this paper creates a bridge between collection of data and their subsequent use in a QMRA model. Typically, QMRA has been conducted with whatever data are available (or assumed values from the literature) to respond to risk assessment questions. Here, a framework was developed detailing how to collect data to better inform a risk assessment. There is a difference between making the most of available data and using data that are strategically gathered to be informative. Future research can develop frameworks to link the collection of data to other QMRA applications.

While water utilities can benefit from information provided by monitoring programs, it is important to acknowledge that routine monitoring of pathogen concentrations is not feasible and/or affordable in many places. Although this study focuses on a large system, some options to reduce sampling costs were noted. Even when it is not always possible to characterize pathogen concentrations in water, understanding how treatment requirements are influenced by different levels of concentration helps to inform decision-making. This work is not a defense for “monitoring at all costs”. Instead, it is argued that monitoring should be conducted strategically to better support decision-making in water treatment and effectively protect public health.

2.5 Conclusions

This paper provides guidance on the development of protocols for monitoring the raw water of treatment plants and the use of monitoring data in QMRA to evaluate treatment needs. The developed framework serves water utilities interested in maximizing the value of monitoring for drinking water treatment decisions and regulators that use monitoring as one of the strategies to control microbial risks in drinking water. The main conclusions are as follows:

- It is important to know the quality of raw water to efficiently treat it (i.e., ensuring public health protection while avoiding unnecessary treatment costs). Tailored monitoring programs are needed to adequately characterize the raw water of a system and meaningfully support water treatment decisions, especially for increased water quality variability in a changing climate.
- Data collection should be planned strategically to reflect the purpose of the monitoring program (e.g., to inform treatment decisions), extract maximum value from the allocated resources, and ensure the studied system is accurately represented.

- In systems with multiple raw water intakes, it is important for the contribution of each intake to be reflected in the sampling approach. There are several methods to choose from depending on the needs and capabilities of each water utility: (1) sampling blended water before treatment, (2) compositing samples of different volumes from each intake, (3) calculating a weighted average concentration from independent samples collected at each intake based on proportional flow contribution, (4) randomly selecting the intake given proportional flow contribution to the total water supply, or (5) representing the flow contribution by adjusting the number of samples per intake. Monitoring for treatment decisions needs to be representative of the water entering the treatment plant because this is the water that will ultimately be consumed.
- It is important to establish a frequency of sampling that can represent a system's needs, which can be informed by observed pathogen concentrations. This frequency can be adjusted to achieve desired precision in estimated treatment requirements given past data. Precisely determining treatment needs contributes to a better balance between water safety and sampling costs (e.g., a fit-for-purpose sampling protocol can save costs if the variability of pathogen concentrations is low).
- When using risk assessment to determine treatment requirements, concentrations used in the model need to be consistent with how risk is measured. Computing annual risk using an individual concentration value assumes that it is sustained all year round, which can substantially overestimate treatment requirements and misinform decisions.
- When compliance rules are established, it is important to set fixed-magnitude safety factors for consistently evaluating the sufficiency of treatment across systems. Instead of log-reduction ratios, the difference between treatment credits and requirements is recommended. Several thresholds could be set to trigger different risk management strategies (e.g., operational changes, regulator notification).
- Treatment requirements may be driven by *Giardia* instead of *Cryptosporidium* if *Giardia* cysts are more abundant, which emphasizes the importance of also including this pathogen in protozoa monitoring programs and/or in regulatory requirements.

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Chapter 3

Spills, storms and sudden failures: Assessing microbial risks when faced with short-term events in drinking water treatment

3.1 Summary

Water utilities have been challenged by the increased occurrence of extreme short-term events threatening drinking water safety such as floods, wildfires, infrastructure failures and accidental discharges. These events often require proactive planning and informative data to support rapid decisions, especially when they are associated with potential acute risks from microbial contamination. Quantitative microbial risk assessment (QMRA) has been applied to support operational and regulatory approaches under typical conditions; however, guidance regarding its use in risk management of unexpected short-term events is limited. Here, the risk implications of an accidental raw sewage discharge upstream of a drinking water treatment plant intake in Calgary, Canada were analyzed to review operational response to the spill and more broadly demonstrate how scenario-based QMRA can be applied to event-driven operational decision-making. The scenarios that most reasonably described the contamination event indicated that existing treatment was sufficient and provided a safety factor of at least 0.4 log. Approaches for microbial risk assessment and management of short-term events are then reviewed, considering implications of *de facto* potable reuse in particular. Microbial risk management could benefit from collaboration between wastewater and drinking water treatment systems as well as development of new risk references for short-term events. This applied framework can be used for emergency preparedness and for increased response capacity of water utilities in time-sensitive contexts.

3.2 Introduction

Drinking water safety can be severely challenged by impactful short-term disturbances that compromise water quality and treatability (Hrudey et al., 2003). From operational failures in coagulant or disinfectant dosing (Momba et al., 2005) to sudden water quality variations caused by climate-related extreme events (Khan et al., 2017), water utilities need to be resilient because a few minutes or hours of insufficient treatment can be crucial for the continuous provision of safe drinking water. Extreme precipitation events have been associated with increased concentrations of microbial contaminants and outbreaks of waterborne disease (Graydon et al., 2022), and they are predicted to become more frequent with climate change (Myhre et al., 2019). In this context, acute risks caused by microbial contaminants are especially concerning due to their rapid health effects. However, pathogen concentrations in water

and corresponding treatment efficiency are not usually monitored with high frequency, hindering evaluation of the impact of such events.

Wastewater is a possible source of microbial contamination in drinking water. Although potable reuse has been gaining increasing relevance for water resource management in contexts of limited water availability, there can be risks associated with it when water reuse is unplanned. Direct and indirect potable reuse are planned forms of reuse involving the use of advanced treatment processes when treated wastewater is part of a drinking water supply; in the case of indirect potable reuse, an environmental buffer provides additional treatment. *De facto* reuse, however, is an unintentional form of reuse in which wastewater is discharged into a water body that is subsequently used as a drinking water treatment plant's source. It is widespread globally (Rice et al., 2013; Swana et al., 2020) and can lead to substantial microbial risks (Nappier et al., 2018) that are higher than risks from planned reuse (Soller et al., 2019). Whereas regulations have recently been developed for planned potable reuse (e.g., SWRCB, 2023), *de facto* reuse is subject to less regulatory scrutiny and its implications are often unquantified.

The impacts of *de facto* reuse in drinking water are notably variable, depending on wastewater quantity and quality as well as streamflow conditions (Rice & Westerhoff, 2015). Management of microbial risks associated with wastewater can be especially difficult if this variability is exacerbated during short periods of contamination caused by extreme events. Wastewater by-pass discharges following wet periods can substantially increase microbial contamination in drinking water intakes (Tolouei et al., 2019). Combined sewer overflows after extreme precipitation have also been associated with increased risk of gastrointestinal diseases for drinking water consumers (Jagai et al., 2015). Wastewater contamination can also be unexpected if infrastructure or treatment failures cause discharge of untreated or insufficiently treated wastewater to surface water, affecting water quality and potentially drinking water treatment downstream (Preisner, 2020).

The unpredictable occurrence and magnitude of wastewater spills often necessitates rapid risk management decisions when spills occur. Except for general considerations in water safety plans, guidance for such decisions is usually lacking as these rare events can easily be overlooked in typical operational and regulatory compliance practices. A drinking water treatment plant in Calgary (Canada) faced this challenge when an accidental wastewater main break in Cochrane caused a raw sewage discharge upstream of its intake in 2023. This event raised concerns about maintaining the

microbiological safety of the drinking water, leading to temporary closure of a water intake and partial diversion of operations to another treatment plant.

Quantitative microbial risk assessment (QMRA) is a framework commonly used to support management of microbiological risks in water, and previous studies have used it to evaluate risks associated with *de facto* potable reuse (Lim et al., 2017; Amoueyan et al., 2019). Nevertheless, there is limited guidance on how to evaluate the impacts of episodic events on drinking water treatment that may pose a high risk. To review the actions taken in Calgary after the wastewater spill in Cochrane and provide a framework for future emergency preparedness, a scenario-based QMRA was used herein to evaluate the sufficiency of treatment provided by the drinking water treatment plant if it had been left in service as usual. Building upon this example, guidance is provided for evaluation of microbial risk caused by short-term high-magnitude disturbances in drinking water treatment.

3.3 Methods

3.3.1 Event description

This study analyzes the risk implications on drinking water of a raw sewage spill caused by an accidental sewer line break in the town of Cochrane, Alberta, Canada in October 2023. The infrastructure ruptured during a planned upgrade of the water main and led to overland flow into the Bow River approximately 23 km upstream of the Bearspaw Water Treatment Plant (WTP). This plant provides 60% of the drinking water supplied to the City of Calgary and has two intakes separated by approximately 2 km that draw water from the Bow River. After timely notification of the provincial emergency coordination centre, spill mitigation efforts started on the day of the contamination event. Vacuum trucks were used to reduce the superficial spill flow before release into the river while the spill was not completely controlled. The spill flow was estimated (for the purposes of this study) to be 14 L/s and to last for up to 24 hours until it was completely controlled.

The Bearspaw drinking water treatment system consists of high-rate sand-ballasted flocculation clarification followed by rapid filtration and chlorine disinfection. It was estimated that bacteria and protozoa did not pose significant risks based on knowledge from routine monitoring programs of typical concentrations in the Bow River and Calgary's raw wastewater. Additionally, there were no cases of cryptosporidiosis in Cochrane reported to Alberta Health Services at that time. However, it was deemed

necessary to assess the continued safety of drinking water with respect to viruses due to higher concentrations that are typical in wastewater. River modellers from the City of Calgary estimated that contaminated water would first reach the plant in approximately seven hours. The mitigation plan involved closing the main intake closest to the spill site while increasing the flow through the downstream intake (as well as increasing the flow through Calgary's other treatment plant on the Elbow River) to ensure the total drinking water storage volume provided by the two plants was augmented. Chlorine dose at Bearspaw WTP was also increased to improve the efficiency of disinfection, resulting in residuals approximately 0.2 mg/L higher at the end of the event period. To review the need for these precautionary actions, this study was conducted with a focus on viral contamination. Figure 3.1 presents the location of the spill site as well as the Bearspaw WTP and its main intake.

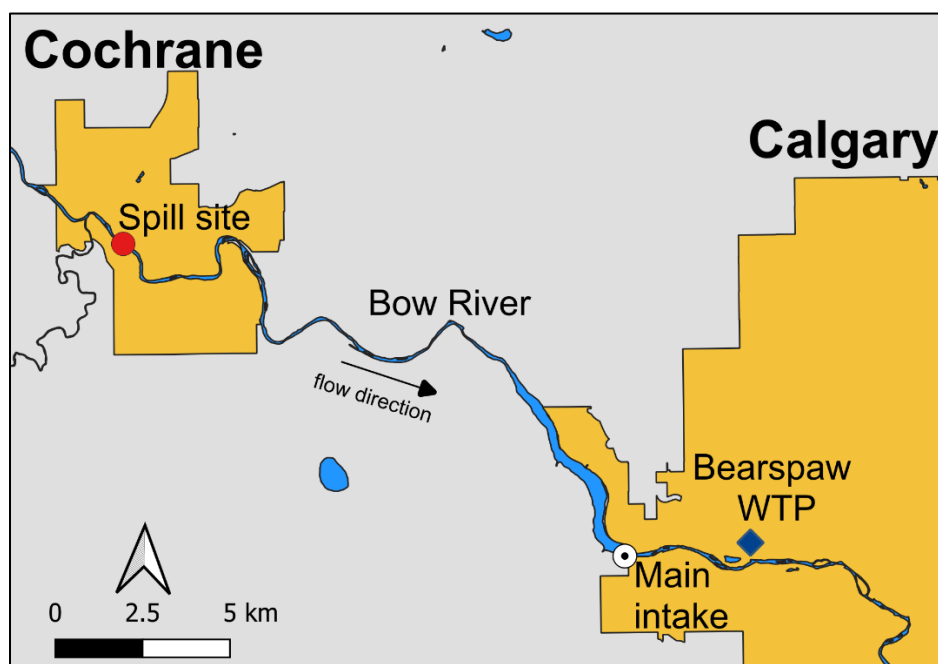


Figure 3.1: Location of spill site and Bearspaw WTP

3.3.2 Risk model

A scenario-based QMRA was used to estimate the annual burden of disease in DALYs (disability-adjusted life years) given background conditions and a brief period impacted by the spill. Annual risk thresholds are typically used in drinking water guidelines, including in Canada. It was assumed that the water treatment plant was under influence of the spill for one day with a baseline concentration of virus in the river for the other 364 days. In each scenario, point estimates were used to characterize the

concentration of viruses in the intake of the treatment plant (C), treatment log-reduction (LR) and daily volume of treated water consumed (V). Although these inputs could be represented by distributions instead of point estimates for a more detailed evaluation of health risks, limited data were available to describe this contamination event. Additionally, this approach provides a simple estimation of risk and its sensitivity to several model inputs that can be conducted quickly to support decisions about water supply in circumstances requiring fast decisions. C , LR and V can be arranged to define the daily dose of virus ingested via consumption of treated drinking water (D), according to Equation 3.1. To account for the duration of the spill, concentration was divided in two components C_0 and C_f representing the concentration of viruses in the baseline condition and after dilution of the spill, respectively.

$$D(C) = C \times 10^{-LR} \times V \quad (3.1)$$

To evaluate daily probability of infection given the dose of virus ingested, an exact beta-Poisson dose-response model for rotavirus with parameters $\alpha = 0.167$ and $\beta = 0.191$ was used (Teunis & Havelaar, 2000). Rotavirus has a high prevalence of infections among children and is the viral pathogen used as a reference for dose-response in Health Canada (2019). The daily probability of infection is presented in Equations 3.2, where ${}_1F_1$ represents the Kummer confluent hypergeometric function. The daily probability of infection was also calculated for the 364 days with baseline concentration ($P(C_0)$) and for the day of the sewage discharge ($P(C_f)$).

$$P(C) = 1 - {}_1F_1(\alpha, \alpha + \beta; -D(C)) \quad (3.2)$$

The annual probability of infection (P_{inf}) was evaluated according to Equation 3.3. To calculate DALYs from annual probability of infection (Equation 3.4), an 88% probability of illness given infection by rotavirus ($P_{ill|inf}$) and a value of 8.28×10^{-3} DALYs per illness ($DALYs/ill$) were used, as in Health Canada (2019).

$$P_{inf} = 1 - \left((1 - P(C_0))^{364} (1 - P(C_f)) \right) \quad (3.3)$$

$$DALYs = P_{inf} \times P_{ill|inf} \times DALYs/ill \quad (3.4)$$

The risk model was also applied in reverse to determine the possible safety factor or extra treatment required to meet the reference risk level of 10^{-6} DALYs per person per year. In each scenario, a fixed volume of 1.45 L (Pintar et al., 2009) was considered as a conservatively high estimate of daily drinking water consumption per person. Although Health Canada (2019) suggests 1 L/day of unboiled tap water

consumption, an increase to 1.45 L/day is understood to be more relevant to the low-humidity environment of Calgary. Values for concentration and treatment as well as the scenarios considered are described in Sections 3.3.3–3.3.5.

3.3.3 Concentration of viruses

The concentration of viruses in river water was defined before and after the sewage discharge (C_0 and C_f , respectively). To estimate the baseline concentration of viruses, three values were considered: 1, 10^2 and 10^3 units/L. Concentration of viruses in water can be reported in different units of measurement (e.g., foci, gene copies) that are not necessarily equivalent. Because there is no standard conversion factor between them, the term “units” is used herein to simply represent any unit of measurement of viruses in water. Although harmonization of units is desirable for comparing reported values, it was not conducted here as the focus was only to have a sense of orders of magnitude of typical concentrations. Schijven et al. (2011) used $10^{-3.6}$ (or 0.00025) units/L as a mean concentration of enterovirus in risk assessment, but values on the order of 10^2 units/L (Albinana-Gimenez et al., 2006) and 10^4 units/L (Lodder & de Roda Husman, 2005) have been reported for viruses in river water. The latter study investigated rivers that were under the influence of untreated sewage; thus, 10^4 units/L was not considered an appropriate value to describe a baseline condition in the Bow River. A study conducted in the Bow River (Pang et al., 2019) reported median values and interquartile ranges for the concentrations of viruses upstream of Calgary. The lowest 25th percentile and highest 75th percentile of concentration values for different viruses were $10^{1.45}$ (or 28) and $10^{3.63}$ (or 4300) units/L, respectively. Here, it is assumed that the highest values are not representative of a baseline condition as they would be unlikely to be sustained for a whole year. Pathogens can also become non-viable in the natural environment due to decay, and detection methods that do not report viable and infectious units can overestimate concentrations. For example, gene copies can overestimate infectious units by up to 100,000 times (Pecson et al., 2021). Thus, 10^3 units/L was considered to be the highest baseline value in this study.

The concentration of viruses in river water after the sewage discharge was estimated using a mass balance (Equation 3.5). In this equation, Q_r represents the Bow River flow of approximately 41,600 L/s on the day of the spill at the monitoring station in Cochrane (Water Office, 2025), Q_d is the estimated sewage discharge of 14 L/s and C_d is the raw sewage virus concentration. This analysis assumes that the discharged sewage would be laterally dispersed within the river water. The residence

time and longitudinal mixing of the sewage in this reach of the Bow River can affect the pattern with which it passes the drinking water treatment plant's intake. However, these temporal variations of concentration should not influence risk estimates because (i) risk is calculated on an annual basis (a timeframe long enough to fully reflect the residence time of the sewage in this reach of the river), and (ii) the linearity of dose-response models ensures that aggregating the exposure in one day or spreading the same total number of pathogens out over several days would not change annual risk estimates. Pathogen decay was also not considered in this analysis, but a brief discussion of its implications is presented in Section 3.4.1.

$$C_f = \frac{C_0 \times Q_r + C_d \times Q_d}{Q_r + Q_d} \quad (3.5)$$

Table 3.1 presents a summary of virus concentrations that have been found in raw sewage (C_d). To simplify the comparison, the last two columns of this table show the mean and maximum concentrations from each study. The average virus concentration in raw sewage is 1.69×10^6 units/L, computed using the mean concentration value of each study with equal weight regardless of the number of underlying data. Therefore, 10^6 units/L was used as a likely estimate of the raw sewage virus concentration in this analysis. A concentration of 10^7 units/L was used as a conservative estimate, which is based on the mean value in Albinana-Gimenez et al. (2006) because it is the highest mean concentration in Table 3.1. A raw sewage virus concentration of 10^8 units/L, based on the average of the maximum concentration values in Table 3.1 (1.39×10^8 units/L) was used as an extreme, likely unrealistic, worst-case scenario of what might be applicable to describe this contamination event. Notably, this value is heavily influenced by one value ($9.17 \log_{10}$ units/L or 1.48×10^9 units/L); the other maximum values were all below 2.52×10^7 units/L. The derivation of log-removal values required under California's framework for direct potable reuse assumes a raw wastewater virus concentration of 10^9 gene copies per litre (SWRCB, n.d.) based on the maximum value of the first study listed in Table 3.1. Using the concentration of 10^9 units/L would likely be too conservative herein because direct potable reuse consists of long-term direct exposure and may warrant additional conservatism, unlike the short-term indirect exposure that occurred in Calgary.

Table 3.1: Virus concentrations reported in raw sewage

Reference	Virus (Number of samples)	Mean concentration (Range) ^{3a}	Unit	Method	Mean conc. (units/L)	Max. conc. (units/L)
Eftim et al., 2017	Norovirus (n = 850)	4.8 (0.02 – 9.17)	log ₁₀ gene copies/L	Meta analysis	6.31×10 ⁴	1.48×10 ⁹
Pouillot et al., 2015	Norovirus GII (n = 566)	3.9 (3.5 – 4.3) ^{3b}	log ₁₀ gene copies/L	Meta analysis	7.94×10 ³	NR
	Male-specific coliphage	6.2 (6.1 – 6.4) ^{3b}			1.58×10 ⁶	NR
	Norovirus GI (n = 253)	1.5 (0.4 – 2.4) ^{3b}			3.16×10 ¹	NR
Bosch et al., 1988	Rotavirus (n = 13)	NR (1.00×10 ³ – 1.40×10 ⁴)	foci/L	Immuno- fluorescence, cell line	NR	1.40×10 ⁴
	Enterovirus (n = 14)	NR (1.00×10 ³ – 1.40×10 ⁴)			NR	1.40×10 ⁴
Fumian et al., 2013	Adenovirus (n = 24)	2.97×10 ⁶ (5.23×10 ⁵ – 7.04×10 ⁶)	log ₁₀ gene copies/L	qPCR/ RT-qPCR	2.97×10 ⁶	7.04×10 ⁶
	Polyomavirus JC (n = 24)	5.98×10 ⁵ (3.26×10 ⁴ – 2.11×10 ⁶)			5.98×10 ⁵	2.11×10 ⁶
	Norovirus GII (n = 24)	6.75×10 ⁴ (1.5×10 ⁴ – 2.03×10 ⁵)			6.75×10 ⁴	2.03×10 ⁵
Nordgren et al., 2009	Norovirus GI (n = 12)	3.2×10 ⁵ (1×10 ⁴ – 2×10 ⁶)	genome equivalents/L	RT-qPCR	3.20×10 ⁵	2.00×10 ⁶
	Norovirus GII (n = 12)	4.1×10 ⁵ (3×10 ⁴ – 1×10 ⁷)			4.10×10 ⁵	1.00×10 ⁷
Albinana-Gimenez et al., 2006	Adenovirus (n = 5)	1.4×10 ⁷ (4.71×10 ⁵ – 2.52×10 ⁷)	genome copies/L	qPCR	1.40×10 ⁷	2.52×10 ⁷
van den Berg et al., 2005	Norovirus (n = 53)	1×10 ⁵ (NR – 1×10 ⁶)	PCR detectable units/L	RT-PCR	1.00×10 ⁵	1.00×10 ⁶
Lodder & de Roda Husman, 2005	Norovirus (n = 5)	2×10 ⁵ (5.11×10 ³ – 8.50×10 ⁵)	PCR detectable units/L	RT-qPCR	2.00×10 ⁵	8.50×10 ⁵

^{3a} Minimum values do not include any non-detects in cases in which they occur, ^{3b} 95% credible interval, NR: not reported

3.3.4 Virus reduction in drinking water treatment

Efficiency of pathogen removal in drinking water treatment is typically assessed indirectly using indicators (e.g., turbidity, total coliforms) or log removal credits awarded to treatment technologies. Less frequently, pilot or full-scale testing using surrogates (Schijven et al., 2011) is conducted to evaluate the sufficiency of treatment. Here, a minimum 8-log virus reduction by drinking water treatment was considered, with 2 log credited to conventional filtration and 6 log credited to chlorine disinfection. According to Health Canada (2019), well-operated chemically-assisted filtration systems can achieve 2 log removal of enteric viruses. However, this treatment credit is likely conservative as overall removal by clarification and filtration cited therein can range from 1.0 to 5.1 log, with most treatment plants achieving 2.2 to 3.8 log removal.

Log reduction credits for chemical disinfection are a function of the residual concentration and contact time (CT). As this treatment efficiency is also impacted by temperature and pH, experimentally derived CT tables are used to determine the required operational conditions (e.g., amount of disinfectant, contact time) to achieve a certain level of microorganism inactivation (U.S. EPA, 1991). To define a range of values for virus log reduction by chlorination, literature addressing drinking water treatment and potable reuse was considered. A 4-log reduction of viruses is required for most surface water sources (U.S. EPA, 2006), so most drinking water treatment studies focus on adjusting and optimizing conditions to reach only a 4-log reduction of viruses (e.g., Rachmadi et al., 2020; Kong et al., 2021). The minimum daily CT values at Bearpaw WTP were around 200 mg·min/L during the day of and after the spill event, which is substantially higher than the minimum CT required to receive a 4 log-inactivation credit according to provincial regulations, in which the maximum CT required is 90 mg·min/L (under the extreme conditions of temperature of 0.5 °C and pH of 10). In contrast, more treatment is required for reclamation of wastewater, especially for production of drinking water. For example, the framework for direct potable reuse in California (SWRCB, 2023) requires a 16-log reduction of viruses between raw sewage and treated drinking water. It credits a maximum of 6 log reduction for each individual treatment process. Critically, it has been experimentally demonstrated that chlorination systems can achieve more than 7 log reduction of F-specific bacteriophage MS2 (Ikehata et al., 2018), which is a common surrogate used for virus reduction in drinking water treatment (Mesquita & Emelko, 2012). Chlorination efficiency of 6-log was considered here in favor of caution as the sensitivity of viruses to chlorination can vary (Rachmadi et al., 2020) and experimental data identifying types of viruses were not available herein. This credit value is being considered for approval

in new chlorine crediting frameworks for potable reuse in California for CT values as low as 10 mg·min/L (Pecson et al., 2020). Nevertheless, additional treatment can be provided by well-operated conventional filtration beyond a 2-log baseline. Summing up filtration and disinfection credits, three values were considered for virus reduction in drinking water treatment: 8, 9 and 10 log.

3.3.5 Scenarios

In Sections 3.3.3 and 3.3.4, three point estimates were selected for each of the three main input variables: baseline virus concentration in the river (1, 10^2 and 10^3 units/L), raw sewage virus concentration (10^6 , 10^7 and 10^8 units/L) and virus log reduction (8, 9 and 10). From these, three base scenarios were initially defined based on the raw sewage virus concentration values: likely (10^6 units/L), conservative (10^7 units/L) and worst-case (10^8 units/L). These were associated with the intermediate values considered for baseline river virus concentration (10^2 units/L) and treatment credit (9 log). The base scenarios were defined according to raw sewage concentration because a wastewater spill is the event analyzed herein. The sensitivity of the results to baseline virus concentration and treatment log-reduction for all raw sewage concentrations was examined using a 3^3 factorial design to explore all possible combinations among the three values of these three variables (Figure 3.2).

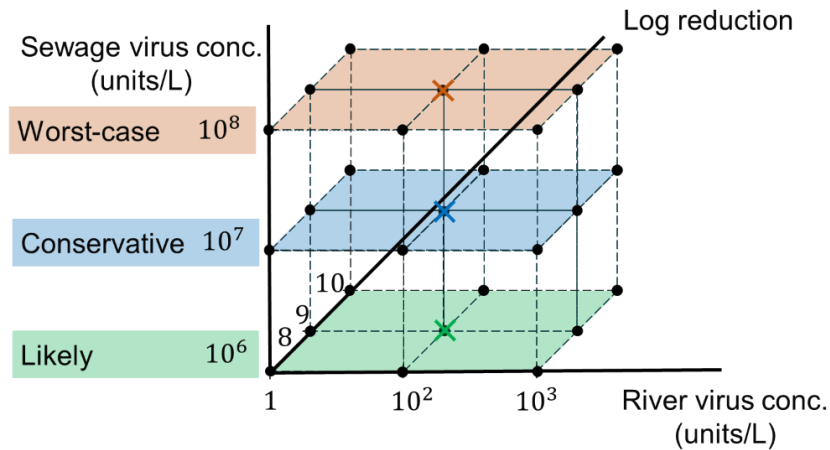


Figure 3.2: Scenarios considered in risk assessment. Each black circle represents a different scenario, and crosses represent the three base scenarios

3.4 Results and Discussion

3.4.1 Wastewater spill event QMRA

Implications of the sewage spill on drinking water safety were assessed for each of the 27 scenarios (Figure 3.2), and the results are presented in Table 3.2. In this table, the three varying inputs are presented, while daily drinking water consumption volume (1.45 L/day), spill flow rate (14 L/s) and river flow (41,600 L/s) are constant. The computed values of treatment needed range from having a safety factor of 3.46 log in excess treatment provided to needing 1.29 log of additional treatment to satisfy the health-based target of 10^{-6} DALYs per person per year. The base scenarios (highlighted in bold) indicate that sufficient treatment would have been provided at the Bearspaw WTP with a safety factor of at least 0.46 log in the worst-case base scenario.

Table 3.2: Description of model inputs and outputs for scenarios considered

Scenario	INPUTS/OUTPUTS					
	Raw sewage conc. ^{3c} (C_d)	Baseline virus conc. ^{3c} (C_0)	Treatment credit (LR)	Intake virus conc. ^{3c} (C_f)	DALYs	Treatment safety factor ^{3d}
Likely	10⁶	1	8	337	3.45×10^{-8}	1.46
		1	9	337	3.45×10^{-9}	2.46
		1	10	337	3.45×10^{-10}	3.46
		10 ²	8	436	1.82×10^{-6}	** -0.26**
		10²	9	436	1.82×10^{-7}	0.74
		10 ²	10	436	1.82×10^{-8}	1.74
		10 ³	8	1,336	1.80×10^{-5}	** -1.25**
		10 ³	9	1,336	1.80×10^{-6}	** -0.26**
		10 ³	10	1,336	1.80×10^{-7}	0.74
Conservative	10⁷	1	8	3,365	1.84×10^{-7}	0.74
		1	9	3,365	1.84×10^{-8}	1.74
		1	10	3,365	1.84×10^{-9}	2.74
		10 ²	8	3,464	1.96×10^{-6}	** -0.29**
		10²	9	3,464	1.96×10^{-7}	0.71
		10 ²	10	3,464	1.96×10^{-8}	1.71
		10 ³	8	4,364	1.81×10^{-5}	** -1.26**
		10 ³	9	4,364	1.82×10^{-6}	** -0.26**
		10 ³	10	4,364	1.82×10^{-7}	0.74
Worst-case	10⁸	1	8	33,644	1.68×10^{-6}	** -0.22**
		1	9	33,644	1.68×10^{-7}	0.78
		1	10	33,644	1.68×10^{-8}	1.78
		10 ²	8	33,743	3.46×10^{-6}	** -0.54**
		10²	9	33,743	3.46×10^{-7}	0.46
		10 ²	10	33,743	3.46×10^{-8}	1.46
		10 ³	8	34,642	1.96×10^{-5}	** -1.29**
		10 ³	9	34,642	1.96×10^{-6}	** -0.29**
		10 ³	10	34,642	1.96×10^{-7}	0.71

^{3c} All concentrations are presented in units/L. ^{3d} Additional treatment provided beyond the minimum to achieve 10⁻⁶ DALYs per person per year. Negative values, highlighted with asterisks, represent extra treatment needed.

The other 24 scenarios show sensitivity of the model to changes in baseline river concentration and treatment log-reduction and mostly support this conclusion. Six out of the ten scenarios indicating that extra treatment would be necessary (highlighted with asterisks) occur at a baseline concentration of 10³ units/L. This is such a high baseline concentration to be sustained throughout a year that even if no spill occurred, a treatment log reduction higher than 9 log would be necessary to counteract it. In the other four scenarios, the minimum treatment credit is assumed with specific combinations of raw

sewage and baseline river concentrations. This underscores the importance of ensuring that the treatment plant is well operated (leading to an overall 9-log reduction of viruses) so that this spill would not impact drinking water safety by exceeding the risk reference. Ensuring that a treatment system can have sufficient performance even under challenging conditions is an important way to be prepared to respond to short-term disturbances, especially when information about microbial contamination is lacking.

To illustrate the effect of the wastewater spill flow rate on risk, two further hypothetical scenarios were run. In these scenarios, the spill flow rate of 14 L/s was halved or doubled assuming the values of the worst-case base scenario (i.e., 10^8 units/L, 10^2 units/L and 9 log for raw sewage concentration, baseline concentration and treatment efficiency, respectively). The reference DALYs were met with a safety factor of 0.29 and 0.58 log for double (28 L/s) and half (7 L/s) of the flow, respectively. Scenarios like these can be useful for risk management, as they can show the effect of operational strategies (e.g., closing valves) once an incident is detected. Alternatively, they can outline maximum tolerable conditions. With these inputs, the spill rate could be increased up to 69 L/s and still meet the risk reference target.

Streamflow conditions can also affect the impact of wastewater discharges on surface water. Monthly flow averages at the Bow River near Cochrane from 2014 to 2023 and in 2023 specifically are presented in Appendix B Section B.1. In this period, reported daily values of river flow have ranged from 33.9 to 397 m³/s. Modifying the river flow on the day of the event (41.6 m³/s) to represent these two extreme flow conditions and assuming the inputs of the worst-case base scenario, the treatment safety factor provided changes from 0.46 log to 0.42 and 0.70 log, respectively. In Calgary, the spill event occurred in a relatively dry season during which wastewater spills can pose greater risks compared to other periods. Having streamflow data is important to guide appropriate response, as flow conditions can change substantially over time, affecting the impact of wastewater discharges (Rice & Westerhoff, 2015). Temporarily increasing flow using water from upstream reservoirs to increase contaminant dilution or accelerate its passage of the WTP intake is a potential mitigation strategy. Alternatively, flow through the plant can be reduced to increase the disinfection contact time and consequently, efficiency of treatment.

The results presented here are presumably conservative because (1) the values considered for concentration are probably overestimated as they do not necessarily represent infectious units and

(2) no pathogen decay in the river was assumed. Crank et al. (2024) showed how neglecting decay can overestimate risk in QMRA. The distribution of the decay constant of rotavirus that they reported was used here for a simple analysis. Using the mean of the untruncated distribution and assuming first-order decay, the intake virus concentration would be reduced to approximately 79% of the initial concentration in the estimated seven hours that the river water flowed from the spill site to the treatment plant intake.

Partial interruption and diversion of water treatment were done in Calgary out of an abundance of caution to avoid potential health risks. The risk framework used here can support decisions of water utilities that face similar challenges but do not have the same flexibility to sustain their water supply while letting the spill pass. It is critical, however, to have informative and ideally case-specific data for use in risk assessment. Case-specific data does not necessarily mean real-time, event-specific data that can be difficult to acquire. Emergency preparedness can be supported through routine monitoring programs with characterization of previous conditions such as streamflow and baseline pathogen concentrations in the river or wastewater. Knowing the resources available to counteract a disturbance (e.g., treatment efficiencies or redundancies, possibility to control flow or increase dilution) is also useful to analyze the impact of different risk management strategies. As a last resort, typical values from the literature can aid definition of scenarios. A factorial design set of scenarios with point estimates is a simple modeling tool that can be used by plant operators as an initial assessment to support decision-making. Building upon this example, challenges and opportunities around the provision of meaningful information for microbial risk management of short-term events are discussed in Sections 3.4.2 and 3.4.3.

3.4.2 Risk evaluation of short-term events

Approaches to evaluate episodic high risks and associated tolerances are not formally addressed in risk assessment of municipal drinking water supplies apart from general consideration in water safety plans (Smeets et al., 2010) or assessment of failure scenarios in direct potable reuse trains (Pecson et al., 2017). The modelling approach applied here can be modified slightly to provide guidance for such evaluation and ensure resilience during periods of degraded raw water quality or treatment performance.

Formulations like Equations 3.1–3.2 can be used to evaluate exposure to pathogens and probability of infection with and without influence of a disturbance affecting drinking water safety. While these

equations can be used to evaluate the magnitude of a disturbance for varying pathogen concentrations or efficiency of treatment, the disturbance's duration and baseline conditions (here, the baseline river concentration) are also important to determine its impact on a system. For example, the intake virus concentration is an intermediate output calculated from the inputs presented in Table 3.2. While it can show by how much water quality changed after the spill, it cannot determine risk alone. As observed in Table 3.2 considering scenarios with 10-log treatment performance, an intake concentration of 33,743 units/L can lead to 3.46×10^{-8} DALYs per person per year while an intake concentration of 1,336 units/L (25 times smaller) results in 1.80×10^{-7} DALYs per person per year (5 times higher). The 100-fold higher raw sewage concentration in the first scenario only lasted for one day, but the year-round 10-fold higher baseline concentration in the second scenario had a greater impact on annual risk.

When evaluating annual risk, duration can be more generally accounted for by modifying Equation 3.3 into Equation 3.6, where t represents the duration of the disturbance in a specific unit of time (e.g., day, hour) and T_{Max} refers to the maximum number of units of time in a year (e.g., for t defined in days, T_{Max} is usually 365). This equation assumes that the change in a system is abrupt and is only characterized in two different timeframes (with and without effect of the disturbance). This simplifying assumption might be appropriate for data-limited contexts.

$$P_{inf} = 1 - \left((1 - P(C_0))^{T_{max} - t} (1 - P(C_f))^t \right) \quad (3.6)$$

This model can be used to enhance emergency preparedness of drinking water treatment utilities. For instance, it is possible to determine what would be the maximum duration of an event or maximum concentration that can be sustained without exceeding a risk reference given a fixed level of treatment. Or, alternatively, the minimum treatment required to counteract a specific concentration that lasts for a specific number of days can be evaluated. Examples of application of Equation 3.6 are presented in Appendix B Section B.2. Baseline concentration conditions can be better characterized through routine monitoring programs (de Brito Cruz et al., 2025 (Chapter 2)). Coupling this with event-based monitoring data, case-specific thresholds and strategies for microbial risk management can be established using the model described here. However, event-based monitoring data should be incorporated into models with caution. While characterization of the raw sewage concentration could be used to better define the extreme event herein, virus concentrations data collected at the drinking water treatment intake could easily misrepresent the impact of the event by missing its peak. Microbial concentration data also exhibit several sources of uncertainty (e.g., random sampling error, analytical

recovery) that can be characterized for better use of collected data for risk assessment and decision-making (Emelko et al., 2010). Overall, this model enables 1) exploration of scenarios, 2) definition of thresholds for combinations of magnitude and duration of a disturbance, and 3) determination of the effect of alternative strategies to counteract a disturbance (e.g., increasing treatment efficiency, reducing spill flow).

Approaches to evaluate the impact of short-term risks using annual risk references can accurately characterize risk over the course of a year. This is useful for characterizing average conditions (e.g., determining typical treatment requirements in a treatment plant) and for compliance, as drinking water regulations generally focus on annual risk. Nevertheless, they do not necessarily ensure that short-term risks are sufficiently managed because the annual timeframe allows for periods of low and high risk to be averaged out throughout a year. Thus, a short-term risk of high magnitude may be impactful for one day and still be averaged out by other days with negligible risk, resulting in an annual risk below the reference level. Although this issue has been recognized and daily risk references have been applied on some occasions (Signor & Ashbolt, 2009), the water industry generally relies on annual risk references when implementing QMRA. A daily risk reference of 2.7×10^{-7} infections per person per day (or, alternatively, 2.7×10^{-9} DALYs per person per day) has been used, but it assumes that this daily risk is sustained year-round for a final annual risk of 10^{-4} infections (or 10^{-6} DALYs) per person. Because these daily risk reference levels do not allow any fluctuation throughout a year, they are stricter than the corresponding annual reference.

In risk analysis theory, it is generally understood that risk assessment will provide information to be used in risk management for better risk control. However, use of annual risk references for evaluation of short-term events illustrates how well-defined and accurate risk assessments might not provide sufficient information to support immediate risk management strategies when the evaluated annual risk is considered acceptable. Short-term risk situations in the water context emphasize how risk assessment should actively consider risk management goals. Traditionally this sector has relied on an acceptable annual risk with the practical obligation of providing safe drinking water all the time. The accidental sewage discharge that impacted Calgary is only one example of how water treatment utilities can be challenged by atypical short-term events. Research has also shown how this problem has been exacerbated by extreme events that can disrupt treatment operations (e.g., after floods or power outages) or suddenly change water quality, impacting treatment (Emelko et al., 2011). A way forward for

managing short-term microbial risks in water might involve the development of other short-term risk references.

In addition to how risk is computed, it is important to consider how the occurrence of rare events is considered in scenario-based QMRA and used to inform decisions. Unlike the point estimate approach used here, probabilistic risk assessments have the advantage of using distributions to determine the full range of risk estimates and their corresponding chances of occurrence. For example, distributions can show that a high level of risk will not happen frequently if it is a result of co-occurrence of several other events that also have a low probability of occurrence. In deterministic risk assessment, care should be taken when extreme values of each variable are used because this can be overly conservative. If a conservative value is taken for all inputs in a model simultaneously, the result may be unrealistic as it is unlikely that all inputs are independently extreme at the same time. The 27 scenarios presented here likely do not have the same probability of occurrence, and this should be considered when making decisions. While probabilistic risk assessment has the advantage of providing this information, it may be impractical to develop advanced models in time-sensitive contexts due to the limited availability of data to describe scenarios and possibly technical expertise to conduct these assessments. Advantages of these modeling approaches should be considered along with the underlying caveats associated with them.

3.4.3 The need for integrated microbial risk management

Analysis of this wastewater spill underscores the importance of knowing microbial concentrations at the intake of a drinking water treatment plant as well as treatment efficiency to evaluate impacts of short-term events. Routine and event-based monitoring or, as a last resort, reported values in the literature can support the estimation of concentrations. Determining treatment efficiency can be more challenging because individual treatment technology efficiencies or regulatory credits may not accurately characterize plant-scale treatment performance when water quality deteriorates or suddenly varies after extreme events (de Brito Cruz et al., 2023 (Chapter 4)). Moreover, one treatment process can affect the efficiency of subsequent processes. For example, water with high concentrations of organic matter can impair coagulation performance, which in turn can affect pathogen removal by filtration (Emelko et al., 2011) and inactivation during disinfection (Mamane, 2008). It is important to be confident of how a treatment system operates at plant scale under challenging conditions to respond to impactful short-term disturbances.

This system perspective is not limited to a drinking water treatment system, which was also highlighted in the *de facto* potable reuse example analyzed herein. *De facto* reuse is a clear example of connection between wastewater and drinking water treatment systems. Wastewater discharge limits are usually established to minimize the impacts of wastewater on aquatic ecosystems or human health due to recreational use of surface water. While these are typical conditions more directly linked to wastewater discharges, unexpected sewage discharges (e.g., wastewater treatment failures, sewer breakage, spills) call into question how water systems are prepared to respond to what is atypical and highlight the overlooked implications of *de facto* reuse. While the spill analyzed here was immediately detected, other spills or leaks could easily be unnoticed for a long time. These issues can become more frequent with aging water infrastructure, but their impacts have not been a focus of drinking water regulations despite broad implementation of *de facto* reuse.

Climate-change-exacerbated disturbances are making these “atypical” events more frequent. Droughts can impact wastewater treatability through occurrence of “high strength” sewage that is less diluted due to less infiltration from storm- or groundwater (Hughes et al., 2021). Additionally, treated wastewater discharges (sufficiently treated or not) will also have a higher proportion in drinking water sources, affecting drinking water treatment. Floods can increase the occurrence of wastewater bypasses and combined sewer overflows that, coupled with increased runoff, will generally result in more deteriorated raw water quality. The compounding effects of such disturbances are frequently overlooked. Hence, a systems perspective is needed not only within a drinking water treatment plant but also to consider the interconnectedness of wastewater and drinking water treatment systems. A One Water approach has been proposed for integrated management of water systems, but its implementation is still incipient in many places (Pokhrel et al., 2022). Possible collaborations between wastewater and drinking water treatment plants involve the development of water safety plans and source water protection strategies. This integration is critical for better management of short-term risk and enhanced resilience of water systems.

3.5 Conclusions

Short-term events have become more common but approaches to analyze their effects on microbial water safety are still limited. This study provides guidance for evaluating impacts of short-term events on drinking water treatment to aid emergency planning and response. The main conclusions are:

- Scenario-based QMRA is a useful tool for the rapid decision-making and prioritization of risk management strategies that are especially needed when short-term events can potentially render treatment insufficient.
- Here, the scenarios that most reasonably described the contamination event indicated that existing treatment was sufficient and provided a safety factor of at least 0.4 log. This type of analysis can help inform operational response decision-making (e.g., interruption of raw water collection, diversion of operations to another treatment plant).
- A deterministic QMRA that considers possible combinations of values (e.g., a factorial design) can be a rapid and simple alternative for modeling many scenarios in contexts in which data availability is limited or time-sensitive decisions are needed.
- Emergency preparedness can be enhanced by defining maximum thresholds for magnitude or duration of a disturbance using the framework developed here. Monitoring data can describe baseline conditions and improve the definition of scenarios, or alternatively, typical values can be used as inputs.
- High-magnitude, short-term events challenge drinking water treatment plants to operate under atypical conditions, which emphasizes the need for integrated management of drinking water and wastewater systems to ensure water supply resilience to such events and protect public health.
- The common annual risk references used to establish health-based treatment goals may not meaningfully support immediate risk management of short-term events. Future research could explore how to connect risk assessment approaches to their use in risk management, which may include the development of new risk reference levels in QMRA.

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Chapter 4

Filter operation effects on plant-scale microbial risk: Opportunities for enhanced treatment performance

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4.1 Summary

Granular media filtration remains a critical treatment process and regulatory requirement for managing pathogenic protozoa in drinking water. It is a dynamic process in which performance inherently varies. While research has focused on characterizing or maximizing (oo)cyst removal in individual filters, the risk implications of combinations of filters moving through different phases of the filter cycle (leading to temporal variation in plant-scale performance) have not been described. Increasing threats from climate-change-exacerbated landscape disturbances leading to more variable source water quality emphasize the need for such evaluations. Here, a modeling framework was developed to investigate the impacts of individual filter performance variation on plant-scale performance. It is shown that improving maximal removal during stable operation does not necessarily improve average performance. The effect of other design and operational strategies like increasing the number of filters or implementing proactive operations (e.g., avoiding breakthrough) are analyzed, thereby providing guidance for increasing treatment resilience.

4.2 Introduction

The paramount objective of drinking water treatment is the prevention of waterborne disease (Hrudey, 2004; Li & Wu, 2019). Drinking-water-associated disease outbreaks continue to occur globally (Widerström et al., 2014; Efstratiou et al., 2017)—the human-infectious protozoa *Cryptosporidium* spp. and *Giardia duodenalis* are of particular concern. In North America, regulatory policies focus on reducing infection risk by requiring drinking water system owners to implement treatment by granular media filtration (or equivalent technology) and disinfection of surface water and groundwater classified as under the direct influence of surface water (U.S. EPA, 1998, 2002, 2006; O. Reg. 170/03, 2003; AEP, 2012). While *Giardia* is the most reported enteric protozoan globally (Adam et al., 2016), *Cryptosporidium* is also ubiquitous in the environment and often a focus for surface water supplies. This is because it is more difficult to remove by filtration and insufficiently treated by traditional oxidant-based disinfection processes such as chlorination (Korich et al., 1990; Li et al., 2001). Virus removal during filtration is also of recent interest because some viruses are resistant to inactivation by disinfection and some removal by filtration is also expected (Nilsen et al., 2019).

Granular media filtration (i.e., physico-chemical filtration with sand and other materials in rapid filters) remains essential in the treatment of *Cryptosporidium* and *Giardia*. All drinking water systems

are vulnerable to increasingly extreme source water quality fluctuations resulting from climate-change-exacerbated landscape disturbances such as heavy precipitation events, wildfires, and hurricanes (IPCC, 2022). While UV irradiation provides effective treatment against the passage of infectious protozoa to treated water supplies, increasingly variable source water quality that can be expected because of climate-change-exacerbated landscape disturbances (Stone et al., 2011) can lead to conditions that potentially challenge coagulation and subsequent (bio)particle removal by filtration or disrupt residuals management (Emelko et al., 2011; Kundert et al., 2014). This, in turn, can reduce the efficacy of downstream UV disinfection (Mamane, 2008).

U.S. and Canadian regulations for treated water quality rely on indirect measures of treatment system performance and provide pathogen removal credits based on indicators of “well-operated” treatment (O. Reg. 170/03, 2003; U.S. EPA, 2006; AEP, 2012). This is due to the impracticality of monitoring pathogen concentrations in treated drinking water (Regli et al., 1991), which requires the analysis of large volumes (on the order of 10^5 – 10^6 L) to confirm drinking water safety and is subject to considerable uncertainty in the case of non-detects and low counts (Emelko et al., 2008; Chik et al., 2018). For example, both the U.S. Environmental Protection Agency (U.S. EPA, 1998, 2002, 2006) and Health Canada (2012, 2019) indicate a 3-log (i.e., thousand-fold or 99.9%) *Giardia* cyst and *Cryptosporidium* oocyst removal credit for conventional filtration systems that meet certain performance criteria. These criteria are mostly related to turbidity: a 95th percentile of combined filter effluent turbidity below 0.3 NTU is required by the suite of the enhanced U.S. surface water treatment rules (U.S. EPA, 1998, 2002, 2006), though a limit of 0.1 NTU for the 95th percentile of filter effluent turbidity is recommended by the Partnership for Safe Water (AWWA, n.d.).

A wide range of oocyst removal by filtration has been reported and used globally in risk assessment (Hijnen & Medema, 2010). Whether derived from bench-, pilot-, or full-scale testing, these values reflect the treatment performance of individual filters. In regulatory policy and quantitative microbial risk assessment, the associated log-removal values for pathogen treatment are generally regarded as a constant within and between similar systems (U.S. EPA, 2006; Health Canada, 2012, 2019; WHO, 2016). Nonetheless, it is recognized that treatment performance can vary depending on the source water quality, treatment technology, and operational conditions, which may include inherent phases of the filter cycle that are characterized by changes in performance (Emelko et al., 2005). Plant-scale treatment performance reflects the collective, concurrent performance of all individual unit treatment processes and can differ from individual treatment-unit-scale performance. Although it has not

previously been discussed, is important to characterize because this plant-scale treatment performance—not individual treatment unit performance—determines ultimate health risk.

Pathogen (and particle) removal by filtration involves physico-chemical attachment of microorganisms to the filter media; this occurs when the pathogens—bioparticles—are sufficiently destabilized through coagulation so that they attach to media grain surfaces or previously deposited particles because of short-range electrostatic attraction forces (O'Melia, 1985; Amirtharajah, 1988; Emelko, 2001; Emelko et al., 2005). Thus, coagulation is essential for maximizing pathogen removal by filtration (Huck et al., 2002; Emelko, 2003; BarkayArbel et al., 2012). Similar levels of protozoa removal by filtration can be achieved when sufficient coagulant is added, regardless of coagulant type (Brown & Emelko, 2009). However, sufficient coagulation does not ensure consistent removal of pathogens while filters are in operation. This is because filtration is a dynamic process with characteristically cyclical operational phases.

A filter cycle comprises at least three distinct phases (ripening, stable operation, and breakthrough), though not all filters are in service or operated through all phases. Ripening is the initial period of effluent quality degradation and subsequent improvement during which backwash remnant particles pass through filters and the removal of pathogens (and particles) from influent streams is dynamic and not maximal (Amirtharajah, 1988; Patania et al., 1995; Huck et al., 2002; Emelko & Huck, 2004). It has been suggested that more than 90% of particles passing through well-operated filters do so during the ripening phase (Amirtharajah, 1988), though operational strategies for minimizing the effects of this phase are also available, like filter-to-waste operation during ripening and modifications in backwashing such as extended terminal subfluidization wash (Amburgey et al., 2003). Stable operation is usually a prolonged period of low and stable effluent turbidity that occurs after ripening; however, the removal efficiency for particles including microorganisms can be more dynamic than for turbidity removal (Darby & Lawler, 1990; Clark et al., 1992; Nilsen et al., 2019). Breakthrough is the final phase of the filter cycle during which filters become overloaded and particles are increasingly likely to detach from or not attach to filter media (Moran et al., 1993). During breakthrough, filter effluent water quality increasingly deteriorates, often rapidly, and it has been associated with order-of-magnitude increases in pathogen passage (Emelko et al., 2003). Because of that, backwashing is necessary to remove deposited materials from the filters and restore performance. Consistently increasing effluent turbidity or particle counts indicate breakthrough and usually trigger backwashing. It can also be initiated due to increasing head loss or scheduled either for convenience or as a precautionary measure. Thus,

characterizing performance variations is important for optimizing filter operation to minimize pathogen passage (Huck et al., 2001).

The passage of microorganisms through individual filters has been shown to vary during both the regular, expected phases of the filter cycle as well as periods of suboptimal operation such as hydraulic surges or sub-optimal coagulation (Patania et al., 1995; Huck et al., 2002; Emelko et al., 2005; Nilsen et al., 2019). Although performance changes throughout the filter cycle are widely reported and recognized, they are usually not reflected in microbial risk assessment or management in drinking water; rather, a constant log-removal credit is commonly used, as discussed above. In this context, Brown (2004) developed a model to assess the risk of *Cryptosporidium* passage through filtration systems in different operational conditions. Nilsen (2020) suggested that pathogen concentration variations caused by variable filtration performance are unlikely to affect risk estimates relative to a model that uses an equivalent mean concentration. Focusing on viruses and bacteria, that analysis described individual filter performance, like most filtration performance studies. However, full-scale water treatment almost always includes multiple filters operated in parallel with staggered backwashes. The dynamic treatment performance that filtration studies reflect has generally not been integrated to describe the risk implications of combinations of filters passing through different phases of the filter cycle and resulting variation in plant-scale performance. Controlling microbial risks through drinking water in public water systems depends on the resulting treatment performance of several filters being operated at the same time and cannot be limited to the analysis of a single filter. Therefore, an understanding of plant-scale filtration performance and how operational conditions contribute to it is needed to better support microbial risk management.

The goal of this study is to provide a modeling framework to evaluate the effects of filtration design and operational conditions on plant-scale filtration performance. Specifically, a simple mathematical model is used to (1) illustrate how temporal variability in oocyst removal performance of a granular media filter throughout a filter cycle affects the combined plant-scale performance of filters operated in parallel, both instantaneously and on average, and (2) evaluate the predicted effects on plant-scale performance of alternative design and/or operational strategies (e.g., changes in number of filters, backwashing schedules, durations and log reductions during individual filter phases). Previously reported, detailed data that describe oocyst removal by filtration during various phases of the filter cycle are used to demonstrate how pathogen removal performance of plant-scale filtration processes—as opposed to individual filters—can be assessed. While the quantitative results are system-specific, they

nonetheless underscore that focusing exclusively on individual unit operation (e.g., filter) performance may preclude the identification of performance optimization and risk management opportunities and/or barriers.

4.3 Methods

4.3.1 Filter cycle variability of pathogen removal in granular media filtration

The variability of pathogen removal during a filter cycle was represented by a step function reflecting ripening, stable operation, early breakthrough, late breakthrough, and backwashing. Breakthrough is divided into two phases to reflect the progressive deterioration of performance. Although a step function omits variations in performance within phases and features abrupt transitions in performance between phases, it is more representative of the cyclical pattern of filter performance than the use of a single log-reduction value and enables simple evaluation of the effects of various performance changes known to regularly (e.g., ripening) or occasionally (e.g., suboptimal coagulation) occur during the filter cycle. Table 4.1 presents the assumed duration and log reduction for each phase of the filter cycle. These values were drawn from pilot experiments assessing *Cryptosporidium parvum* oocyst removal by filtration at the Britannia Water Treatment Plant in Ottawa, Canada (Huck et al., 2001). That study was illustratively used herein due to the availability of extensive performance data during ripening, stable operation, breakthrough, and other operational conditions, which are not available elsewhere. As the goal of this work is to investigate the effect of filter cycle variability on plant-scale filtration performance, the relative difference among log reductions and durations during the various phases of a filter cycle is more important than the values themselves. Data for other pathogens and treatment performance values based on site-specific information, or hypothetical scenarios, may be used to support planning and risk management.

Table 4.1: Filter cycle details

Filter cycle phase	Duration (h)	Log-reduction
Ripening	0.5	4.7
Stable operation	60	5.3
Early breakthrough	1	2.8
Late breakthrough	0.5	1.2
Backwash	0.5	-

The raw data from all ripening and stable operation experiments conducted at the Ottawa pilot plant were used to calculate the average performance (expressed as an effective log reduction) corresponding to each of these two phases. It should be noted that such high stable operation log reductions can only be attained in certain water types with optimized coagulation and operation of the filters. Breakthrough conditions were defined by increasing filter effluent turbidity beyond 0.2 NTU, with early breakthrough remaining below 0.3 NTU (Huck et al., 2001; Emelko et al., 2003). To represent the wide range of performance that could be achieved as stable operation gives way to breakthrough, one experiment was selected from each set of tests at early and late breakthrough; specifically, the ones leading to the greatest change in breakthrough performance were selected (i.e., the highest removal during early breakthrough and the lowest removal during late breakthrough). The phase durations for ripening and stable operation were similar to values reported in Huck et al. (2001). Here, the relatively short durations of the breakthrough and backwashing periods are hypothetical. It is important to note that the effects of ripening and breakthrough are often limited or avoided in practice with filter-to-waste operation and timely backwashing, respectively; however, they are included here to illustrate their effects on system performance if such practices are not followed. Because turbidity is monitored to assist these operational practices, deteriorated effluent turbidity may be avoided; however, Nilsen et al. (2019) showed diminished removal of viruses and bacteria persisting beyond the ripening phase with respect to turbidity as well as deteriorating removal commencing prior to turbidity breakthrough. Although the study did not assess (oo)cyst removal, it suggests that excellent control of filtration with respect to effluent turbidity may not be sufficient to ensure high and stable pathogen removal throughout the period that the filter is in service. Emelko et al. (2003) showed that oocyst removal can deteriorate before turbidity breakthrough. Accordingly, the analyses performed here may be emblematic of the effects of reduced pathogen removal at the bounds of stable operation for systems that employ filter-to-waste operation during ripening and that commence backwashing promptly following the arrival of turbidity breakthrough.

4.3.2 Model for analysis of several filters operated in parallel

The pathogen removal performance of a system of parallel filters was evaluated using the effective log-reduction metric, which expresses average treatment performance as a log reduction and emphasizes that log-reduction values themselves should not be averaged because doing so overstates average treatment performance (Schmidt et al., 2020). The model considers n similar filters running in parallel,

receiving settled water with a constant influent pathogen concentration and with a combined flow that is evenly divided among the operating filters. The presumption of evenly divided flow simplifies the model by averting the need for a volume-weighted approach. However, it presumes an increase in flow through operating filters during backwashing of one or more filters to maintain a constant total filtered water production and does not reflect accumulating head loss through a filter cycle. Appendix C Section C.1 provides a comparison between this model and one considering no redistribution of flow during backwashing (i.e., with constant filter flow and reduced total volume of produced water during a backwash). The indices i and t represent individual filters and time, respectively, and the variable $Op_{i,t}$ indicates if a filter is in service ($Op_{i,t} = 1$) or is being backwashed ($Op_{i,t} = 0$). The filters can be in differing phases of their respective filter cycles at a certain point in time; therefore they achieve different instantaneous log reductions of pathogens ($LR_{i,t}$) when they are not being backwashed. The instantaneous combined performance of the filters in operation is represented by the combined log-reduction $LR_{combined,t}$, according to Equation 4.1.

$$LR_{combined,t} = -\log_{10} \left(\frac{\sum_{i=1}^n 10^{-LR_{i,t} \times Op_{i,t}}}{\sum_{i=1}^n Op_{i,t}} \right) \quad (4.1)$$

To assess the overall filtration performance, the combined performance of all filters over a full filter cycle is averaged. This metric is presented in Equation 4.2, which considers time discretized in T one-second intervals.

$$LR_{overall} = -\log_{10} \left(\frac{1}{T} \sum_{t=1}^T 10^{-LR_{combined,t}} \right) \quad (4.2)$$

Given n filters, a defined pattern of filter performance throughout a filter cycle (phase durations and log reductions), and the initial condition of each filter (e.g., time since completion of backwashing) as inputs, the analysis presented here yields the combined log-reduction pattern over time and the overall log reduction to evaluate system performance in a particular scenario. Figure 4.1 illustrates a system with n filters being operated in parallel over time and the representation of combined and overall log reduction in this system.

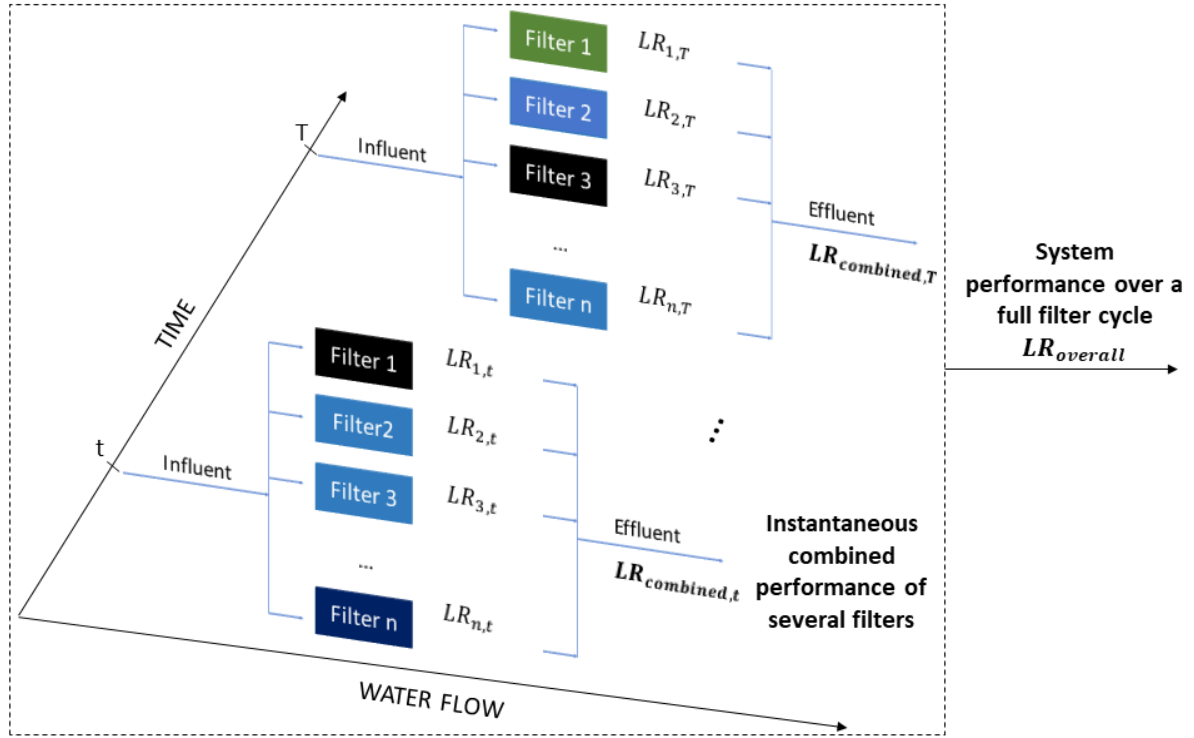


Figure 4.1: Combined and overall log reduction in a system with n filters operated in parallel. The different colors represent the different phases of a filter cycle (e.g., black = backwashing, light blue = stable operation, dark blue = ripening, green = late breakthrough)

To evaluate and compare the proportion of pathogens passing through the filter among the different phases of an individual filter cycle, the percent passage¹ (PP) is calculated, as expressed in Equation 4.3. LR_p and D_p represent, respectively, the log reduction and the duration associated with phase p of the filter cycle (of m phases in service). The influent concentration of the pathogen is assumed to be constant over time so that only the effect of treatment performance is considered. The percent passage metric, by integrating both the log reduction and the duration of the phases of a filter cycle, is useful to evaluate how the different phases contribute to total microbial risk. Ultimately, it can indicate which phase contributes most to pathogens reaching the filter effluent (thus posing a potential risk) and, conversely, which phases have negligible contribution to risk.

$$PP_p = \frac{10^{-LR_p \times D_p}}{\sum_{p=1}^m 10^{-LR_p \times D_p}} \times 100\% \quad (4.3)$$

¹ fraction of all pathogens passing through filter during a full filter cycle attributable to a particular phase

4.3.3 Application of parameter sweep method to evaluate impacts of changing model inputs

A simple parameter sweep approach defines the set of scenarios presented in this study. In it, only one parameter is changed at a time relative to a base case to explore the effect of each design or operational practice individually. Although the alternative scenarios are not comprehensive, they illustrate the sensitivity of the model to each one of these parameters.

In this work, the “base case” uses the filter cycle information as described in Table 4.1 with four parallel filters and evenly staggered backwashes. From this base case, eight sets of scenarios were explored to evaluate the effect of varying operational contexts or specific model inputs. Although some of these parameters are fixed with plant design and cannot be operationally varied, these analyses underscore the importance of detailed knowledge of system characteristics to improve treatment. Instead of representing a common or a proper way of operating a plant, the base case includes all phases of a filter cycle and a wide range of log reduction values among them to better investigate the model sensitivity to each individual change. The values of the parameters in each scenario are summarized in Table 4.2 and the code used in this paper is presented in Appendix C Section C.2. The eight analyses are:

1. **Number of filters operated in parallel.** To represent a wide range of the number of filters that could be operated in water treatment plants of different capacities, five scenarios were analyzed with 2, 4, 8, 20, and 50 filters operated in parallel. The minimum number of filters is 2 to allow operation during backwashing and 50 was chosen to represent plants in big cities. The biggest water treatment plant in the world in Rio de Janeiro has 132 filters (CEDAE, n.d.).
2. **Duration of maximum pathogen removal performance (stable operation).** The duration of stable operation is an important factor in filtration optimization as lengthy stable operation simplifies operations by reducing the frequency of backwashing, which ultimately saves energy costs. The length of a typical filter run is predominantly comprised of stable operation, whose duration depends on filter design and operation, and water quality (e.g., influent turbidity). Here, five scenarios with 15, 30, 60, 90, and 120 h of stable operation, followed by breakthrough were analyzed.

3. **Magnitude of maximum pathogen removal performance (stable operation).** From a treatment perspective, filter performance is frequently associated with a high pathogen removal capacity. Accordingly, research has focused on developing technologies or applying aids to increase pathogen removal by filtration during stable operation (Lin et al., 2013). This analysis explored the impact of different values of log reduction during stable operation (4.7, 5.0, 5.3, 6.0, and 7.0 log) upon system performance. The lowest value is equal to that of ripening in the base case to avoid a removal during stable operation lower than the one during ripening, and 5.3 log represents the base case.
4. **Duration of minimum pathogen removal performance (early and late breakthrough).** An operational strategy to limit pathogen passage is reducing the occurrence of breakthrough with earlier backwashing, as soon as stable operation ends and the limit for head loss, effluent turbidity, or operating time is reached (Kline, 2007). The effect of this strategy was investigated considering five pairs of early and late breakthrough duration (1 h, 0.5 h; 1 h, 0.25 h; 1 h, 0 h; 0.5 h, 0 h; 0 h, 0 h) that successively trim operation in late breakthrough and then early breakthrough conditions.
5. **Magnitude of minimum pathogen removal performance (late breakthrough).** Breakthrough is the phase of the filter cycle most vulnerable to pathogen passage; thus, it is important to know how much treatment can deteriorate during this critical period and how sensitive overall system performance can be to breakthrough. Although in practice early and late breakthrough performance would be linked, this analysis considered only the effect of late breakthrough because this is the phase with minimum pathogen log reduction during the filter cycle. Five scenarios (0, 0.6, 1.2, 2.0, and 2.8 log) were considered. A log-removal of zero presumes equality of attachment and detachment while 2.8 log is the log-reduction value assigned to early breakthrough in the base case.
6. **Backwash staggering.** Most of the available discussion related to filtration performance focuses on methods to ensure effective backwashing (Amburgey & Amirtharajah, 2005; Slavik et al., 2013). In contrast, the issue of how different backwashing schedules affect the whole system's performance is evaluated herein. Five alternative schedules are used to analyze the impact of overlapping periods of backwashing and breakthrough in different filters: case *a* (evenly staggered backwashes), case *b* (a random schedule with no backwash

overlapping), case *c* (backwashes separated by 10 h), case *d* (backwashes separated by 0.5 h), and case *e* (backwashes separated by 0.25 h).

7. **Chemical pre-treatment/coagulation.** The degree of sensitivity of pathogen removal performance in filtration to coagulation varies substantially among systems. It depends on factors such as the coagulation mechanism, type of coagulant used, water quality, and plant design. Sub-optimal coagulation can also have different meanings (under- or overdosing of coagulant) and effects on filtration depending on how long the condition persists. Here, three scenarios were tested: optimal coagulation (i.e., the degree of coagulation leading to the 5.3 log reduction, in which filter effluent turbidities were below 0.1 NTU) in the base case, and two other sub-optimal coagulation scenarios. Two experiments were selected to represent the sub-optimal coagulation scenarios according to data reported by Huck et al. (2001). In sub-optimal coagulation cases I and II, the coagulant doses were reduced by 52% and 47% from the optimum doses, leading to 1.4 and 3.1 log reduction during stable operation, respectively. Concerning the effect of coagulation on performance, only data during stable operation are available. In the absence of data to evaluate the impact of sub-optimal coagulation on the other phases of the filter cycle, ripening, and early breakthrough log reductions were changed as needed so that they were no higher than the sub-optimal coagulation performance during stable operation.
8. **Filter-to-waste operation.** Filter-to-waste operation during ripening is a common practice for avoiding subsequent treatment and distribution of water with deteriorated post-filtration quality (Soucie & Sheen, 2007). In this analysis, the total volume of water filtered during ripening would be discharged to waste. This was compared against four other scenarios without filter-to-waste operation including the base case and lower values of log reduction during ripening (4.7, 3.3, 2.0, and 1.2 log) to show the relative benefit of filter-to-waste operation in each case. These values varied from the removal during ripening (4.7 log) to the removal during late breakthrough (1.2 log) in the base case.

Table 4.2: Summary of parameter values used in each analysis

Model Input	Base Case	Alternative values tested ^{4a}
Number of Filters	4	(1) 2, 4, 8, 20 and 50 filters
Ripening	0.5 h at 4.7 log	(7) 0.5 h at 1.4, 3.1, and 4.7 log (8) 0.5 h of filter-to-waste, 4.7, 3.3, 2.0, and 1.2-log
Stable Operation	60 h at 5.3 log	(2) 15, 30, 60, 90, and 120 h at 5.3 log (3) 60 h at 4.7, 5.0, 5.3, 6.0, and 7.0 log (7) 60 h at 1.4, 3.1, and 5.3 log
Breakthrough	Early: 1 h at 2.8 log Late: 0.5 h at 1.2 log	(4) Early: 1, 1, 1, 0.5, and 0 h at 2.8 log Late: 0.5, 0.25, 0, 0, and 0 h at 1.2 log (5) Late: 0.5 h at 0, 0.6, 1.2, 2.0, and 2.8 log (7) Early: 1 h at 1.4, 2.8 and 2.8 log
Backwash	0.5 h, evenly spaced	(6) Alternative staggering: random, spaced by 10 h, spaced by 0.5 h, and spaced by 0.25 h

^{4a} Alternative values tested in analyses (1 to 8) are shown (e.g., only the number of filters varies relative to the base case in analysis 1).

Notably, the performance of a filtration system can also be impacted by other factors like filter design (Swertfeger et al., 1999; Papineau et al., 2013) and hydraulics (Han et al., 2009; Edzwald, 2011). These effects were not considered in the present study because changes in performance vary on a case-by-case basis.

4.4 Results and Discussion

Figure 4.2 presents the combined log reduction of pathogens at plant scale (blue step function) and the overall log reduction averaging the combined performance over a full filter cycle (dark green line) for the base case of four parallel filters with evenly staggered backwashes. As a result of the step function assumed for each filter's log-reduction pattern throughout the filter cycle, the combined log reduction also follows a step function with each step corresponding to a transition in the number of filters in each of the various phases of the filter cycle. In this figure, the combined log reduction starts at 5.1 when Filter 1 starts the ripening phase and Filters 2, 3, and 4 are in stable operation (Point A). After 0.5 h (Point B), ripening ends and Filter 1 joins the other three filters in stable operation, making the combined log reduction 5.3. All filters remain in stable operation for another 13.125 h until stable

operation ends for Filter 4 and the combined log reduction decreases to 3.4 (Point C) with three filters in stable operation and Filter 4 in the early breakthrough phase. One hour later, Filter 4 moves to the late breakthrough phase while the other filters are still in stable operation, resulting in a combined log reduction of 1.8 (Point D). After 0.5 h at this level, when Filter 4 gets backwashed, all the other filters are in stable operation, and the combined log reduction returns to 5.3 again (Point E). When the backwash ends, the described process repeats with Filters 1, 2, and 3 in stable operation and Filter 4 at the beginning of ripening.

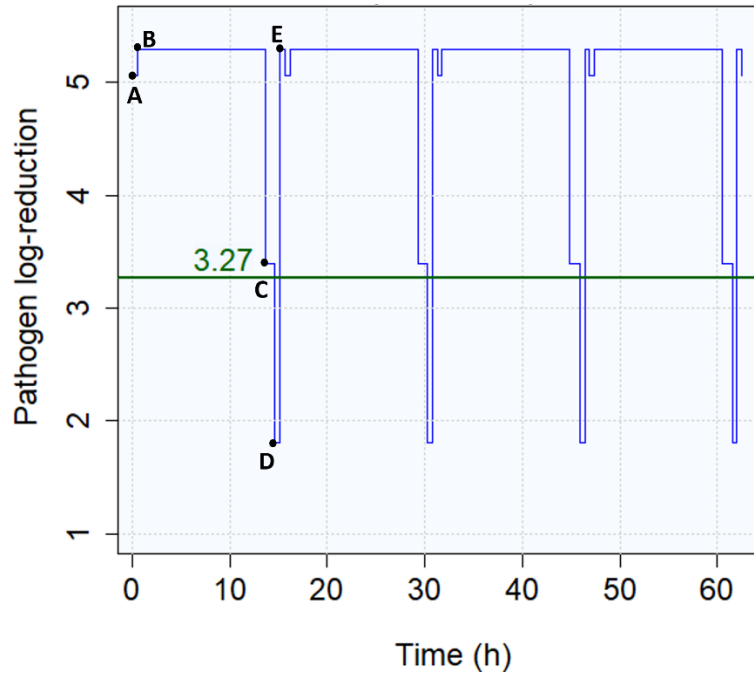


Figure 4.2: Temporal variation of combined log reduction of pathogens over one full filter cycle with four filters and evenly staggered backwashes. The blue lines represent temporal variation in the combined log reduction and the dark green line (and corresponding value) indicates overall plant-scale log reduction of pathogens. Key transitions associated with the dynamic periods experienced by the individual filters are indicated. At (A), Filter 1 starts ripening and Filters 2, 3 and 4 remain in stable operation. At (B), ripening ends and all filters are in stable operation. At (C), early breakthrough begins in Filter 4. At (D), late breakthrough begins in Filter 4. At (E), Filter 4 is backwashed and subsequently ripens. This pattern repeats as successive filters undergo breakthrough, backwashing, and ripening for each of the filters

The overall log-reduction value represents the pathogen removal performance of the entire system of filters (i.e., plant-scale treatment performance) over the period spanning one full cycle of each filter, in the absence of any performance disruptions. Notably, overall log reduction is substantially impacted by operational phases other than stable operation. In this case, these phases represent only 3.2% (2 of

62 h) of the filter cycle and are still responsible for reducing performance from the 5.3 log achieved when all filters are in periods of stable operation (and presumed maximum performance) to a combined average performance of 3.27 log at plant-scale. This simple case study underscores that low values often drive average performance when it is evaluated on a logarithmic scale, as is commonly done in describing the treatment of waterborne pathogens.

4.4.1 Number of filters operated in parallel

The treatment performance impact of splitting influent flow between more or fewer filters operated in parallel is illustrated in Figure 4.3. The maximum and minimum values differ depending on the number of filters at each phase of the filter cycle. For example, with 50 filters it is not possible to have them all in stable operation with evenly staggered backwashes, thus 5.3 log pathogen removal is never achieved at plant-scale, even though individual filters can achieve this level of treatment performance. Although operating fewer filters enables higher levels of plant-scale pathogen removal during some points of the filter cycle when filters are concurrently in stable operation, it also notably enables lower levels of performance at other periods of the filter cycle, as can be seen by the minimum values of the blue lines in each panel of Figure 4.3. The minimum level of pathogen removal achieved at plant-scale increases with increased numbers of filters because having more filters in concurrent operation with better performance dilutes (or averages out) the effect of one or more poorly performing filters. Hence, changing the number of filters does not impact overall plant-scale filtration performance (3.27 in all panels); however, increasing the number of filters reduces performance variability (variability decreases from left to right among the panels in Figure 4.3). This type of analysis may be useful for operations planning to increase treatment resilience because it enables the evaluation of trade-offs between maximum and minimum performance during brief periods of the filter cycle. Further work is needed to evaluate the implications of brief plant-scale performance variations on health risk.

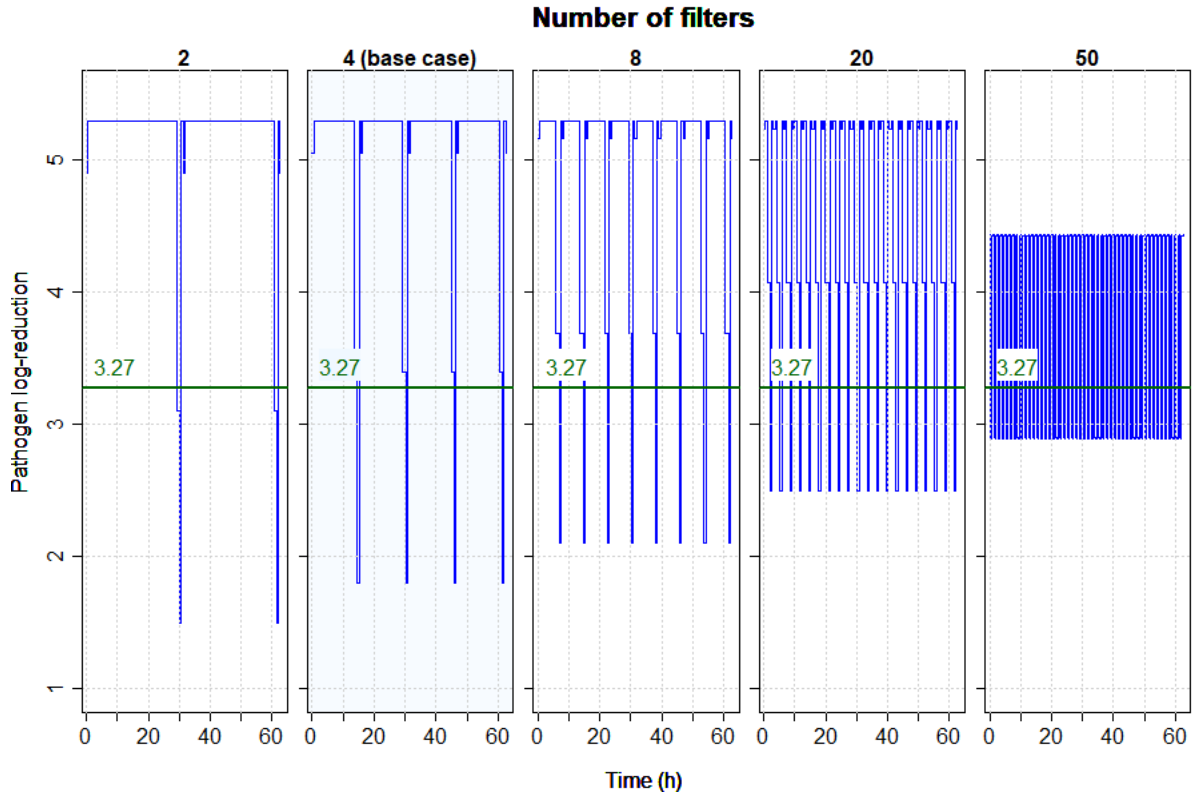


Figure 4.3: Temporal variation of combined log reduction of pathogens over one full filter cycle with varying numbers of filters and evenly staggered backwashes (analysis 1). The blue lines represent temporal variation in the combined log reduction and the dark green lines (and corresponding values) indicate overall plant-scale log reduction of pathogens

4.4.2 Duration of maximum pathogen removal performance (stable operation)

Figure 4.4 illustrates how the length of the stable operation period affects plant-scale performance, presuming the level of removal during stable operation is maintained. As expected, a longer duration of stable operation improves overall plant-scale pathogen removal (represented by the increasing green values from left to right among the panels in Figure 4.4). This is because longer periods of stable operation result in larger proportions of the filter cycle during which higher pathogen removals are achieved. In this example, the proportion of time in which combined log reduction is greater than three, which is a common minimum threshold for protozoan removal established by guidelines (U.S. EPA, 2006; Health Canada, 2019), was 88.6%, 93.8%, 96.8%, 97.8% and 98.4% for 15, 30, 60, 90, and 120 h of stable operation, respectively. Hence, filter design and operation leading to a longer stable operation phase result in increased overall plant-scale treatment performance, therefore reducing the

probability of microbial contaminant passage to treated water. The length of a typical filter run should be predominantly composed of stable operation and is reflected in many performance assessment metrics such as unit filter run volume (AWWA, 2011). Periods of deteriorated source water quality tend to reduce the length of stable operation and can reduce filtration performance because of increased solids loading to filters (Polyakov, 2009), especially when chemical pre-treatment (e.g., residuals management in clarifiers) is strained (Kundert et al., 2014).

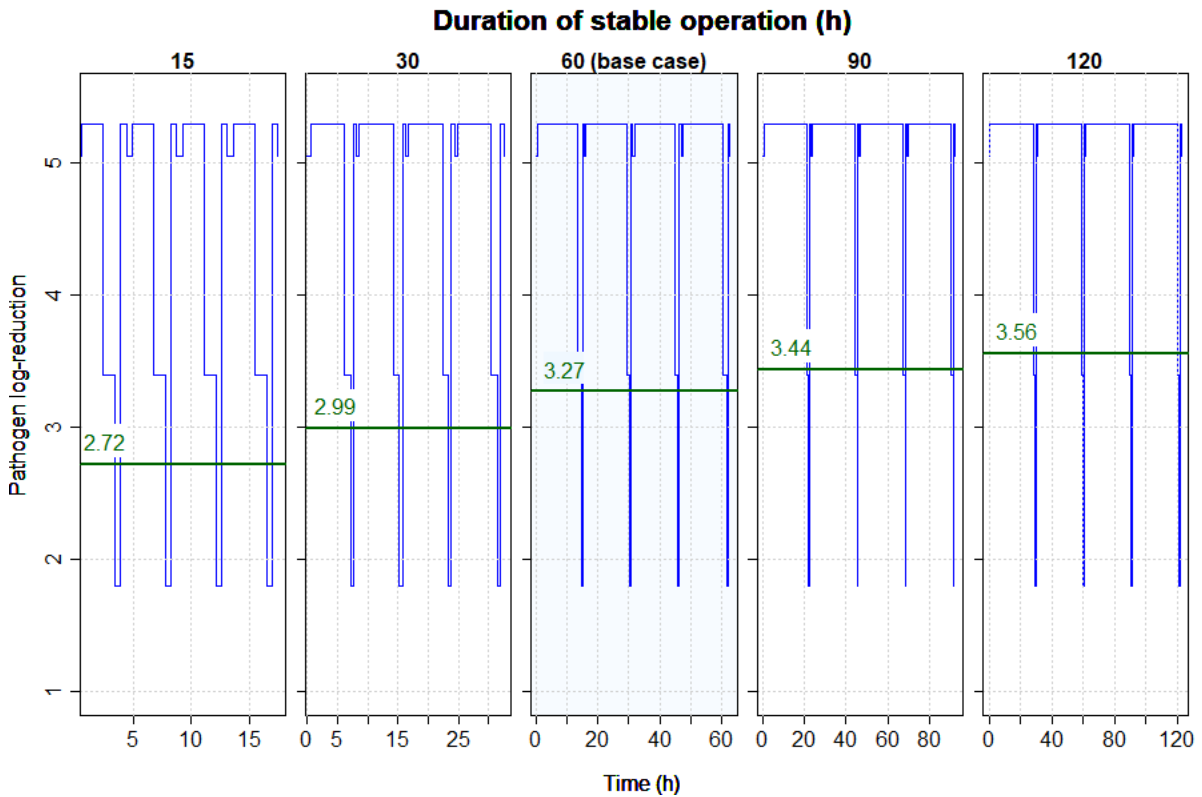


Figure 4.4: Temporal variation of combined log reduction of pathogens over one full filter cycle with four filters, evenly staggered backwashes, and varying durations of the stable operation phase (analysis 2). The blue lines represent temporal variation in the combined log reduction and the dark green lines (and corresponding values) indicate overall plant-scale log reduction of pathogens

Extending the length of stable operation while avoiding breakthrough, which is not represented in this analysis, will lead to the same positive impact on plant-scale performance because stable operation would have a greater contribution to the overall log reduction. This result is particularly relevant for systems treating high-quality source water because filters are often backwashed more frequently than necessary under the belief that more frequent backwashing is better for ensuring treated water quality and managing microbial risks.

4.4.3 Magnitude of maximum pathogen removal performance (stable operation)

The analysis presented in Figure 4.5 demonstrates the impact of increased maximum pathogen removal during stable operation on combined performance. Higher maximum pathogen removals lead to better combined performance when all operating filters are in stable operation but do not change the periods of time at which combined performance is lowest, as indicated by the increasing maximum values and consistent minimum values, respectively, of the blue lines from left to right among the Figure 4.5 panels. For example, the percentage of time with pathogen removal lower than 3 log was equal to 3.2% in all cases tested. As discussed above, the lowest pathogen removal values can substantially impact overall filtration performance; thus, overall performance does not change substantially even when maximum pathogen removal is increased by orders of magnitude. Comparing the second and the last scenario in Figure 4.5, overall pathogen removal improved only trivially (from 3.27 to 3.28) when maximum pathogen removal increased by more than 2 log. This is because the maximum pathogen removal becomes trivially different from 100% (e.g., 99.99% at 4 log and 99.999% at 5 log) relative to the minimum log reduction (e.g., 98.42% at 1.8 log). In the base case, approximately 0.9% of the pathogens passing through a filter during a full cycle do so during stable operation, so reducing this passage by improving performance during stable operation necessarily has limited effect on the overall performance.

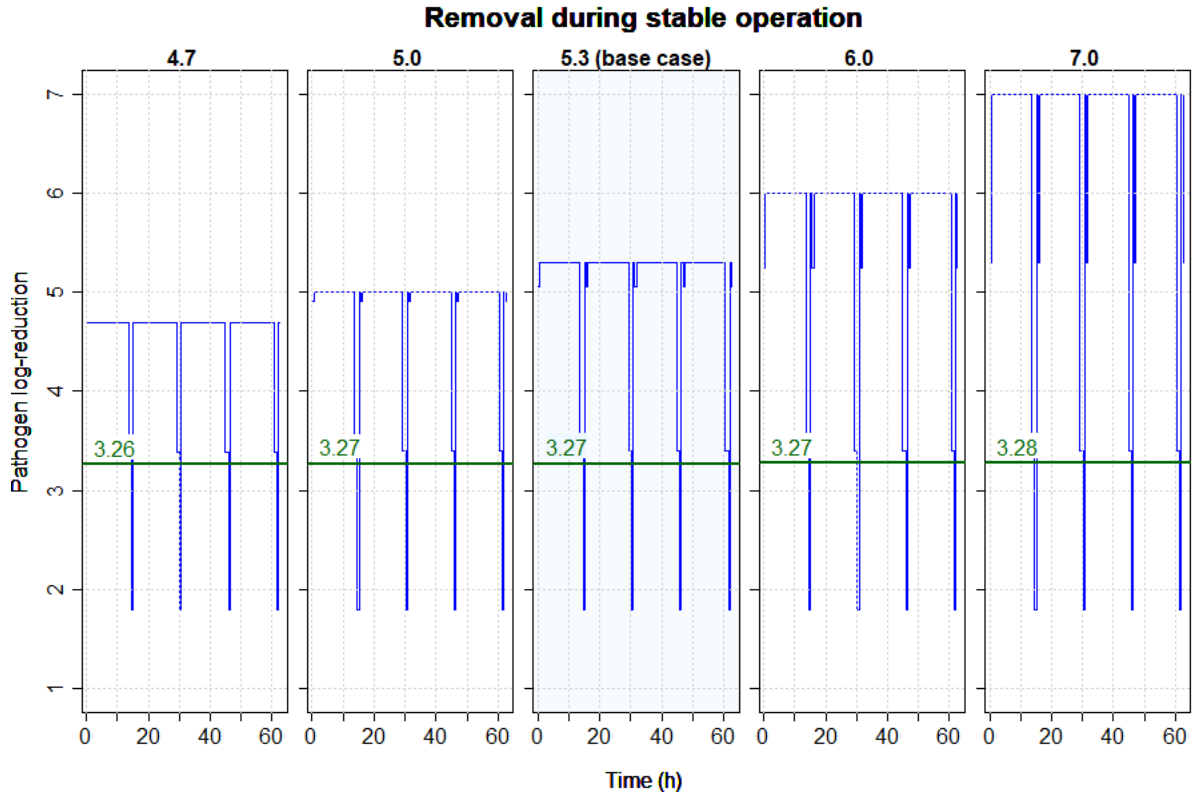


Figure 4.5: Temporal variation of combined log reduction of pathogens over one full filter cycle with four filters, evenly staggered backwashes, and varying removals during stable operation (analysis 3). The blue lines represent temporal variation in the combined log reduction and the dark green lines (and corresponding values) indicate overall plant-scale log reduction of pathogens

Focusing only on stable operation, efforts to improve filtration performance can focus on either improving the level of pathogen removal achieved or increasing the duration of the stable operation period. However, increasing the pathogen removal performance of individual filters during stable operation has a negligible effect on overall plant-scale performance if the percentage of pathogens passing during stable operation is minimal compared to the other phases of a filter cycle. This result can be counterintuitive because of the natural tendency to consider performance data on linear rather than logarithmic scales, especially if the focus is put on the long durations of stable operation compared to the other phases of the filter cycle. Comparing the results in Figure 4.5 to the previous analysis (Figure 4.4) suggests that efforts to improve plant-scale pathogen removal performance may sometimes be more impactful when directed toward increasing the duration of stable operation rather than striving to achieve inconsequential improvements in maximum pathogen removal by individual filters. Therefore, if water providers seek to increase overall treatment performance, pathogen removal

performance during stable operation may not be the most important parameter to focus on, especially if performance is substantially lower during other operational periods—end-of-run breakthrough is of particular concern (Emelko et al., 2003, 2005).

4.4.4 Duration of minimum pathogen removal performance (early and late breakthrough)

The phases of the filter cycle during which performance is the poorest can substantially impact overall plant-scale filtration performance, as discussed above. Figure 4.6 demonstrates how decreasing the duration of the breakthrough phase improves the average performance of the system (as illustrated by the increasing green values from left to right among the panels). Whereas substantial increases in the duration of stable operation were needed to get better overall filtration performance (Figure 4.4), relatively small reductions in the duration of periods with minimum performance (i.e., breakthrough, here) have a substantial effect. This is because truncating the periods of low removal allows them to have less influence on the temporal average performance. Here, eliminating 0.5 h of the worst performance from each filter cycle (third scenario) improved overall pathogen removal performance more than an additional 60 h of stable operation would improve it. The difference in overall removal between the base case and the case with breakthrough eliminated is 2 logs, as indicated by the green values in the first and last panels of Figure 4.6. In the base case, 94% of the pathogen passage would occur during late breakthrough, so eliminating that phase by backwashing sooner is highly impactful. Thus, minimization or elimination of the phases of the filter cycle during which performance is the poorest can be a significant operational strategy for increasing overall plant-scale pathogen removal by filtration and increasing public health protection. The importance of these operational strategies is indicated by the continued development of tools such as online monitoring equipment that detects bacteria breakthrough to signal microbiological risk (Fujioka et al., 2019).

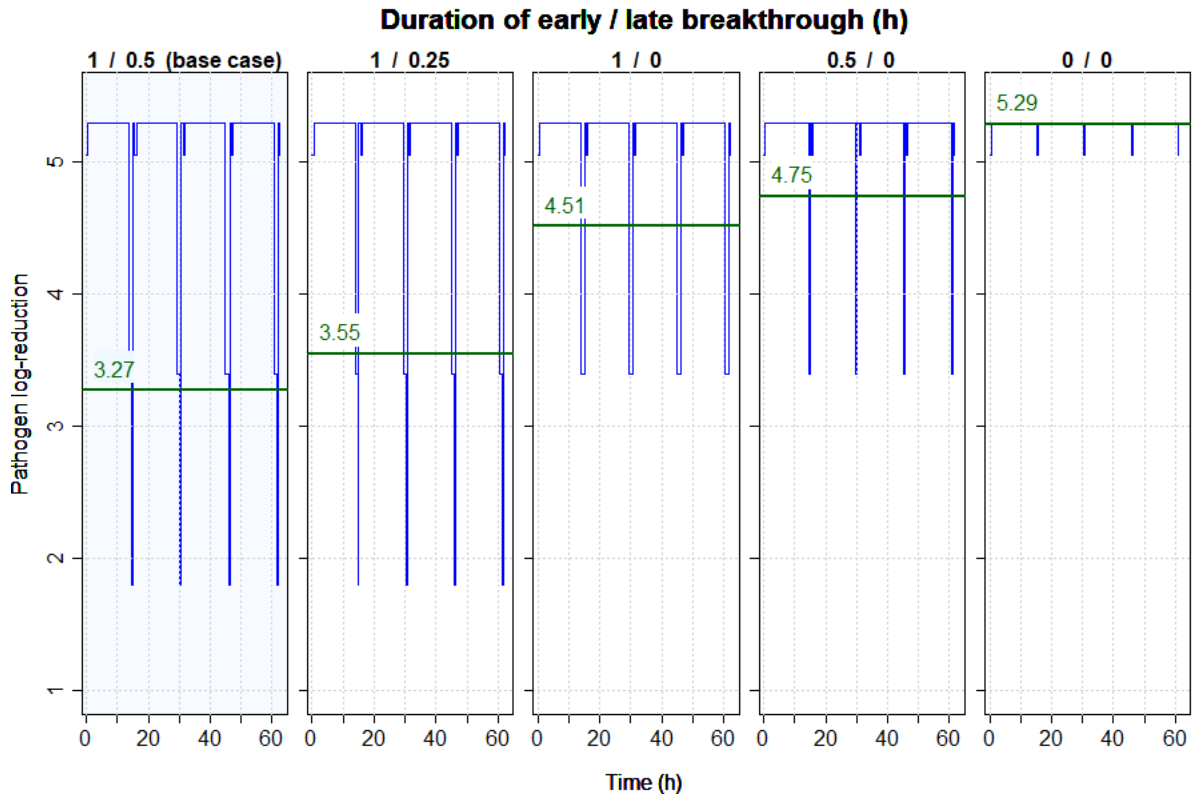


Figure 4.6: Temporal variation of combined log reduction of pathogens over one full filter cycle with four filters, evenly staggered backwashes, and varying durations of early and late breakthrough (analysis 4). The blue lines represent temporal variation in the combined log reduction and the dark green lines (and corresponding values) indicate overall plant-scale log reduction of pathogens

This analysis emphasizes the value of monitoring individual filter performance to avoid breakthrough (Huck et al., 2002). Limiting maximum individual filter effluent turbidity can improve overall plant-scale treatment performance by reacting to individual filter breakthrough while filter effluent blending still leads to acceptable combined filter effluent turbidity. The magnitude of this impact would require system-specific data for quantification. Nonetheless, given that the onset of turbidity and pathogen breakthrough can occur quickly at the end of a filter cycle (Emelko et al., 2003), it is important to eliminate or decrease the duration of breakthrough, thereby limiting individual filter effluent turbidities at the end of the filter cycle. Operational strategies like proactive backwashing can substantially enhance overall plant-scale filtration performance. Optimizing the timing of backwashing to eliminate periods of pathogen breakthrough while realizing the full benefits of stable operation by not backwashing too soon is an operational challenge.

4.4.5 Magnitude of minimum pathogen removal performance (late breakthrough)

Higher minimum pathogen removal during the filter cycle (i.e., during late breakthrough) led to substantial increases in overall plant-scale filtration performance, as shown by the increasing green values from left to right among the panels in Figure 4.7. In contrast to the negligible effects of increasing pathogen removal during stable operation (Figure 4.5), this effect was similar to that of decreasing the duration of phases in the filter cycle with minimum pathogen removal (Figure 4.6); overall pathogen removal performance increased as the minimum pathogen removal during the individual filter cycles increased. This emphasizes the importance of resilience in water treatment: performance is not only governed by how well a system can perform and how long it can perform well—it is also important to understand how much treatment deterioration occurs and can be tolerated during sub-optimal conditions. For example, it has been shown that short periods of failure and/or interruption in treatment can have a substantial impact on health risks and may not be counterbalanced by periods of good performance (Hunter et al., 2009).

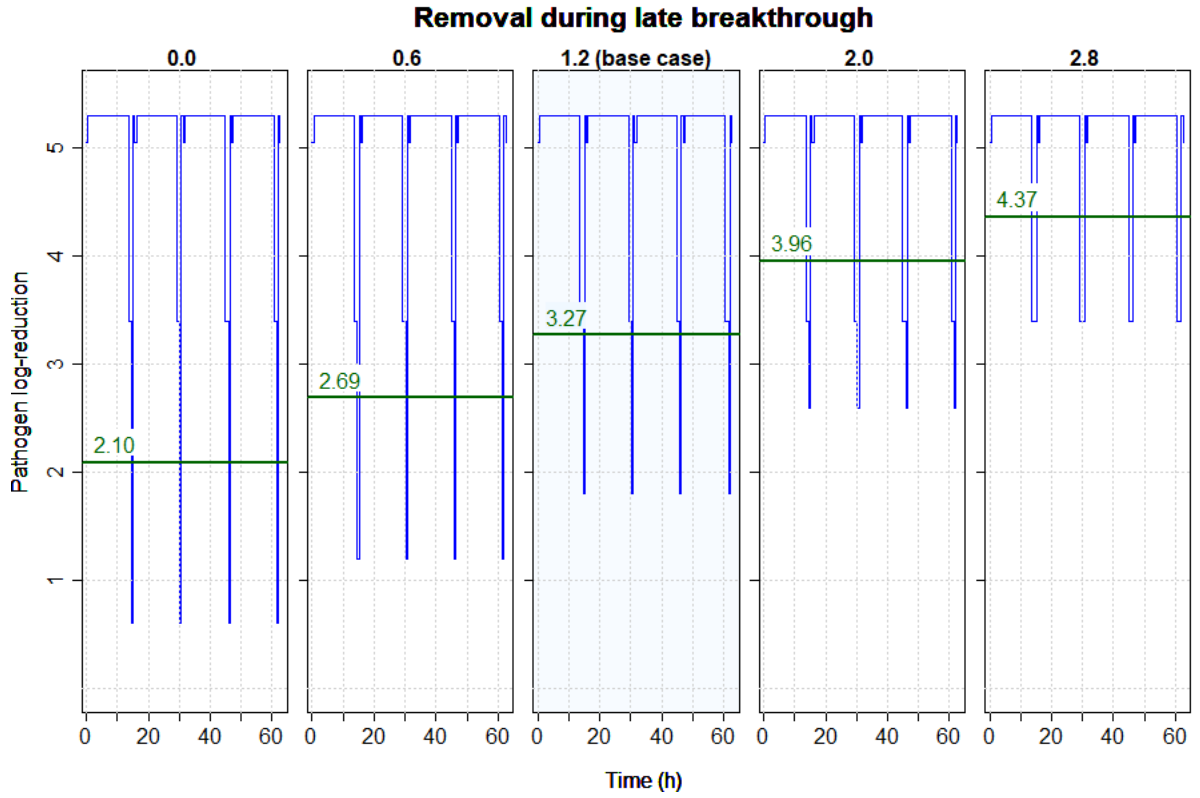


Figure 4.7: Temporal variation of combined log reduction of pathogens over one full filter cycle with four filters, evenly staggered backwashes, and varying removals during late breakthrough (analysis 5). The blue lines represent temporal variation in the combined log reduction and the dark green lines (and corresponding values) indicate overall plant-scale log reduction of pathogens

4.4.6 Backwash staggering

The effect of backwash staggering is illustrated in Figure 4.8. Case *a* represents the base case where the backwashes of the four filters are evenly spaced. In all other cases, the backwashes are not evenly spaced. In case *b*, backwash staggering was randomized. In the remaining cases, backwashes are spaced by 10, 0.5, and 0.25 h (cases *c*, *d*, and *e*, respectively). By reducing the time between backwashes, the phases of the filter cycle with the poorest pathogen removal performance increasingly overlap. In case *c* no backwashes or breakthrough periods overlap, in case *d*, backwashes do not overlap but up to three filters may be in breakthrough at one time (two in early breakthrough, one in late breakthrough), and in case *e* up to two filters can be offline for backwashing at a time and it is possible for all four filters to be in breakthrough at the same time (two in early breakthrough, two in late breakthrough).

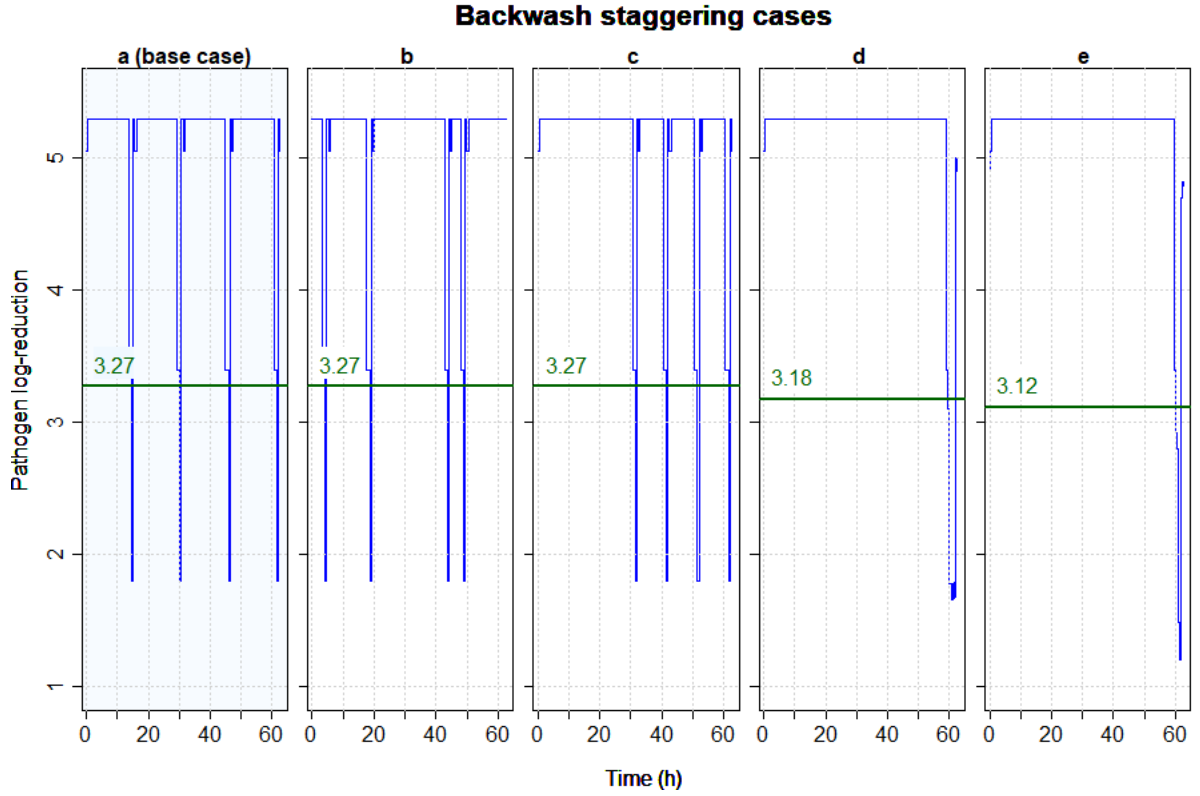


Figure 4.8: Temporal variation of combined log reduction of pathogens over one full filter cycle with four filters and varying backwash staggering patterns (analysis 6). The blue lines represent temporal variation in the combined log reduction and the dark green lines (and corresponding values) indicate overall plant-scale log reduction of pathogens. Case a: base case, case b: random backwash staggering, case c: backwashes spaced by 10 h, case d: backwashes spaced by 0.5 h and case e: backwashes spaced by 0.25 h

Generally, the results show that the effect of backwash staggering on overall filtration performance (green values) is minimal; however, the minimum pathogen removal values (minimum values of blue lines) will differ depending on whether the phases of the filter cycle with the poorest pathogen removal performance coincide. It can be concluded that uneven backwash staggering presents similar performance to the base case if at least three of the filters are always in stable operations (cases b and c). Because cases d and e allow several filters to be in the breakthrough phase at the same time, a substantial reduction in combined performance is expected around the time filters are backwashed. A slight reduction in overall performance occurs in these cases because the flow is redistributed to filters exhibiting breakthrough while others are being backwashed. For example, case e includes a brief period of time during which two filters are undergoing backwashing and the two filters in service are in late

breakthrough. The increased flow through filters in service while other(s) are being backwashed can further reduce filter performance, but this effect was not considered in this analysis.

Because redistribution of the influent flow to other filters while a filter is being backwashed was presumed, the number of filters that can be backwashed at the same time without impacting operation depends only on how much flow the other filters can handle while maintaining equivalent performance. In this case, a good operational strategy for maintaining overall pathogen removal would be to avoid overlapping filter cycle phases with deteriorated pathogen removal when staggering filter backwashes. Ideally, backwashes should be conducted while other filters are in stable operation. This analysis was repeated without flow redistribution during backwashing, and the results are presented and discussed in Appendix C Section C.1. In summary, without flow redistribution, the overall performance is not impacted by backwash scheduling because each filter processes the same amount of water regardless of other filters being backwashed; thus, various periods of treatment performance are not differently weighted by different flows.

4.4.7 Chemical pre-treatment/coagulation

As discussed in Section 4.3.3, the effect of coagulation conditions is variable among systems. In the present investigation depicted in Figure 4.9, a 1.9- and a 0.4-log decline in the overall log reduction of pathogens (green values) were observed when coagulation was not optimized in sub-optimal coagulation cases I and II, respectively. This analysis has an important contrast with Section 4.4.3. The analysis presented in Figure 4.5 showed that increasing the removal achieved during stable operation had negligible effect on overall filtration performance. Reducing the already small number of pathogens passing through the filter during this phase would be ineffective when breakthrough is the principal problem. Here, on the other hand, decreasing the removal achieved during stable operation due to sub-optimal coagulation affects overall filtration performance. The difference is that the filtration performance during stable operation in the unoptimized scenarios (1.4 and 3.1 log) is not much better than the poorest pathogen removal achieved during the filter cycle (1.2 log). As a result, stable operation also contributes significantly to pathogen passage throughout a filter cycle, which explains the differences between the overall log reduction results in Figure 4.9. If breakthrough is prevented, stable operation would affect overall filtration performance even more. Thus, the impact of coagulation on overall filtration performance is often critical. In a study conducted by Westrell et al. (2003), many microbial risks in the drinking water system studied were due to sub-optimal particle removal.

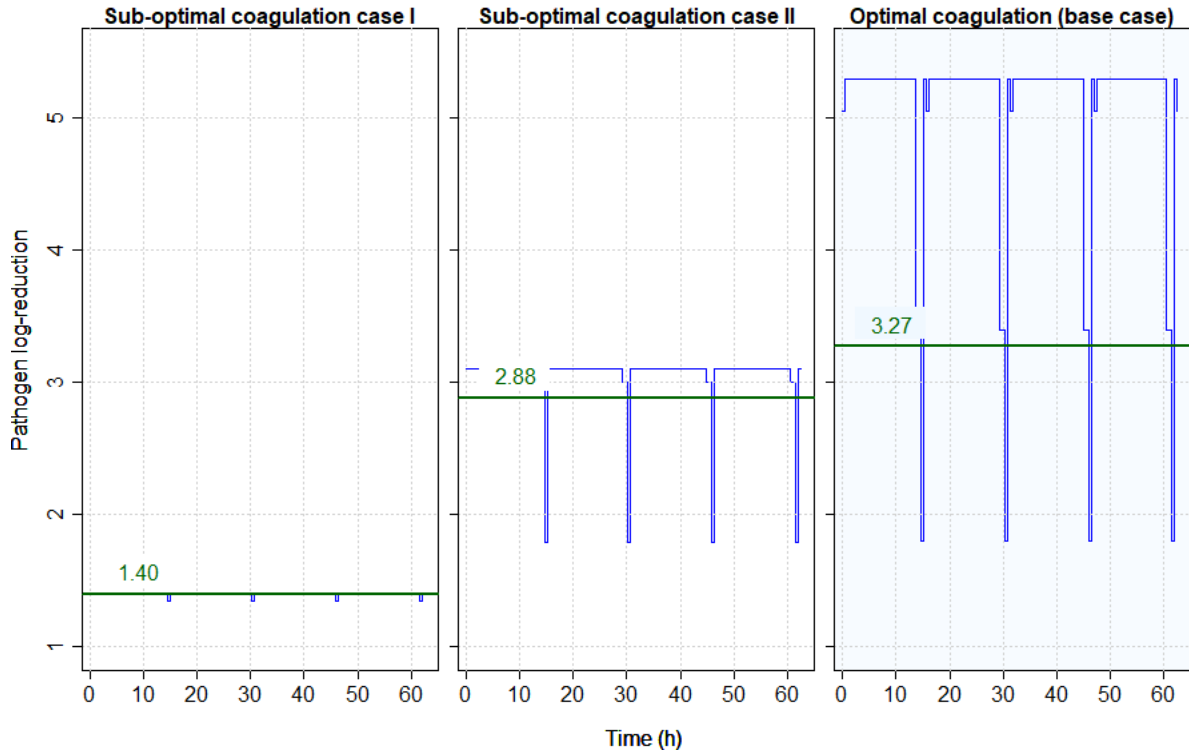


Figure 4.9: Temporal variation of combined log reduction of pathogens over one full filter cycle with four filters, evenly staggered backwashes, and varying coagulation conditions during stable operation (analysis 7). The blue lines represent temporal variation in the combined log reduction and the dark green lines (and corresponding values) indicate overall plant-scale log reduction of pathogens

4.4.8 Filter-to-waste operation

Figure 4.10 presents the effect of filter-to-waste practice on treatment performance. By comparing the filter-to-waste scenario to another scenario with the filter in service during ripening, it is possible to evaluate how much overall plant-scale performance (green values) may be improved by filter-to-waste operation. In this example, even when pathogen log reduction during ripening is poor (e.g., 2.0 log), there is relatively little improvement in overall log reduction if filter-to-waste operation is implemented. The fifth panel with a log reduction of 1.2 during ripening, on the other hand, shows a more marked deterioration in overall performance if filter-to-waste operation is not implemented. When filter-to-waste is not conducted, the period of deteriorated performance during ripening is averaged out by other filters in stable operation and over the course of the filter cycle by a prolonged period of stable operation. When ripening is not the worst phase of the filter cycle, the effect of filter-to-waste operation

during ripening will generally be limited and the worst phase is the greater concern. Here, late breakthrough is the period of worst performance (accounting for 94%, 94%, 82%, and 49% of the pathogen passage with log reductions of 4.7, 3.3, 2.0, and 1.2 during ripening, respectively); thus, it is more impactful to avoid operation during breakthrough conditions than during ripening. Decreasing the performance during ripening increases the proportion of pathogens passing through the filters during this phase (0.03%, 0.7%, 13%, and 49%, respectively), increasing the value of filter-to-waste operation.

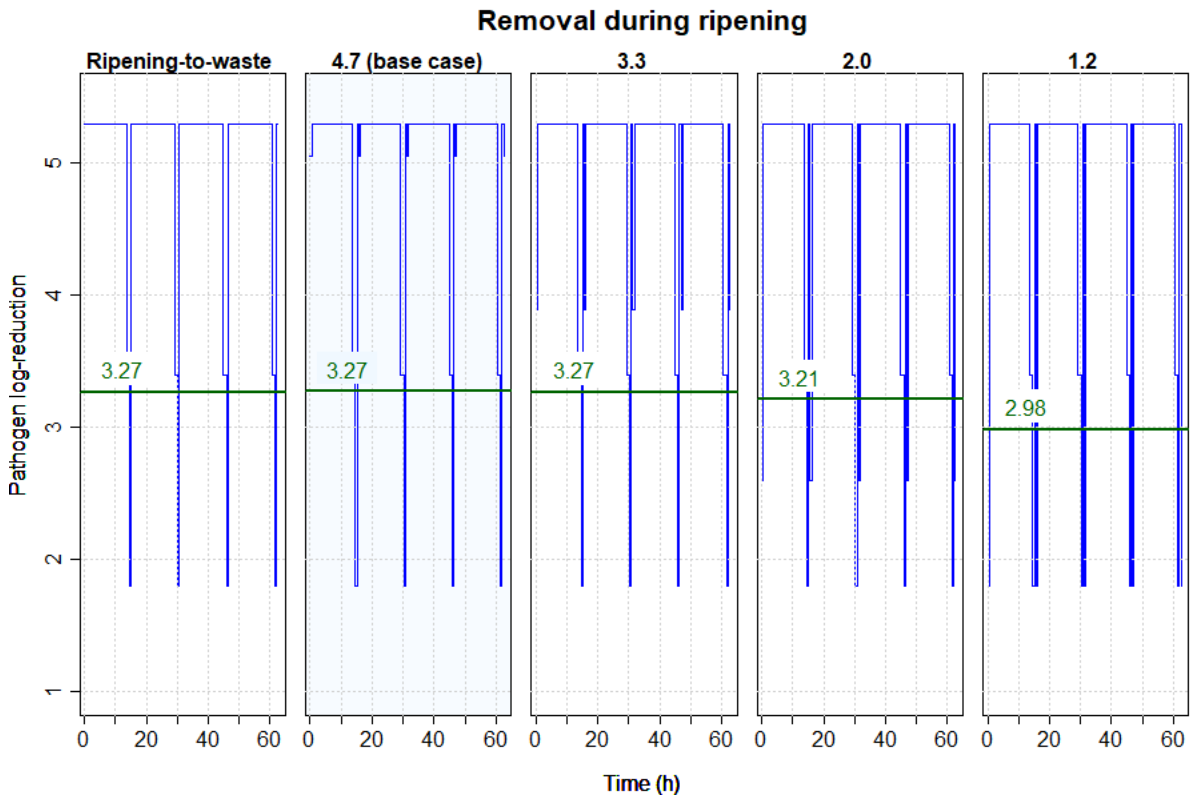


Figure 4.10: Temporal variation of combined log reduction of pathogens over one full filter cycle with four filters, evenly staggered backwashes, and varying removals during ripening (analysis 8). The first case illustrates the filter-to-waste procedure under the base case condition. The blue lines represent temporal variation in the combined log reduction and the dark green lines (and corresponding values) indicate overall plant-scale log reduction of pathogens

From a performance perspective, this practice is beneficial if pathogen removal during the ripening phase is substantially lower (e.g., 1.2 log in this example) than overall plant-scale pathogen removal considering filter-to-waste (e.g., 3.27 log in this example). However, other factors should also be considered when analyzing the benefit of filter-to-waste operation. From a risk management perspective, filter-to-waste contributes to the provision of safe water by providing a means to divert

effluent at any time if one or more events (e.g., sudden changes in water quality or insufficient coagulation) could lead to pathogen passage through filters and, eventually, to waterborne outbreaks.

4.4.9 Implications for practice and research

Moving from single filter analysis to a deeper understanding of filtration operation at plant scale is critical to improve filtration performance. Due to the linearity of dose–response models at low doses (Haas et al., 1999), effects in treatment performance are carried over 1:1 to risk (e.g., a 1-log change in treatment leads to an approximately 1-log change in risk). Therefore, the results presented here are important to the management of microbial risks in drinking water and to support progress toward Sustainable Development Goal 6 to “Ensure availability and sustainable management of water and sanitation for all” (United Nations, 2023). The analyses conducted herein demonstrate how changes in several model inputs (removal and duration of various phases) can impact system performance in removing waterborne pathogens. These inputs are in turn influenced by design and operations in water treatment plants. Table 4.3 links elements of design and/or operational considerations to each of the eight sets of scenarios investigated. For example, if water treatment design changes the number of operating filters during an expansion project, or if filters are taken out of operation due to failures or maintenance, there will be changes in filtration performance as illustrated in the number of filters analysis. Stable operation can be impacted by design, which usually targets maximizing performance during this phase, or other operational conditions like water quality, coagulation, and hydraulic changes. While backwash staggering is mostly an operational concern (possibly within flow constraints based on design), filter-to-waste operation requires modifications in the infrastructure to waste or recirculate water to the beginning of treatment. Pathogen removal during breakthrough is not practically specified as a part of design or operation but it is a function of the filter design. The duration of breakthrough, on the other hand, depends on the monitoring technologies available to support its detection and the operational strategy of timely backwashing. Given the substantial impact of this phase on overall filtration performance, it is valuable to know how sensitive the system is to breakthrough, especially if pathogen removal deteriorates before effluent turbidity. Characterizing the efficacy of pathogen removal and duration of each phase of the filter cycle could help practitioners know how system performance can be improved. The results of this research can be leveraged to support decision-making as it pertains to reducing the impact of filter operation and design decisions/practices to control potential pathogen passage.

Table 4.3: Elements of design and operation with potential to lead to changes in plant-scale pathogen removal performance

Analysis	Design	Operation
(1) Number of filters	Water treatment plant design	Filters taken out of operation (e.g., maintenance, low demand)
(2) Duration of stable operation	Filter design (configuration, media type(s) and depth, etc.)	Water quality after pre-treatment (e.g., turbidity)
(3) Removal during stable operation	Filter design (configuration, media type(s) and depth, etc.)	Coagulation optimization, Hydraulic loading
(4) Duration of breakthrough	Monitoring infrastructure to inform backwash initiation (e.g., turbidimeters, particle counters, software for data analysis)	Timely backwashing
(5) Removal during breakthrough	Filter design (configuration, media type(s) and depth, etc.)	— ^{4b}
(6) Backwash staggering	Production/flow constraints on number of filters in service	Backwash scheduling/initiation
(7) Coagulation	Monitoring infrastructure to support coagulant dosing (e.g., zeta potential analyzers, streaming current monitors)	Coagulation optimization (e.g., choice of coagulant, coagulation conditions)
(8) Filter-to-waste operation	Infrastructure for implementation	It may be an operational decision, given existing infrastructure

^{4b} Although no element of operation is identified that would affect the removal during breakthrough, knowledge about the sensitivity of overall plant-scale performance to the degree of pathogen removal deterioration during breakthrough can enhance operational decisions.

4.5 Conclusions

Plant-scale filtration is a process comprised of smaller individual systems with inherent variations in performance, therefore it is critical to understand how periods of vulnerability affect overall system (i.e., plant-scale) performance. Accordingly, the impact of individual filter design or operation on plant-scale pathogen removal performance of filtration was investigated here and the effects that changes in duration or performance during the various phases of the filter cycle have on the combined performance of several filters, either temporally or averaged over time, were demonstrated using a modeling approach. The developed framework allows assessment of whether various changes improve, degrade, or have a trivial effect on overall plant-scale performance. Hence, this framework can be used as a tool in water utilities to investigate opportunities to enhance filtration performance in the removal of microbial contaminants. The main conclusions that can be drawn from this work are as follows.

- Increasing the number of filters in asynchronous operation makes combined performance less variable without changing the overall plant-scale pathogen removal performance (Section 4.4.1).
- Increasing the pathogen removal performance of individual filters (i.e., “higher log reduction”) is not necessarily better with respect to the protection of public health. Specifically, improving filter performance during stable operation (with adequate coagulation) has a limited effect on overall plant-scale pathogen removal if the lowest pathogen removals during the filter cycle are substantially lower than those during stable operation. If portions of the filter cycle with lower pathogen removal performance are unavoidable, a longer duration of stable operation may lead to better overall plant-scale performance than higher pathogen removal performance during stable operation. In systems treating high-quality source water, avoiding unnecessary backwashing that decreases the length of the stable operation period is also beneficial to overall filtration performance (Sections 4.4.2 and 4.4.3).
- Avoiding end-of-run breakthrough can markedly impact combined and overall filtration performance. Operationally, prompt backwashing following or just before the onset of breakthrough may be the most practical and beneficial change that is possible (Sections 4.4.4 and 4.4.5).
- Different backwash staggering schedules change the combined pathogen removal pattern, although minimal or no changes are observed in the overall plant-scale performance, depending on the adopted flow distribution regime during backwashing (Appendix C Section C.1). When flow is redistributed to other filters during backwashing, overlapping of phases with poor pathogen removal should be avoided to prevent increased production from filters with low removal performance. In general, this practice also limits the severity of brief periods of deteriorated performance. Ideally, filters should be backwashed when other filters are in stable operation (Section 4.4.6).
- Considerable deterioration of the log reduction during stable operation caused by unoptimized coagulation will often compromise the system performance, underscoring the critical importance of sufficient chemical pre-treatment by coagulation for ensuring filtration performance (Section 4.4.7).

- From a performance perspective, filter-to-waste operation is beneficial if the pathogen removal during ripening is substantially lower than the overall plant-scale removal during the remainder of the filter cycle (Section 4.4.8).

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Chapter 5

Drinking water QMRA and decision-making: Sensitivity of risk to common independence assumptions about model inputs

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5.1 Summary

When assessing risk posed by waterborne pathogens in drinking water, it is common to use Monte Carlo simulations in Quantitative Microbial Risk Assessment (QMRA). This method accounts for the variables that affect risk and their different values in a given system. A common underlying assumption in such analyses is that all random variables are independent (i.e., one is not associated in any way with another). Although the independence assumption simplifies the analysis, it is not always correct. For example, treatment efficiency can depend on microbial concentrations if changes in microbial concentrations either affect treatment themselves or are associated with water quality changes that affect treatment (e.g., during/after climate shocks like extreme precipitation events or wildfires). Notably, the effects of erroneous assumptions of independence in QMRA have not been widely discussed. Due to the implications of drinking water safety decisions on public health protection, it is critical that risk models accurately reflect the context being studied to meaningfully support decision-making. This work illustrates how dependence between pathogen concentration and either treatment efficiency or water consumption can impact risk estimates using hypothetical scenarios of relevance to drinking water QMRA. It is shown that the mean and variance of risk estimates can change substantially with different degrees of correlation. Data from a water supply system in Calgary, Canada are also used to illustrate the effect of dependence on risk. Recognizing the difficulty of obtaining data to empirically assess dependence, a framework to guide evaluation of the effect of dependence is presented to enhance support for decision-making. This work emphasizes the importance of acknowledging and discussing assumptions implicit to models.

5.2 Introduction

Quantitative Microbial Risk Assessment (QMRA) is a framework for assessing health risk resulting from exposure to pathogenic microorganisms in which factors influencing risk are analyzed from the source of contamination to the individual exposed (Haas et al., 1999). For example, QMRA is an important tool to support the provision of microbiologically safe drinking water, aiding decisions like the choice of adequate treatment technology (Hadi et al., 2019) and the development of water safety plans (Smeets et al., 2010). As drinking water is intrinsically related to public health protection, it is important to consider the practical implications of model assumptions when estimating risk. For example, factors impacting risk can have multiple values due to variability (e.g., temporal or spatial

variations of pathogen concentrations in the environment) and/or uncertainty (e.g., imprecision in fitted parameters due to limited data); therefore, it is common to represent these factors by probability distributions. To account for variability and/or uncertainty in model inputs, Monte Carlo simulations have been widely applied in QMRA since the late 1990s (Teunis et al., 1997; McElroy et al., 1999). This method allows characterization of exposure and resulting risk by randomly sampling from input distributions. This sampling process is repeated multiple times to consider a wide range of possible values, leading to more detailed information about the distribution of risk.

An underlying assumption of how Monte Carlo has been used in most risk analyses is that the random variables are independent (Smith et al., 1992). Dependence is commonly understood as a direct and causal relationship (i.e., two events are dependent if one is directly impacted by another). However, two variables can be statistically dependent even if there is no causal link between them. Using the classical example of “correlation does not imply causation”, ice cream sales and drowning deaths are correlated (both increase during warmer periods) without one causing the other. Hence, two factors that do not directly affect each other can exhibit dependence if both are affected by a third common factor. In drinking water QMRA, examples of model inputs are the raw water pathogen concentration, treatment efficiency and volume of water consumed. In this context, for example, independence means that a value of consumed volume drawn in Monte Carlo simulations has no association with the drawn value of pathogen concentration. However, if high contaminant concentrations happen to be particularly prevalent during periods of higher water consumption, then pathogen concentrations and volume of water consumed are dependent. For example, seasonality could explain this dependence as it may influence the concentration of pathogens in water sources as well as the consumption of water. Alternatively, if contamination of a water source leads to a boil water advisory, the corresponding reduction in the volume of unboiled water consumed associated with higher concentrations would be an extreme example of causative dependence between these two variables.

While there is potential correlation between variables in QMRA, this has not generally been considered when calculating risk estimates or even reflected as an assumption or an issue potentially leading to bias. Another possible association in drinking water QMRA is between the efficiency of treatment and source microbial concentration. According to Haas & Kaymak (2003), disinfection models that include dependence between initial microbial density and inactivation efficiency have better correspondence with experimental data when investigating the inactivation of *Giardia muris* by ozone. They also observed that the disinfection efficiency of *Escherichia coli* with monochloramine is

significantly greater at higher initial microbial densities in certain conditions (Kaymak and Haas, 2008). Likewise, Ofori et al. (2017) noted a reduction in disinfection performance at low concentrations in the examination of chlorine dioxide oxidation of *E. coli*. Documented instances of simultaneous occurrence of increased microbial concentrations and treatment failures provide other practical examples of dependence. This was exemplified by the Walkerton outbreak in Canada in 2000. Flooding events caused both well contamination including *E. coli* O157:H7 and failure to maintain chlorine residuals, and this contributed to 2300 illnesses and 7 deaths (Hrudey et al., 2003). The higher disinfectant demand due to deteriorated source water quality was not met; therefore, the treatment failure was not entirely independent from the simultaneously elevated pathogen concentration. This association resulted in a high-risk situation and made this outcome more likely than if microbial concentration and treatment performance were independent. Such associations may become more likely given the sudden water quality variations caused by climate-change-exacerbated disturbances, which can concurrently increase contaminant concentrations and impair water treatability (Emelko et al., 2011; Lipczynska-Kochany, 2018). These disturbances have been identified as a contributing factor to waterborne outbreaks (Charron et al., 2004; Graydon et al., 2022). Therefore, knowledge about the effect of dependence among input variables on risk estimates becomes important not only in theory, but also in practice.

In the 1990's, some studies explored the effect of correlation in risk assessment (Smith et al., 1992; Bukowski et al., 1995). Since then, the independence assumption has been more extensively discussed in some fields of risk analysis, like economics (e.g., Arreola Hernandez et al., 2017) and hydrology (e.g., Botai et al., 2020), in which clear association among variables requires the use of multivariate distributions. Haas (1999) discussed dependence in the general context of risk analysis, presenting approaches to model dependent random variables. Despite this author being one of the foremost QMRA researchers (Haas et al., 1999), this issue gained little attention in the field of QMRA as only a few studies have mentioned or integrated correlation in QMRA. Jaidi et al. (2009) applied a correlation coefficient between analytical recovery and (oo)cyst counts per unit volume used as estimates of concentration, and they showed the impact on risk of integrating this correlation. Evolving from this discussion, Schmidt and Emelko (2011) noted that the number of microorganisms observed in a sample is necessarily dependent upon analytical recovery and presented a probabilistic framework that explicitly accounted for this dependence in how pathogen concentrations are characterized without the need for case-specific correlation information. The effect of correlation in time between influent and effluent treatment samples was discussed by Smeets et al. (2008), while Donald et al. (2011) mentioned

the correlation between parameters of the approximate beta-Poisson dose–response model when incorporating parameter uncertainty into QMRA.

The limited discussion of dependence—and associated assumptions of independence—in QMRA may be explained by data limitations, often making an empirical assessment of dependence impractical. Regardless, whether and how much the effect of independence assumptions can be impactful in QMRA needs to be investigated because risk estimates often inform important decisions including system-specific risk management approaches (e.g., Hadi et al., 2019) and the development of (or compliance with) drinking water regulations (Schijven et al., 2011; Gerrity et al., 2023). The goal of this study is to evaluate the effect of independence assumptions among model inputs in drinking water QMRA using both hypothetical scenarios and data from a water supply system. The main objective is to present a framework for characterizing these effects to support the evaluation of their relevance to decision-making.

5.3 Methods

To show the impact of independence assumptions on risk in QMRA models, three analyses are presented. The first two are based on drinking water QMRA using hypothetical model inputs. For illustrative purposes, a third analysis applies monitoring data and treatment credits from a water supply system in Calgary, Canada.

5.3.1 Hypothetical scenarios to investigate dependence in drinking water QMRA

The risk of infection by *Cryptosporidium* spp. through consumption of drinking water is a key example in which the independence assumptions of QMRA model inputs can be explored—it is depicted in Figure 5.1. Here, several hypothetical scenarios are explored using an extreme range of degrees of correlation within a QMRA model with the following assumptions: the influent oocyst concentration is comprised only of viable and pathogenic oocysts, each input is assumed to vary daily, and there is no variation in exposure among individuals.

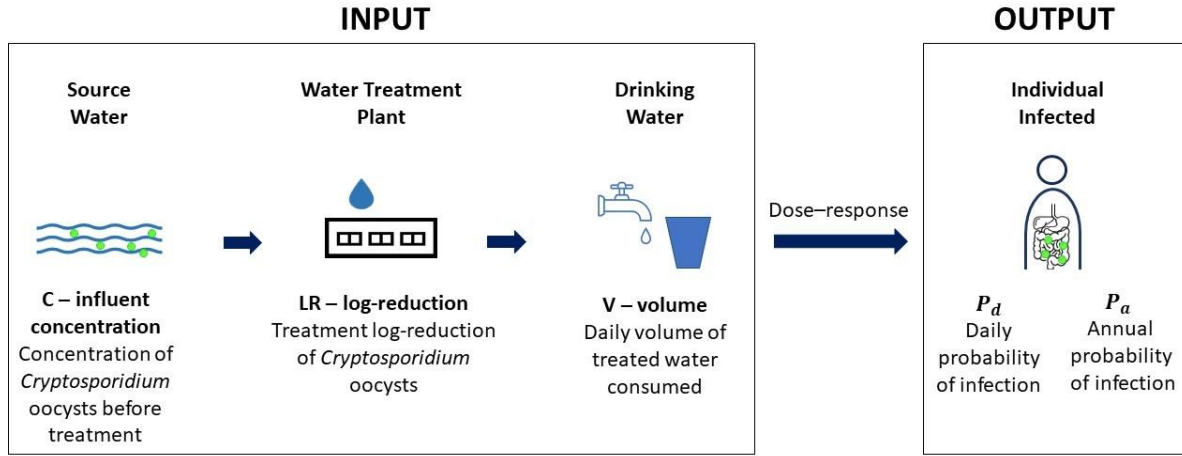


Figure 5.1: Illustration of the QMRA model used in this study

Although dependence can involve two or more variables, it is explored between only two inputs at a time in this study. Analysis 1 examines the dependence between the concentration of *Cryptosporidium* oocysts before treatment (C) and treatment log-reduction (LR), while analysis 2 considers dependence between the influent concentration and daily volume of treated water consumed (V). An exponential dose-response model is used to link all these variables, considering that the probability of infection from one oocyst (r) is 0.018 (Messner et al., 2001). The daily probability of infection (P_d) is expressed in Equation 5.1. The final output of this model is the annual probability of infection (P_a), presented in Equation 5.2. The indices i and j represent days and years, respectively.

$$P_{d,i,j} = 1 - e^{-r \times C_{i,j} \times 10^{-LR_{i,j}} \times V_{i,j}} \quad (5.1)$$

$$P_{a,j} = 1 - \prod_{i=1}^{365} (1 - P_{d,i,j}) \quad (5.2)$$

Here, two of the three input variables in Equation 5.1 are represented by probability distributions (C and LR in analysis 1 and C and V in analysis 2), while the other is a constant (V in analysis 1 and LR in analysis 2). Monte Carlo simulations in QMRA conventionally include several implicit independence assumptions by drawing the value from any one distribution independently from the values of other distributions for a given day as well as assuming temporal independence between days (i.e., using the same distributions for every day). Practically, examples of temporal dependence would include dependence in Equation 5.1 inputs between days (e.g., the pathogen concentration on one day depends on the concentration in the preceding days) or delayed or cumulative effects. Temporal dependence is outside the scope of this paper and is only noted to be clear about the assumptions and limitations of

the Monte Carlo QMRA employed. Incorporating dependence requires the use of multivariate or conditional distributions, linking the occurrence of values of two or more variables. The Monte Carlo simulation of 1000 years in this study incorporates dependence between the two variable inputs in Equation 5.1 using a multivariate distribution but presumes no temporal dependence by using the same distributions for every day.

The scenarios illustrated here are analyzed under the lens of correlation, a specific form of dependence in which variables are linearly associated (i.e., correlation measures how well the change in one variable as a function of another can be modeled by a line). Dependence more generally describes any type of association between two or more variables, and some ways to incorporate it are briefly discussed in the framework presented in Section 5.4.5. As a simple approach to account for correlation, the two dependent input variables are first assumed to have normal distributions so that a bivariate normal distribution can be used to easily represent the joint distribution between these correlated variables. However, lognormal distributions are often chosen to represent concentration and volume in QMRA (e.g., Jaidi et al., 2009; Pecson et al., 2017) since these variables cannot have negative values and are commonly right skewed. Therefore, an approach is also used to model correlation between two lognormal variables using the bivariate normal distribution given that lognormal distributions can easily be transformed into normal distributions. The derivation of this approach is presented in Appendix D Section D.1.

Four scenarios are analyzed here, two in each analysis, as presented in Table 5.1. The main difference between the two scenarios in each analysis is the type of distribution (Figure 5.2) used to represent the dependent variables (normal or lognormal). The parameters of these distributions are hypothetical but were chosen to represent realistic distributions in drinking water risk assessment. Ongerth (2013) reported median *Cryptosporidium* oocyst concentrations in the United States varying from 0.005 to 0.5 oocysts/L. Here, mean oocysts concentrations are close to 0.005 oocysts/L. The log-reduction distributions have an average of 3 log because this is a common minimum removal target for *Cryptosporidium* (Health Canada, 2019). Volume distributions have an average of 1.5–2 L per person per day (Pintar et al., 2009). A range of standard deviations was chosen to test the impact of variability of correlated variables on risk. These parameters were also selected so that the uncorrelated case has a mean annual probability of infection that is lower than 10^{-4} infections/person/year, a common reference point used in QMRA. Concentration and consumed volume are in units of oocysts/100 L and L/day,

respectively, while log-reduction is unitless. A constant consumed volume of 1.45 L/day is used in scenarios 1 and 2, while a log-reduction of 3 is used in scenarios 3 and 4.

Table 5.1: Description of marginal probability distributions used in the hypothetical scenarios

	Scenario	Marginal distribution ^{5a}	Mean	Standard deviation
Analysis 1 – Dependence between concentration (C) and treatment (LR)	1 (normal distributions)	$C \sim Normal(0.75, 0.17^2)$	0.75	0.17
		$LR \sim Normal(3, 0.35^2)$	3.00	0.35
	2 (lognormal distributions)	$C \sim LogNormal(-3.15, 2.19)$	0.47	5.17
		$LR \sim LogNormal(1.2, 0.3)$	3.47	1.07
Analysis 2 – Dependence between concentration (C) and volume (V)	3 (normal distributions)	$C \sim Normal(0.75, 0.17^2)$	0.75	0.17
		$V \sim Normal(2.0, 0.4^2)$	2.00	0.40
	4 (lognormal distributions)	$C \sim LogNormal(-3.15, 2.19)$	0.47	5.17
		$V \sim LogNormal(0.31, 0.45)$	1.51	0.71

^{5a} In scenarios 1 and 3, normal distributions are represented by $Normal(\mu, \sigma^2)$, where μ and σ are the mean and standard deviation of the normal distributions, respectively. In scenarios 2 and 4, lognormal distributions are presented by $Lognormal(\lambda, \zeta)$, where λ and ζ are the mean and standard deviation of the natural logarithm of the lognormal distributions, respectively. The arithmetic mean and standard deviation of the lognormal distributions are given by $e^{\lambda + \frac{\zeta^2}{2}}$ and $\sqrt{(e^{\zeta^2} - 1)(e^{2\lambda + \zeta^2})}$, respectively.

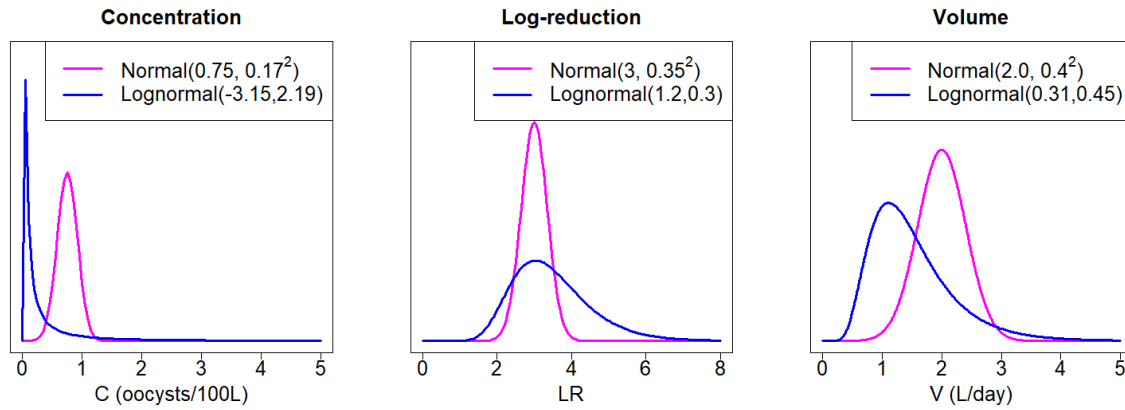


Figure 5.2: Probability density functions of the marginal distributions used in the hypothetical scenarios, as summarized in Table 5.1

The Pearson correlation coefficient (ρ) represents different degrees of correlation and is conveniently a parameter of the bivariate normal distribution. This coefficient can vary between -1 and 1 , so risk

analyses were conducted for five cases considering the correlation coefficients -1, -0.5, 0, 0.5 and 1 when using normal distributions. In these scenarios, $\rho = 0$ means that the normal variables are uncorrelated. These variables are also independent because the statistical definition of independence (the joint distribution is equal to the product of the marginal distributions) is met when $\rho = 0$. When using normal distributions, the Pearson correlation coefficient was integrated in the Monte Carlo simulations simply as one of the parameters of the bivariate normal distribution. When lognormal distributions are used with the proposed correlation approach described in Appendix D Section D.1, ρ is also used as a parameter of the corresponding bivariate normal distribution but is limited according to the parameter values chosen for the lognormal distributions, as explained in Appendix D Section D.2. The five values chosen for comparison are $\rho_{min}, \frac{\rho_{min}}{2}, 0, \frac{\rho_{max}}{2}, \rho_{max}$, with ρ_{min} and ρ_{max} being the minimum and maximum Pearson correlation coefficients of each scenario, respectively. The R scripts (R Core Team, 2021) used for the analyses presented in scenarios 1 and 2 are provided as examples in Appendix D Section D.3.

5.3.2 Case study to investigate dependence in a QMRA model

Building on the analysis of hypothetical dependence between pathogen concentration and treatment efficiency, this case study evaluates health risk from *Giardia* cysts in drinking water using 5 years of pathogen concentration and treatment credit data from a drinking water system located in Calgary, Canada. The rationale for exploring this scenario is to assess the effect that seasonality in environmental pathogen concentrations and treatment efficiency may have on risk. It is not intended to be a complete and rigorous analysis of risk, as that work has been done elsewhere (not published) and only a simple practical illustration of implications of dependence is within the scope of this work.

The drinking water system is comprised of two water treatment plants, Glenmore and Bearspaw, with water drawn from the Elbow and Bow rivers, respectively. A conventional treatment process including coagulation, flocculation, sedimentation, filtration and disinfection is applied in both plants. The City of Calgary has a monitoring protocol to evaluate protozoa concentrations in the raw water twice a month using Method 1623.1 (U.S. EPA, 2012). Spike recovery analyses are conducted for each sample to better estimate the percentage of (oo)cysts that can be retrieved from the water matrix using this method. Although *Cryptosporidium* data are collected, they are not presented here because oocyst detections were rare and much lower than for *Giardia* cysts and the corresponding treatment credits are relatively constant. Data from January 2016 to December 2020 at the Glenmore and Bearspaw water treatment

plant intakes, including *Giardia* cyst counts, volumes analyzed and sample-specific recovery, were used to estimate concentrations according to Equation 5.3. Non-detects were treated as counts of zero instead of censored values to avoid introducing bias to concentration estimates (Chik et al., 2018). To simplify this illustrative analysis, Bayesian approaches to evaluate random error in concentration estimates that are typical of our other work (e.g., Emelko et al., 2010) were not used. A total of 246 concentration values, 123 from each treatment plant, were used in the analyses.

$$Concentration = \frac{Giardia\ cyst\ count}{Sample\ volume \times Recovery} \quad (5.3)$$

Treatment credit values (determined using a process established by the regulator) were used as a proxy for characterizing removal and/or inactivation of *Giardia*. Daily treatment credits at the Bears paw water treatment plant from the same timeframe as concentration data were used because the credits for the Glenmore plant are relatively constant (Figure D.1, Appendix D Section D.4). These credits include filtration and chlorine disinfection credits. The filtration credit varies between 3 and 4 log based on individual and combined filter effluent turbidity. The disinfection credit varies between 1.1 and a cap of 3 log based on calculations using the residual chlorine concentration and contact time. The total treatment credit is given by the sum of credits associated with these two processes. During the winter season, the water temperature drops, which reduces the efficiency of chlorination at the Bears paw plant. The Glenmore water treatment plant has bigger chlorination tanks, which allows increased contact times during this period of the year. As a result, chlorination efficiency can still be maintained; because of that, treatment data from this plant were not considered here. The 1819 treatment credit values reported by the Bears paw treatment plant from 2016 to 2020 were used without any further manipulation.

Like in analysis 1, the risk of infection was calculated according to Equations 5.1 and 5.2, using $r = 0.0199$ as the probability of infection by one cyst (Rose and Gerba, 1991) and a fixed volume of 1.45 L/day (Pintar et al., 2009). To maintain similarity with the analyses described in Section 5.3.1, a thousand years are simulated in the two risk scenarios presented in this case study, assuming (i) independence and (ii) dependence between pathogen concentration and treatment efficiency. First, concentration and treatment data were paired by associating a concentration value to a treatment credit datum using the closest date for which concentration data are available. The scenario illustrating dependence draws concentration and treatment data jointly to reflect this temporal pairing. In the scenario representing independence, concentration and treatment data were drawn individually using

the same paired dataset to ensure equivalence of the dependent and independent scenarios except for paired and independent drawing. The idea behind these scenarios is to examine the effect on risk of reductions in treatment credits at the Bearspaw treatment plant combined with typical *Giardia* cyst concentrations at this time of the year. Due to the limited variability in Glenmore treatment credits (Figure D.1, Appendix D Section D.4) as well as limited seasonality exhibited in the Bearspaw *Giardia* concentration data (Figure D.2, Appendix D Section D.4), a hypothetical scenario is run coupling the Glenmore concentration data that exhibit greater seasonality together with the more variable treatment credits characteristic of Bearspaw. Practically, this scenario is illustrative of what the risk might have been for water from the Glenmore treatment plant if the system had been designed with less contact time. In summary, four scenarios are presented representing both dependence and independence of variables at the two sites. Both concentration and treatment data are from the Bearspaw plant for the Bearspaw scenarios, while the Glenmore scenarios illustratively used concentration data from Glenmore and treatment data from Bearspaw because the Glenmore treatment credits are relatively constant.

5.4 Results and Discussion

In the following sections, results are presented using jitter plots, which illustrate the variation of one variable in relation to a categorical variable. Here, they are used to represent risk data over the simulated years for each considered degree of correlation. A small amount of noise on the x-axis is introduced in jitter plots to allow a better visualization of the distributions without overlapping many data points. Empirical cumulative distribution functions of risk are also provided in Appendix D Section D.5.

5.4.1 Effects of correlation between concentration and treatment log-reduction on risk

The first analysis is an example of a conventional Monte-Carlo-based QMRA modified to include varying degrees of correlation between the source water pathogen concentration and treatment log-reduction. Figure 5.3 and Figure 5.4 present the annual probability of infection for 1000 simulated years as well as the mean and coefficient of variation (i.e., standard deviation divided by mean) of these values for scenarios 1 and 2 (defined in Table 5.1), respectively. In both scenarios, the average risk of infection decreases as the concentration and log-reduction become more positively correlated. This result is expected because more treatment is desirable to reduce the risk posed by higher pathogen concentrations. Plant operators are typically responsible for adjusting treatment set points and operations to ensure sufficient treatment when source water quality changes. However, failures or

delays can occur and some treatment disruptions (e.g., decrease in chlorination efficiency during winter, as presented in the Calgary case study) may require more than a quick operational adjustment. If concentration and treatment are negatively correlated, mistakenly presuming independence will lead to underestimation of risk. It is also notable how the annual probability of infection tends to be less variable with increasing correlation coefficients. This trend can be explained by the relationship between influent concentration and treatment log-reduction, which leads to the effluent concentration and then to risk. Intuitively, the lowest and highest effluent concentrations (and thus risk) occur when the maximum treatment efficiency is applied to the minimum influent concentration and the minimum treatment efficiency is applied to the maximum influent concentration, respectively. The probability of these extremes occurring is greatest in the most negatively correlated case, and that is why it tends to be more variable. Because higher log-reduction counteracts higher influent concentrations, more positive correlation suppresses variation in the effluent concentration and in risk.

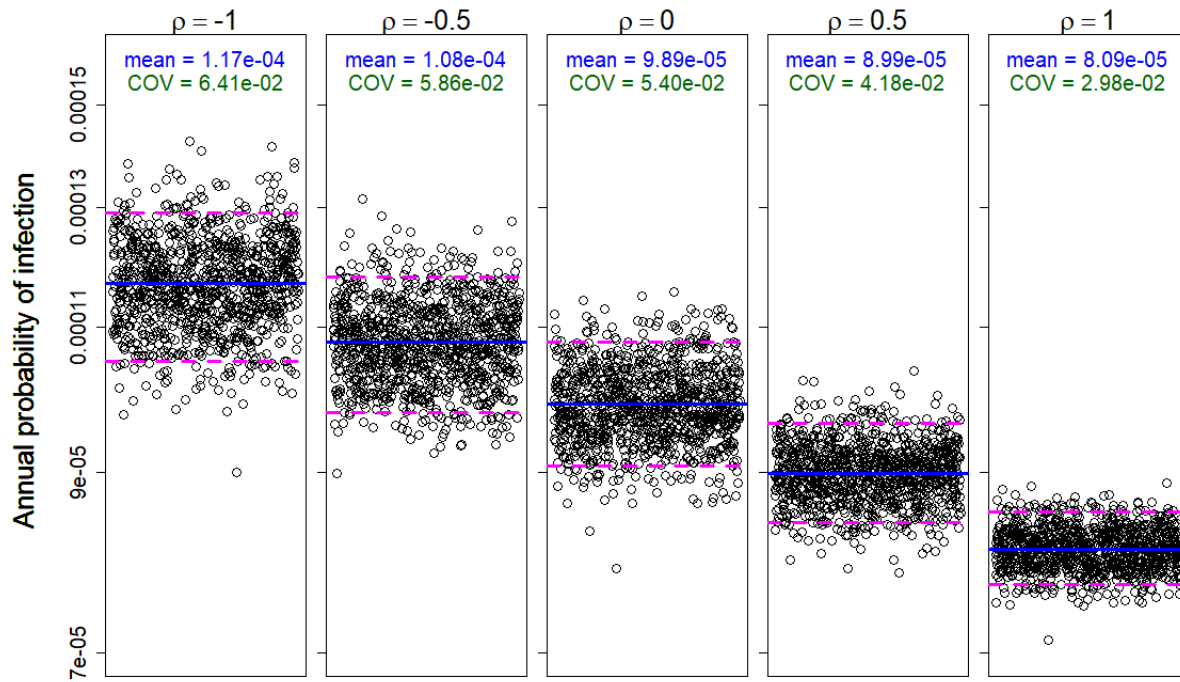


Figure 5.3: Annual probability of infection in each of 1000 simulated years given different correlation coefficients between normally distributed concentration and treatment log-reduction (Scenario 1). The blue line indicates the mean value and COV represents the sample coefficient of variation. The pink dashed lines indicate the 5th and 95th percentiles

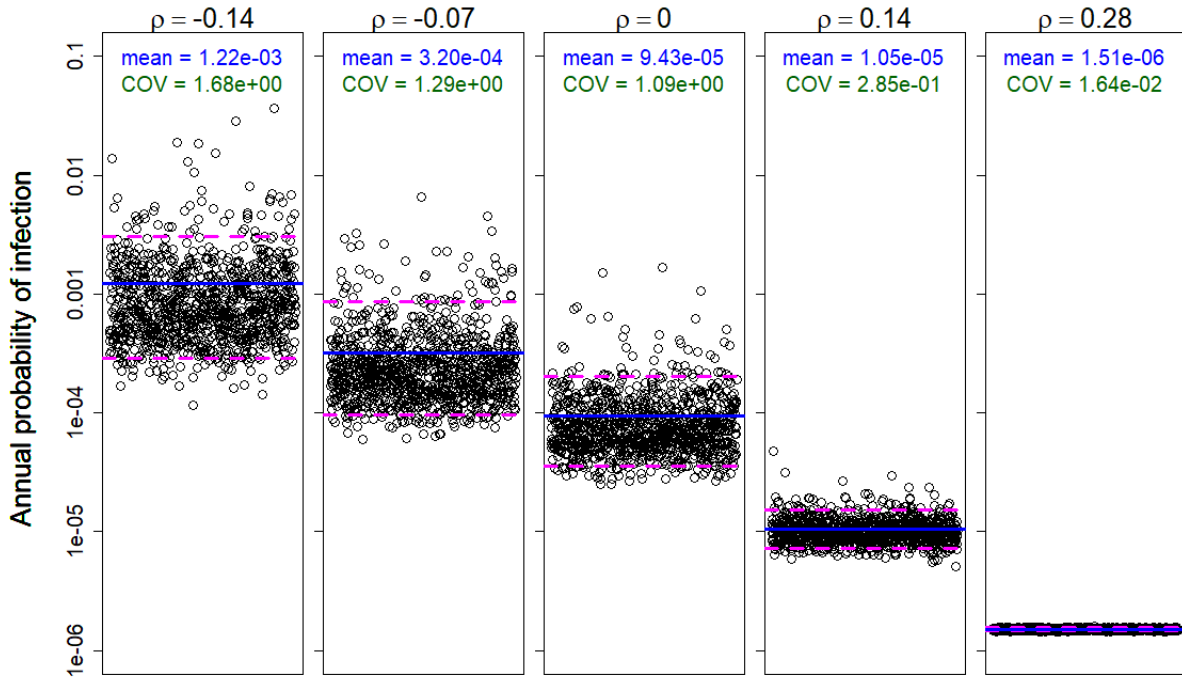


Figure 5.4: Annual probability of infection in each of 1000 simulated years given different correlation coefficients between lognormally distributed concentration and treatment log-reduction (Scenario 2). The blue line indicates the mean value and COV represents the sample coefficient of variation. The pink dashed lines indicate the 5th and 95th percentiles

The effect of correlation depends on the variability of the assumed distributions. Low variances of the concentration and log-reduction distributions were chosen to avoid negative values in the normal distributions of scenario 1, whereas greater variability was possible in the lognormal distributions of scenario 2. In scenario 1, the mean risk at the lowest correlation coefficient was only 1.2 times higher than the mean risk assuming no correlation ($\rho = 0$), meaning that risk would be underestimated by a factor of 1.2 if independence was mistakenly assumed. Conversely, risk would be overestimated by a factor of 1.2 if independence was mistakenly assumed and these parameters were fully positively correlated. However, this effect is more prominent in scenario 2: the mean risk in the most negatively correlated case ($\rho = -0.14$) is nearly 13 times higher than in the uncorrelated case, and the uncorrelated case is approximately 62 times higher than the most positively correlated case ($\rho = 0.28$). When risk is close to a reference level of 10^{-4} infections per person per year, overlooking existing dependence can lead to wrong decisions when managing microbial risk. This situation is

illustrated both in scenarios 1 and 2, in which a negative correlation increases the mean risk above the reference level.

In decision-making, it is also important to know how variable risk estimates are. Despite the same trend of decreasing standard deviations of risk with increasing correlation coefficients, the magnitude of change differs between scenarios 1 and 2. While the coefficients of variation differ approximately two-fold between extreme correlation cases in scenario 1, the corresponding difference in scenario 2 is more than 100-fold. Thus, correlation can have a substantial impact on the variability of risk estimates. To explore whether this difference between scenarios 1 and 2 is attributable to the change in mean and standard deviation or the change from normal to lognormal distributions, another scenario (Figure D.9, Appendix D Section D.6) was run with two lognormal distributions having approximately the same mean and standard deviation as the scenario 1 normal distributions: $C \sim \text{LogNormal}(-0.31, 0.22)$ and $LR \sim \text{LogNormal}(1.09, 0.12)$. Like in scenario 1, the annual probability of infection means and coefficients of variation were very similar (differences within 4% and 15% for mean and coefficient of variation, respectively) with Pearson correlation coefficients varying from -0.97 to 1 ; therefore, the greater change in risk observed among correlation cases in scenario 2 than in scenario 1 is principally a result of the greater variances chosen for the lognormal distributions rather than the change in distribution shape. As has already been reported by Bukowski et al. (1995), the effect of correlation on risk is higher when the variances are large. Conversely, the effect of correlation could be limited when the variances are small, as illustrated in scenario 1.

5.4.2 Effect of correlation between concentration and volume of water consumed on risk

The effect of correlation between concentration and consumed volume on annual risk is presented in Figure 5.5 and Figure 5.6 for scenarios 3 and 4 (Table 5.1), respectively. As expected, the mean annual risk tends to be higher as the variables become more positively correlated since more contaminated water coinciding with periods of high consumption will lead to greater risk. The ratios of mean risk between the worst case (highest mean risk) and the uncorrelated case are 1.04 and 2.60 in scenarios 3 and 4, respectively. This represents underestimation of risk if independence is mistakenly presumed. As mentioned before, these differences depend on the variances of the distributions. If pathogen concentrations and daily volume of water consumed do not vary substantially, the difference in mean risk among various degrees of correlation cannot be large, as represented in scenario 3. On the other

hand, if only one of the distributions has a large variance, like the concentration of pathogens in scenario 4, greater changes can be observed.

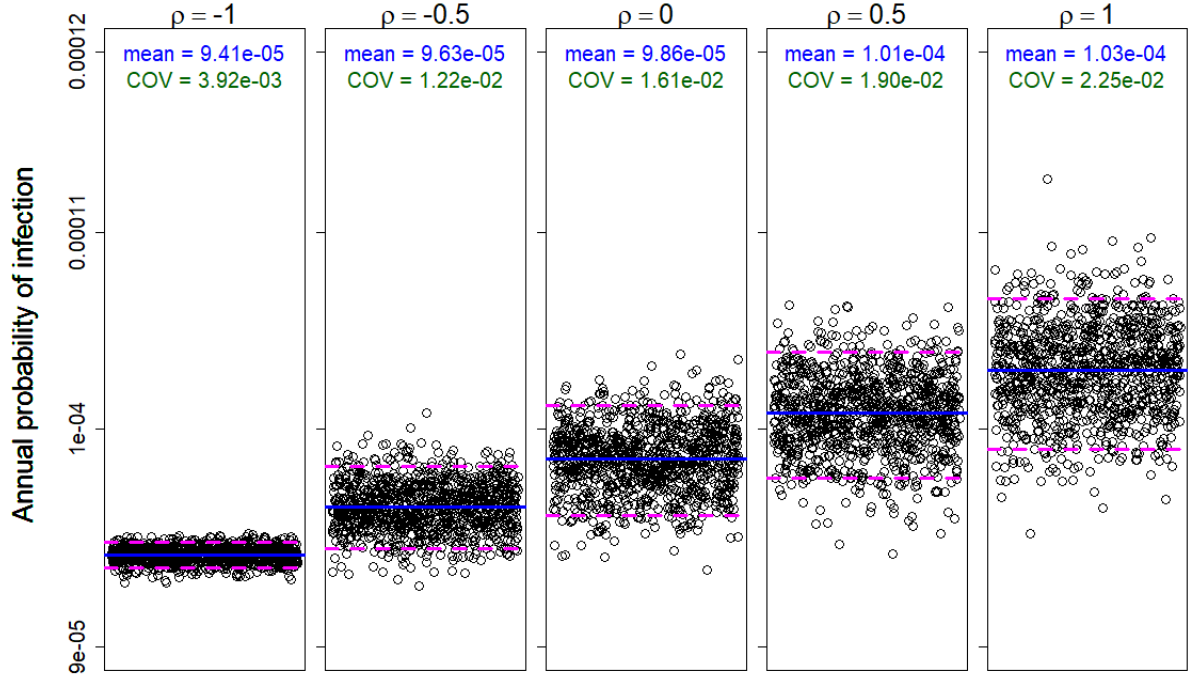


Figure 5.5: Annual probability of infection in each of 1000 simulated years given different correlation coefficients between normally distributed concentration and volume of treated water consumed (Scenario 3). The blue line indicates the mean value and COV represents the sample coefficient of variation. The pink dashed lines indicate the 5th and 95th percentiles

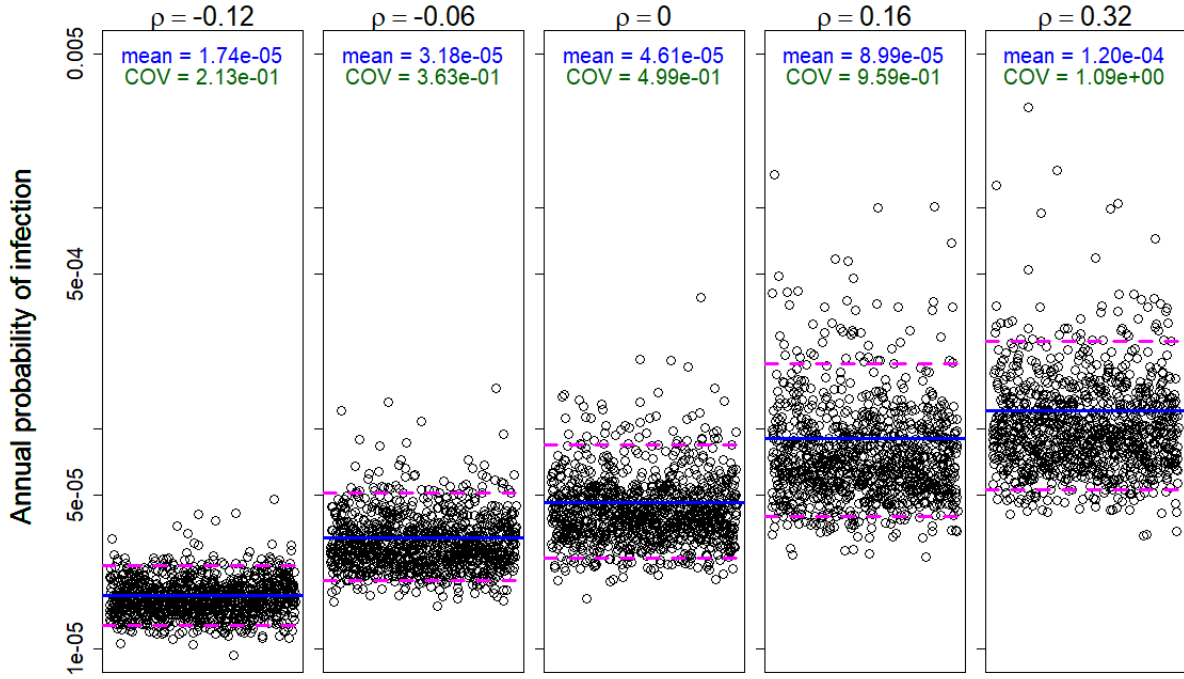


Figure 5.6: Annual probability of infection in each of 1000 simulated years given different correlation coefficients between lognormally distributed concentration and volume of treated water consumed (Scenario 4). The blue line indicates the mean value and COV represents the sample coefficient of variation. The pink dashed lines indicate the 5th and 95th percentiles

Comparing scenario 4 to scenario 2, in which the variances of pathogen concentration are both large, it can be observed that the impact of correlation between concentration and volume on risk tends not to be as big as the effect of correlation between concentration and treatment. This is because of the difference in the mathematical relationship between volume and treatment with the dose of pathogens consumed ($Dose = Concentration \times 10^{-Log-reduction} \times Volume$) and the typical values that these variables have in drinking water treatment. For example, a shift between an insufficient (0.5 log) and a good (4 log) treatment performance changes the dose of pathogens consumed (assuming constant volume and concentration) by a factor of more than 3000 ($10^{-0.5}/10^{-4}$) due the non-linear relationship between log- reduction and dose. On the other hand, varying the volume of water consumed from 4 L to 0.5 L—which are arguably reasonable limits for variation between days or between people—changes the final dose of pathogens (considering constant treatment and concentration) by only a factor of eight.

Therefore, even if concentration and volume are correlated, the impact on risk tends to be smaller compared to the impact of correlation between concentration and treatment.

As observed in analysis 1 (Section 5.4.1), the coefficients of variation in scenarios 3 and 4 also follow the same trend as the mean in relation to the correlation coefficients (i.e., both the average and the variability of risk increase or decrease with a change in correlation). This is important for risk characterization and decision-making because if uncorrelatedness is presumed when variables are in fact correlated, a situation can not only have a higher risk on average but also be more difficult to manage due to increased variability in risk. Therefore, when both the mean and the variance of risk estimates increase, there are greater implications for risk control. Conversely, there are lesser implications for risk control if a case of dependence decreases the mean and variance of risk. The other possibilities when only one of the metrics increases and the other decreases can be more or less consequential for risk management depending on the magnitude of changes. However, without case-specific analysis, it is not possible to know the magnitude and direction of the effect of correlation on the mean and variance of risk.

5.4.3 Case study: dependence between parasite concentration and treatment performance

Figure 5.7 presents the risk distributions resulting from a case study considering *Giardia* concentrations and treatment credits at the Glenmore and Bearspaw water treatment plants in Calgary. The empirical cumulative distribution functions of these risk distributions are also presented in Appendix D Section D.5, Figure D.8. When characterizing risk at the Bearspaw treatment plant, the difference between the independent and dependent scenarios is subtle and leads to a mean risk only 1.1 times higher in the dependent scenario. This scenario has a correlation coefficient of only -0.10 between concentration and treatment credits. It is worth noting that dependence between these datasets may not be linear, and therefore, not well described by a correlation coefficient. The difference in risk between the two scenarios is larger when the Glenmore concentration data were illustratively combined with the Bearspaw treatment data. In this case, the correlation coefficient between concentration and treatment efficiency is -0.25 in the dependent scenario in which concentration and treatment data are temporally paired. This change results in a mean risk 1.4 times higher than the one in the independent scenario. The different results between the Glenmore and Bearspaw *Giardia* cyst concentration data can be explained by the greater seasonality observed at Glenmore compared to Bearspaw, as illustrated in

Figure D.2 and Figure D.3 (Appendix D Section D.4). At Glenmore, the concentrations are higher during the winter season, which would be problematic if lesser contact time led to reduced treatment credits during winter. Although the results of the independent and dependent scenarios are statistically different in both plants (p-value of Mann-Whitney test is less than 10^{-8}), they may not be meaningfully different for decision-making in this case. Dependence, which currently has relatively trivial effect on computed levels of risk, may become an important point to consider if concentrations in Bearspaw present greater seasonality in the future, especially if high concentrations are prevalent in the winter. Regardless, analysis 3 illustrates another way of evaluating temporal dependence and shows its effects in a drinking water system. It is worth noting that even in the dependent scenarios, the annual risk is well below the reference value of 10^{-4} infections per person per year, affording a significant safety factor for this particular system.

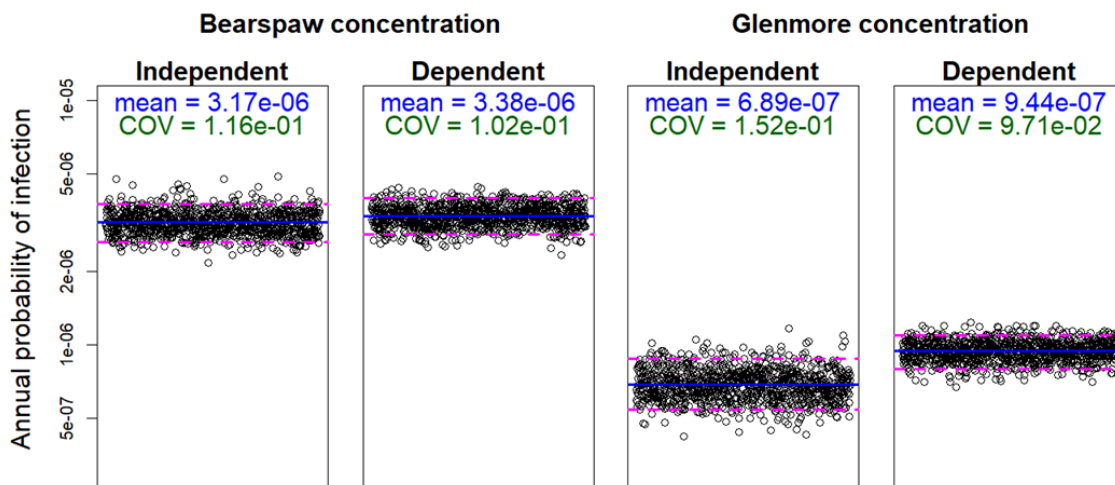


Figure 5.7: Annual probability of infection in each of 1000 simulated years considering concentration (at Glenmore or Bearspaw) and treatment efficiency (at Bearspaw) to be either independent or dependent (i.e., paired). The blue line indicates the mean value and COV represents the sample coefficient of variation. The pink dashed lines indicate the 5th and 95th percentiles

5.4.4 Practical challenges and strategies for exploring dependence in QMRA inputs

The presented examples show different implications of assuming independence when there is dependence, on both the average and variability of risk. There are situations (e.g., scenario 3) in which dependence would have little impact on risk estimates, while in others (e.g., scenario 2) the difference between results is so large that neglecting dependence could misinform decision-makers. In the

drinking water context, dependence between pathogen concentration and treatment efficiency is of particular concern because when microbial raw water quality deteriorates, there must be enough treatment to ensure that higher pathogen concentrations will not lead to excessive risk. Treatment efficiency tending to deteriorate concurrently with microbial raw water quality would be problematic, likely leading to higher risk than what is calculated if independence is mistakenly presumed. Therefore, it is valuable to know if dependence can have impacts on risk assessment and what can be done to better support decision-making.

To approach this problem, the first question to be raised is if the variables of a risk model (i.e., the factors influencing risk) are dependent. The answer to this question is case-specific. Scatter plots can assist in the investigation of dependence between variables, and correlation coefficients are also useful with the caveat that they are limited to represent linear relationships so that a lack of correlation does not prove independence. However, one of the challenges in applying QMRA to drinking water supplies is the availability of data to empirically assess dependence. For instance, quantitative information about pathogen removal or inactivation by treatment barriers is scarce (Pettersen and Ashbolt, 2016). The sufficiency of treatment is typically evaluated using indicators; for example, Schijven et al. (2011) described a way to assess removal of naturally occurring and relatively abundant microorganisms as a surrogate for protozoan pathogens. In these situations, spiking (oo)cysts into pilot systems is needed to describe treatment performance (Emelko et al., 2003). Data about pathogen concentrations in environmental samples are also affected by several sources of variability and/or uncertainty (Schmidt and Emelko, 2011) that could require a large and/or detailed dataset for accurate description. If it is difficult to characterize important variables (like pathogen concentration or treatment efficiency) independently in drinking water QMRA, it would be even more difficult to assess the interaction among them (e.g., through a monitoring program that simultaneously evaluates pathogen concentrations and treatment performance).

Paired data can provide useful information about dependence, which can be further incorporated in risk models. Monitoring should therefore be conducted in a paired fashion (e.g., every concentration datum has a corresponding treatment efficiency datum) at least some of the time to begin assessing dependence, if possible. Teunis et al. (1999) discussed the use of paired and unpaired concentration data when evaluating treatment efficiency to support drinking water risk assessment. Conducting paired experiments is complicated by variable residence times and mixing conditions in full-scale treatment processes. To overcome the difficulties of collecting paired data, pairing can also be imposed after data

are collected if each unpaired value from the more comprehensive time series is matched with a value in the less comprehensive time series using the nearest time, as the case study presented in Section 5.4.3 paired concentration and treatment efficiency. Alternatively, risk assessment can be divided into specific conditions in which each condition has a specific distribution to describe the variables influencing risk. For instance, it may not be feasible to conduct paired experiments to evaluate dependence of water consumption and pathogen concentration in raw water, but if concentration and consumption data can be separated by season, a risk assessment drawing from different distributions for different seasons will better reflect the effect that seasonality might have on risk estimates.

If it is not possible to empirically assess (in)dependence, it is recommended to test the effects of potential dependence and the direction of bias that ignoring it might create (i.e., whether risk would be over- or underestimated if independence is assumed). To investigate the sensitivity of the model to dependence, some approaches are discussed in Section 5.4.5 to either formally incorporate dependence in QMRA models or preliminarily investigate its potential impact on risk. Finally, it is worth noting that the implications for decision-making will be highly case-specific, as discussed in Section 5.4.2. Using scenarios, a quantitative characterization of the effects of dependence can support use of the independence assumption in risk assessment if results are not sensitive to dependence and can also inform treatment and/or monitoring decisions to control microbial risk in drinking water.

5.4.5 Mathematical approaches for incorporating dependence in QMRA models

When data are collected in a paired fashion (i.e., data from different variables are collected under the same conditions), the structure of dependence can be evaluated empirically from the data. The simplest approach to account for dependence would be resampling entire sets observed under the same conditions rather than fitting distributions from which to draw. When values of two or more random variables are drawn together, any effect of dependence on the probability of their co- occurrence can be reflected rather than assuming independence. This method was illustrated in the Calgary case study presented in Section 5.4.3. Although this approach can be useful when distributions cannot be fit to data, it can lead to inaccurate results if the number of data is small and/or the data cannot represent the distributions of the actual variables well.

As an alternative to using the raw data, if it is possible and desired to fit a multivariate distribution (i.e., a probability distribution that explains the occurrence of multiple variables at the same time), there are several methods available in the literature: non-parametric methods, multivariate parametric

distributions, entropy and copulas (Hao and Singh, 2016). Parametric distributions are known functions defined using parameters (e.g., the multivariate normal distribution used to link two dependent normal and lognormal distributions in Sections 5.4.1 and 5.4.2). They are simple to work with, but there is a limited number of well-described and easy-to-use parametric multivariate distributions. Parametric distributions are also limited for situations with complex dependence structures such as tail dependence (i.e., dependence in the extreme values of a bivariate distribution) or to describe specific distribution shapes (e.g., bimodality). Non-parametric methods and entropy (i.e., a measure of uncertainty inherent to a random variable's possible outcomes) are alternative ways to characterize multivariate probability density functions given data. One of the most common ways to characterize multivariate distributions is through the copula theory. A brief introduction to copulas and how they can be used is presented in Appendix D Section D.7.

Typically, available data in QMRA are not paired. In these situations, it is recommended to use hypothetical scenarios to analyze the sensitivity of the model to dependence. Exploring scenarios is a powerful way to develop risk management strategies linked to specific conditions when data are scarce. The analyses presented in Sections 5.4.1 and 5.4.2 are examples of analyses of sensitivity to dependence and they can guide other risk analysis situations involving two normal or lognormal random variables. To measure non-linear dependence between non-normal distributions, dependence metrics like Spearman's ρ and Kendall's τ may be more appropriate than the Pearson correlation coefficient (Hao and Singh, 2016); however, these metrics are limited to representing a monotonic association between variables (i.e., if one variable is either ever-increasing or ever-decreasing as the other variable increases). The Iman–Conover method (Iman and Conover, 1982) is another approach to simulate dependence among datasets regardless of their distributions. It consists of reordering samples based on the rank correlation desired among them. This method can be applied using the package *mc2d* in R (Pouillot and Delignette-Muller, 2010). Figure 5.8 summarizes the discussion of Sections 5.4.4 and 5.4.5 to guide decision-makers and risk modellers in the evaluation of the effect of dependence on risk analysis.

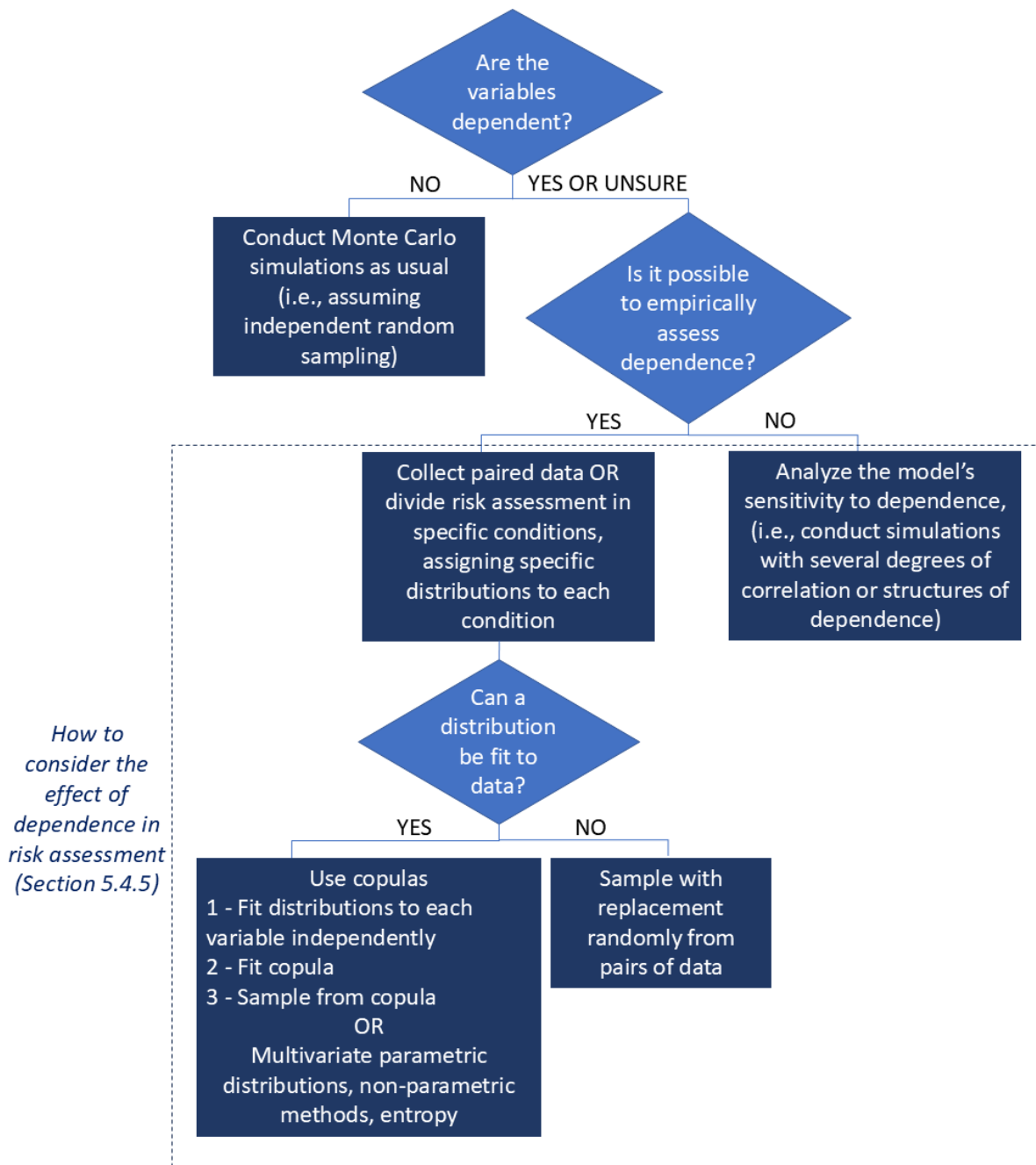


Figure 5.8: A framework to guide evaluation of the effect of dependence for decision-making

5.5 Conclusions

Independence among input variables is a common assumption when risk is evaluated using QMRA. However, this work shows that assuming independence when this assumption is not valid can affect risk profiles (either under- or overestimating risk), which could impact decision-making to control microbial risk in drinking water. A framework is provided to support investigation of the impact of dependence in risk assessment. In summary, the conclusions are as follows:

- In drinking water, dependence between pathogen concentrations and treatment efficiency is especially concerning if deteriorated water quality occurs concurrently with reduced treatment performance, which results in higher risk.
- Both the mean and the variance of risk estimates vary with different degrees of correlation, and the impact of correlation on risk can either be subtle or reach more than an order of magnitude. If independence is mistakenly presumed and risk is higher than estimated, it might also be more difficult to manage because risk can be more variable at the same time. Case-specific analyses are required to evaluate the effect of dependence.
- Impacts of dependence on risk distributions depend strongly on the variances of the input variables; the higher their variances, the greater the impact of correlation can be.
- Paired sampling of QMRA inputs is desirable, where plausible, so dependence can be evaluated. Mathematical tools such as resampling and copulas can be useful to incorporate complex patterns of dependence in Monte Carlo simulations.
- To meaningfully support decision-making, QMRA studies incorporating two or more distributions should at a minimum acknowledge, discuss, and defend presumed independence and consider the magnitude of bias that could occur if it were mistakenly presumed, even when suitable data are not available to model dependence.

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Chapter 6

No risk, no resilience: Leveraging risk insights to enhance operational resilience in the provision of safe drinking water

6.1 Summary

The need for resilience has increasingly been debated in the water sector to mitigate risks from adverse events. Resilience is a broad, interdisciplinary concept that can have many formal and informal interpretations. In water supply systems, the sufficiency of treatment to ensure drinking water safety has been challenged by events such as infrastructure failures and source water quality degradation associated with climate-change-exacerbated disturbances. Contributions of risk frameworks to description of resilience have, however, not been practically described in the context of drinking water safety, which is a critical need for public health protection. In this context, the potential health effects posed by sudden or unforeseen changes can be more difficult to manage when associated with acute risks from microbial contaminants because rapid decisions are needed to control such risks. This work focuses on the role of operations in drinking water treatment to increase resilience and improve microbial risk management. Operational resilience is defined and hypothetical case studies are used to demonstrate that descriptions of resilience must reflect risk not only as motivation, but as an integral part, to make resilience an actionable tool for risk management. Beyond risk descriptors, frameworks are needed to explore, comprehensively describe and ultimately operationalize resilience in drinking water treatment.

6.2 Introduction

Climate change, population growth, pollution, urbanization, wars: threats to water security keep evolving in a rapidly changing world. Managing risks from these threats is critical to ensure water quality and availability needs are fulfilled in multiple systems that depend on water such as drinking water, sanitation, recreation, ecosystems and economic development (Mishra et al., 2021). Historically, risk assessment approaches have been used for evaluation of risk (i.e., describing the chances and potential impacts of losses given an adverse event) to support risk management (i.e., decision-making related to risk prioritization, application of mitigations strategies, allocation of resources) and enhance water safety (van den Berg et al., 2019). In the context of systems' responses to adverse events, the term resilience is also applied to describe a system's ability to recover from adversities. The need for resilience in water systems has been increasingly discussed to counteract the effects of known or unknown adverse events and ultimately manage risks (Rodina, 2019). As part of an ongoing discussion, some authors advocate for the need to shift "from risk to resilience" as risk assessment can be

undermined in contexts of rapid and unpredictable changes (Fiksel, 2015; Aven, 2019). Other authors recognize the value of resilience for risk management and, conversely, the importance of considering risk when conducting resilience assessments (Aven, 2022). Contributions of risk frameworks to description of resilience have, however, not been practically described in the context of drinking water safety, which is a critical need for public health protection.

Risk and resilience can be studied from multiple perspectives with different threats, systems and dimensions (e.g., social, technological, ecological) in the water context. Considering the technical dimension of the provision of safe drinking water, water supply systems usually involve several barriers to prevent water contamination from the source to the tap, applied in the main elements of such systems: source water, treatment, drinking water distribution (Canadian Council of Ministers of the Environment, 2002). Water treatment has a critical role in this context and is highlighted in the U.S.'s multiple barrier approach for public health protection as the risk management barrier (U.S. EPA, 2006). Within water treatment, risk and resilience can also be studied under multiples perspectives (e.g., infrastructure, logistics, monitoring, operations). For example, several studies have sought to evaluate the role of treatment technologies (Howard et al., 2010; Rajib et al., 2012; Blackburn et al., 2023) or infrastructure (Schramm & Felmeden, 2012; Kohlitz et al., 2020; Pamidimukkala et al., 2021) in building resilience to climate change. Nevertheless, the existence of infrastructure does not ensure that it is appropriately operated and the contribution of operational strategies to resilience has received lesser attention.

Water treatment performance varies over time, and these variations have been exacerbated by events causing sudden changes in source water quality or treatment failures. Because treatment is a risk management barrier, this dynamic nature of treatment can consequently impact risk. In the drinking water context, the potential health effects of sudden or unforeseen changes in water quality can be more difficult to manage when associated with acute risks because these require faster recognition and interventions for control. Most acute risks in drinking water are related to microbial contamination, and microbial risk is typically assessed using Quantitative Microbial Risk Assessment (QMRA), an established risk assessment framework that supports treatment decisions (e.g., de Brito Cruz et al., 2025 (Chapter 2)) and development of water safety plans (Smeets et al., 2010). This work focuses specifically on description of the role of operations to increase resilience to adverse events related to microbial risks in drinking water treatment. Operational resilience is defined and case studies are used to demonstrate (1) potential limitations for risk management of not integrating risk into resilience descriptions,

(2) how risk assessment can be used to describe the value of resilience strategies and prioritize them and (3) how operational resilience can be used to better manage microbial risks.

6.3 The concept of risk in QMRA

Risk assessment approaches have been extensively used in water safety plans for evaluation of risk and prioritization of risk management strategies, either as qualitative or semi-quantitative frameworks such as risk matrices and Failure Mode and Effects Analysis (FMEA) or more complex human health frameworks such as QMRA (Medema & Smeets, 2009; Dominguez-Chicas & Scrimshaw, 2010). Simplistically, risk can be defined as the product of occurrence of an adverse event (usually described using probabilities) and the severity of its consequences on a system. Defining an adverse event as the presence of pathogens in water, the probability of occurrence could be 100% as it can be assumed that there are always microbial contaminants in many water sources and treatment cannot practically remove every pathogen all of the time. Safety of drinking water is based on the notion of “acceptable risk”, which means that it is impractical to reduce risk to zero. Given pathogen occurrence, risk in QMRA would measure only the consequences of having pathogens in drinking water, represented in terms of health effects caused by varying levels of exposure to pathogens.

Returning to the foundational definition of risk, other more diverse perspectives are also possible. For example, if a health effect (e.g., infection, illness) is considered to be the adverse event, then associated probabilities can be estimated and coupled with measures of consequences such as disability-adjusted life years (DALYs). DALYs, another common risk endpoint used in QMRA, have the advantage of accounting for the consequences of health effects by including measures of severity and duration. However, this comes with the caveat that DALYs do not consider asymptomatic cases (Emelko et al., 2019), which can be particularly relevant when diseases are contagious. Notably, there is a long chain of events (from shedding of pathogens to impacts of ingestion of contaminated water), and the “adverse event” of interest and “risk” can be defined in multiple ways and have different units. For example, microbial risk is commonly measured in probability of infection or DALYs, but could also be expressed using mortality rate or health-care costs.

6.4 Resilience and its relationship to QMRA

The term resilience has been applied to characterize systems' responses to changes in several fields including ecology, finance, psychology, and engineering. Generally, resilience definitions have referred to a system's ability to withstand, recover from or adapt to disruptions caused by adverse events (e.g., Wang & Blackmore, 2009). In the initial discussions of resilience in water systems, the term was defined using a temporal frame, as the time needed to recover from a failure state (e.g., Hashimoto et al., 1982; Moy et al., 1986). Resilience has gained broader meaning and, more recently, most definitions involve the ideas of recovering from and absorbing (or withstanding) a perturbation (e.g., Wang & Blackmore, 2009; Roach et al., 2018). Anticipation of threats and adaptation are also concepts related to resilience (e.g., NIAC, 2009), which is sometimes also defined as a function of a defined outcome (e.g., ensure continuity of drinking water services) (e.g., Quitana et al., 2020). Because resilience is an interdisciplinary, broad term that can carry diverse interpretations, many definitions have been proposed (Rodina, 2019) to describe water resilience in different dimensions (e.g., social, technological, ecological). For example, resilience in water systems can involve the efficiency of treatment infrastructure (Pamidimukkala et al., 2021) or social mediation of water access (Kohlitz et al., 2020) when these systems are perturbed by adverse events. Research has suggested that having several interpretations of resilience poses challenges to understanding and operationalization of this concept (Johannessen & Wamsler, 2017). Despite the increasing number of studies discussing water resilience recently (Rodina, 2019), actionable tools for implementation of the resilience concept in drinking water risk management are not broadly available.

A common graphical representation of resilience is presented in Figure 6.1, in which the curve represents a system function that is potentially lost over time following a perturbation. P_0 is the initial performance and $P(t)$ is a function representing performance variations over time (Bruneau et al. 2003; Quitana et al., 2020). Figure 6.1 also presents some of the multiple scenarios that can be analyzed under this perspective. A system can recover after a perturbation (i.e., bounce back to an initial state) either completely (scenarios i and ii) or partially (scenario iii), in which case the final steady-state of the system function analyzed might be different from the original one. The magnitude (y axis) and duration (x axis) of loss are two quantitative metrics related to resilience, whose relationships can vary as illustrated in scenarios i (big loss, rapid recovery) and ii (small loss, long recovery). Scenarios iv, v and vi show variations in the pathways of degradation (loss of function) and restoration (recuperation of function). For example, these scenarios can be used to illustrate filter performance after a coagulation

failure. Depending on the extent to which coagulant dose needs are not met, for how long they are not met and the operational actions taken to return filter operation to its previous condition, changes in filter performance and time taken to recover can be subtle or substantial, as well as the rates of performance degradation and restoration.

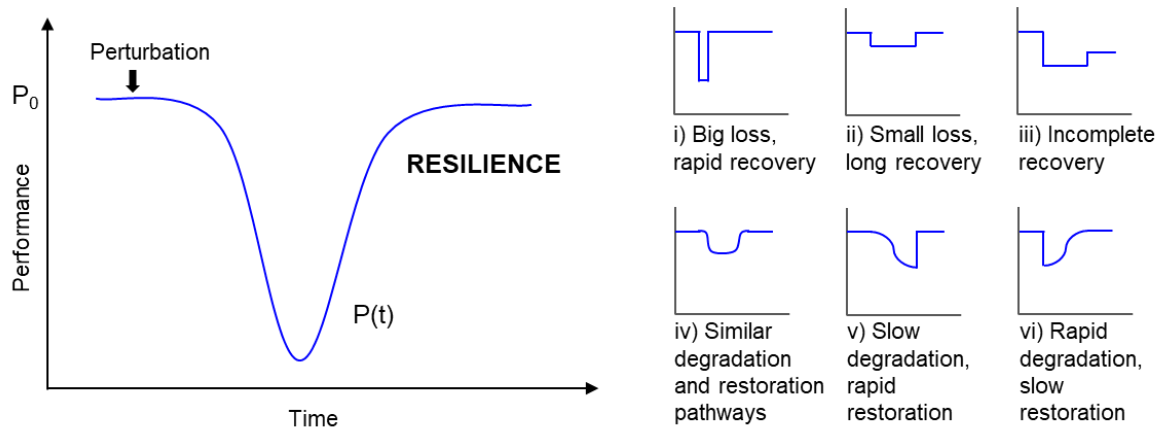


Figure 6.1: Graphical representation of resilience considering various patterns of performance variation over time

The contribution of an initial system condition (baseline) matters because a high-performing system might remain resilient given a partial recovery that would not be tolerated in a system that performs closer to acceptable thresholds. Notably, many resilience definitions in engineering systems (e.g., Hashimoto et al., 1982) are based on thresholds from which it is possible to differentiate satisfactory states from failure states. In the drinking water microbial risk context, a threshold indicating failure to provide safe drinking water cannot currently be defined over time because there are many pathways that can lead to “unsafe” drinking water, defined by exceedance of a given health endpoint. Indicators of treatment performance such as turbidity or log-removal credits are typically used to indirectly assess microbial water quality because it is impractical to continuously determine pathogen concentrations in drinking water (Regli et al., 1991). However, these indicators cannot completely indicate failure on their own, which makes evaluation of resilience from this perspective more difficult. For example, there might be pathogens passing through filters even if the effluent turbidity is lower than 0.3 NTU, a typical acceptable turbidity threshold (Ballantyne et al., 2024). Conversely, turbidities greater than 0.3 NTU do not necessarily confirm presence of pathogens in water because turbidity can also be caused by other particles

A broader definition of resilience is therefore needed to describe water quality challenges that cannot be completely described with only one variable that can readily be assessed over time. Herein, the scope of resilience is narrowed to define operational resilience as the capacity of a system to limit the risk consequences of insufficient treatment performance when adverse events perturb the system. It is important to note that the challenge of defining a failure state to describe resilience persists even if risk curves (instead of a single performance metric) are assessed over time because there is no instantaneous acceptable risk threshold in drinking water QMRA. Risk can be mathematically assessed over any event period, but it is typically assessed on an annual basis or at most on a daily basis because there are only acceptable risk thresholds for these two timeframes.

Adverse events analyzed through the lens of operational resilience can be treatment failures or changes in source water pathogen concentrations (happening concurrently or not). Notably, source water quality changes unrelated to changes in pathogen concentration can also result in insufficient treatment of pathogens (e.g., when affecting coagulation and potentially filtration downstream). For simplicity, only treatment failures are illustrated herein to easily refer to situations that can be described with figures similar to Figure 6.1, but other events can be similarly described as long as the effects of operational changes are coupled with the other corresponding factors influencing risk. Therefore, this definition of operational resilience can not only involve recovery from treatment failures but also systems' capacity for adaptation or transformation. For example, operational resilience can involve the use of an alternative water source to reduce risk consequences from a huge contamination event in the source water of a treatment plant. This was one of the operational strategies implemented by a water utility to respond to the wastewater spill event described in Chapter 3. While the risk of this strategy was not analyzed therein, it can also be evaluated and compared to the other discussed operational strategies (e.g., changes in treatment efficiency or spill flow).

6.5 Bridging microbial risk and operational resilience

Microbial risk and operational resilience are framed by linking concentrations of pathogens in source water to potential health effects caused by ingestion of contaminated water. This framing is relevant because it represents the context in which operational interventions can be applied for reducing risk during drinking water treatment. The general and simple definition of risk as a product of probability of occurrence and consequences is used to describe relationships between risk and resilience.

Describing the occurrence of adverse events is important to address risks. However, describing probabilities associated with such occurrences can be challenging when faced with rapid changes and increased variability. Milly et al. (2008) explained that climate change is undermining the assumption of stationarity (i.e., the idea that natural systems fluctuate within fixed patterns of variability), which has historically been relied upon for design, operations and risk management of water systems. Consequently, it is not always possible to know to what extent past observations can inform the probability of future event occurrences. Even if the probability of occurrence of adverse events cannot be well characterized (e.g., accurately describing probabilities of pathogen concentrations in water), describing the range of possible consequences given an adverse event using probabilities can be useful from a resilience perspective because this can give information on which parts of a system are more vulnerable or should be prioritized to increase overall system resilience.

Evaluating consequences of adverse events is also important for characterizing risk because an event with a low probability of occurrence can still have catastrophic impacts on a system. In complex systems such as drinking water, consequences can also be impacted by dependencies among different factors influencing risk. For instance, risk of contamination in treated water depends on the quality of the source water as well as the efficiency of treatment processes. The association of a high degree of contamination with higher treatment efficiencies will lead to a lower risk in comparison to a high degree of contamination associated with low treatment efficiencies (de Brito Cruz et al., 2024 (Chapter 5)). This example illustrates that systems affected by adverse events (in this case, a drinking water supply system) may have capacities (in this case, the efficiency of water treatment) that can directly influence the magnitude of consequences. Referring to the simple risk definition (i.e., *risk = probability of occurrence × consequences*), the probability of occurrence depends solely on an adverse event and its drivers. Consequences, however, depend not only on the magnitude of the adverse event but also on system capacities to respond to it and reduce consequences from it. Thus, risk is inherently dependent on the resilience of systems.

Resilience cannot be described solely by system capacities. It is critical to know if and how these capacities are effectively used to reduce risk. Conversely, consequences should also be considered when making investments to improve a system's resilience. Beyond the growing efforts to define strategies to develop resilience to various events in the water sector, it is also important to measure the value of these strategies for risk management to better support decision-making, risk prioritization and allocation of resources. Probabilities of occurrence and consequences (described quantitatively or not)

bridge the concepts of risk and resilience and are foundational concepts in risk science to measure the value of risk management strategies. However, they are not necessarily integrated in some resilience descriptions, which underscores barriers to a useful and practical implementation of resilience.

Resilience has been assessed qualitatively or semi-quantitatively using expert judgement (e.g., Luh et al., 2017) or quantitatively with metrics that are often based on analyses of performance variations over time. A common metric is the area between an initial performance level (P_0) and the actual performance of the system (P_t) following perturbation during the period between t_0 and t_f , which can be mathematically evaluated using Equation 6.1 (e.g., Bruneau et al., 2003; Cubillo & Martinez-Codina, 2019; Quitana et al., 2020). This metric, graphically represented in Figure 6.2, has been referred to as resilience loss (R). The case studies presented herein present limitations of this metric and underscore the importance of incorporating foundational risk concepts (i.e., information—quantitative or not—about probabilities of occurrence and consequences from a system perspective) into resilience descriptions.

$$R = \int_{t_0}^{t_f} (P_0 - P(t)) dt \quad (6.1)$$

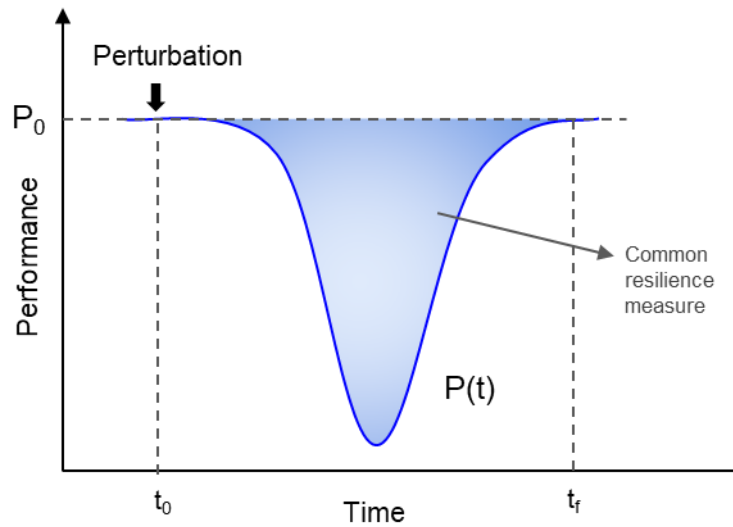


Figure 6.2: A common resilience metric from performance variations over time

6.6 Case studies

Three hypothetical case studies of relevance to drinking water treatment are used to describe relationships between microbial risk and operational resilience. Case study 1 demonstrates limitations of a common resilience metric (Equation 6.1) and why risk perspectives need to be integrated into description of resilience. In case study 2, the importance of risk assessment to describe the impact of resilience strategies is illustrated using three scenarios that present different treatment responses after disinfection failures. Case study 3 illustrates the contribution of operational resilience for risk management in drinking water treatment, in which the benefits of increasing disinfectant dose in two different periods are compared. QMRA is used as a tool to indirectly measure resilience by quantifying the benefits of different operational strategies for risk management. Risks are compared using Equation 6.2 that assesses risk in a given event period (Δt) where t_0 and t_f represent its bounds, and $P_{inf}(t)$ describes the instantaneous probability of infection. The derivation of this equation is presented in Appendix E Section E.1, and the calculations conducted herein consider time in units of days.

$$P_{\Delta t} = 1 - e^{\int_{t_0}^{t_f} \ln(1 - P_{inf}(t)) dt} \quad (6.2)$$

6.6.1 Case study 1: The need to integrate risk into resilience descriptions

A simple example (Example 1), in which two drinking water treatment plants (WTPs) are affected by a flood event that leads to a power outage for 10 h, is used here to illustrate the application of Equation 6.1 for evaluation of resilience. WTP 1 loses 10% of its treatment capacity (i.e., level of treatment provided) while WTP 2 loses 50% in this period, as depicted in Figure 6.3. Using Equation 6.1, the loss of resilience in WTP 1 is 100 %·h while in WTP 2, it is 500 %·h. Comparing these absolute values, the resilience metric presented in Equation 6.1 indicates that WTP 2 is less resilient than WTP 1. However, these values do not reflect the consequences of “losing resilience”. Although this metric has been referred to as resilience loss, it actually does not represent how much resilience was lost over time because resilience is not a synonym of performance. Losing resilience would mean losing the ability to limit risk caused by reductions in performance which is not equivalent to losing performance when impacted by an adverse event.

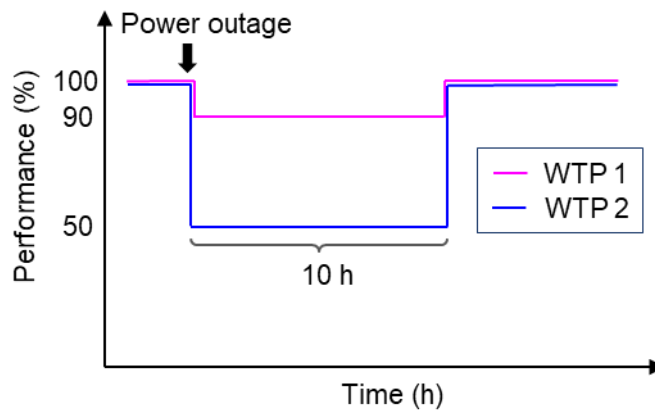


Figure 6.3: Performance losses in two water treatment plants after a power outage (case study 1, example 1)

In addition to the inaccuracy of this terminology, resilience metrics that simply couple performance states and time without accounting for the consequences of losing performance over time limit practical implementation of resilience (e.g., for comparative purposes). In the example above, it is important to know how bad it is to lose 100 or 500 units of performance·time and this can depend on how much performance is actually needed in each system. The consequences of this power outage might be similar in both systems if WTP2 has treatment redundancies implemented and does not need to use all its treatment capacity for achieving its treatment goal in such a way that losing 50% of its treatment capacity is as impactful for this system as is for WTP 1 losing 10%. To address this problem, some studies have added multiplicative weights to equations similar to Equation 6.1 to indicate the severity of consequences as well as thresholds associated to acceptable or critical performance levels (e.g., Cubillo & Martinez-Codina, 2019). However, it is also important to understand how severity is being assessed. The contribution of duration and magnitude of loss to risk might not be linear. For example, if limiting performance reductions is more important for reduction of consequences than cutting recovery times, a metric that equally values the magnitude of loss and duration may indicate that a system is more resilient to an adverse event, although it has worse consequences compared to other systems. This is further illustrated in case study 2 (Section 6.6.2.1). Especially in drinking water, it is critical to know the implications of these performance losses because the provision of safe water is directly linked to public health protection.

Resilience descriptions can also benefit from risk science because it can provide targets to support evaluation of resilience. To illustrate this idea, an example with defined thresholds in the drinking water

treatment context can be analyzed (Example 2). Drinking water regulations typically use indicators of treatment performance to control risk from microbial contaminants in drinking water. For example, turbidity is commonly used to indicate operational performance of filtration systems. In Canada, national guidelines recommend that turbidity measured at the effluent of individual filters should be less than or equal to 0.1 nephelometric turbidity units (NTU) at all times. If this is not possible, it is acceptable that turbidity is less than or equal to 0.3 NTU in at least 95% of measurements, either per filter cycle or per month; however, turbidity can never exceed 1.0 NTU, which would indicate a significant operational problem to be addressed immediately (Health Canada, 2012). Notably, these thresholds are not necessarily derived from risk frameworks but by risk perceptions resulting from correlations between turbidity and pathogen removal, although there is no fundamental relationship between them. Figure 6.4 shows these thresholds in a turbidity versus time graph, in which turbidity values are presented in decreasing order as turbidity is inversely related to filter performance. If a filter's effluent turbidity follows the pattern shown in Figure 6.4, analyzing the whole area from the initial system condition until complete recovery would not be as meaningful for risk management as defining resilience targets associated to each threshold because crossing these thresholds represents different consequences for this system (i.e., some areas are more consequential than others). For example, the area above the 0.1 NTU mark, although it represents impacts from perturbation, cannot be equally valued with the area below the acceptable threshold of 0.3 NTU.

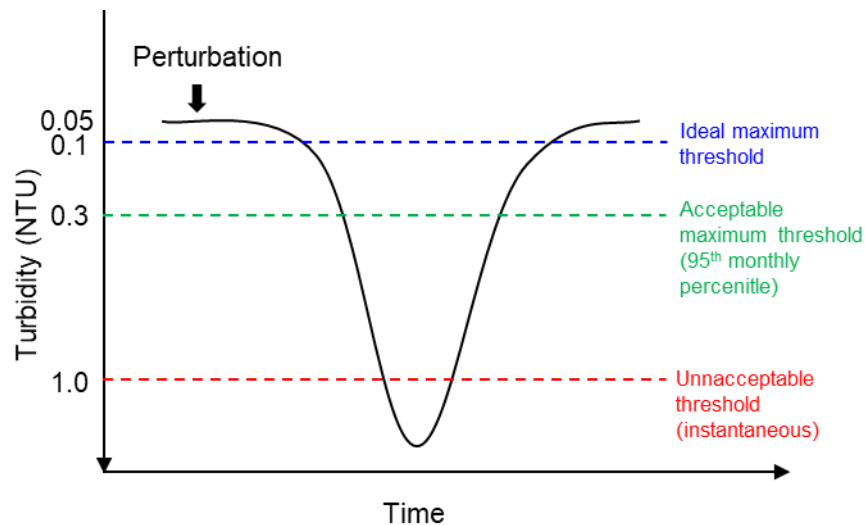


Figure 6.4: Performance loss and associated turbidity thresholds (case study 1, example 2)

An additional insight from risk frameworks that can be useful for resilience is the notion of describing probabilities or chances of occurrence. While most risk assessment frameworks attempt to estimate the chances of occurrence of adverse events, some of them also include description of the chances of failures in systems given an event. For example, in FMEA, the probability of failure given a defined failure mode is scored, commonly qualitatively or semi-quantitatively. Describing these probabilities is important for resilience description because it can better inform decision-making about not only the consequences of adverse impacts on a system but also their chances of occurrence. Therefore, to be meaningful and actionable, resilience should be integrated with measures of consequences, chances of failure and ideally well-defined thresholds, which can be informed by risk assessment frameworks when the overall goal of resilience is to support risk management.

6.6.2 Case study 2: Risk is important to describe resilience

In this case study, risk from *Giardia duodenalis* in drinking water is evaluated in a water treatment plant. Under typical operating conditions, the treatment plant is credited with a 6-log reduction for *Giardia*, of which 3 log are attributed to conventional filtration and 3 log to chlorine disinfection. Three operational responses (scenarios 1, 2 and 3) to improve treatment efficiency and manage *Giardia* health risks in drinking water are analyzed following hypothetical failures in the chlorination system. The risk in each scenario is evaluated using QMRA to compare the effect of these operational strategies, illustrated in Figure 6.5. For simplicity, it is assumed that transitions between different treatment efficiency phases are instantaneous in all scenarios. They consider a baseline concentration of 0.05 cysts/L, a daily drinking water consumption volume of 2 L, and an exponential dose–response model with parameter $r = 0.01982$ (Rose & Gerba, 1991).

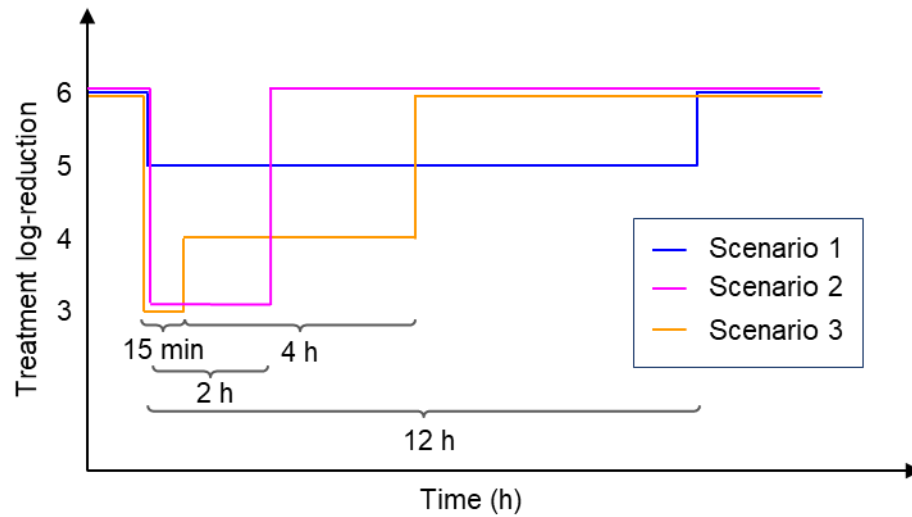


Figure 6.5: Treatment changes of scenarios described in case study 2

Scenario 1 represents a partial failure of the chlorine dosing system due to a sensor failure. A sub-optimal chlorine dose was added for 12 hours until operators manually verified the added dose, detected the problem and fixed it. It is estimated that only 2 log could be credited to disinfection during the failure period.

In scenario 2, the chlorination system is completely shut down, but the plant has the capacity to activate an ozone system before filtration. Operational modifications are necessary so the water coming from the sedimentation basin could flow through the ozone tanks. The current infrastructure enables the change, and a standard operating procedure is available. After 2 h from the beginning of the chlorination failure, the ozone system is operated and can provide 3 log of *Giardia* reduction, replacing the chlorination system until it is restored.

Scenario 3 relies only on coagulation optimization to increase pathogen removal by filtration after a complete failure of the chlorination system. The plant used zeta potential analyzers to adjust coagulant dose and better control particle charge neutralization. A total chlorination failure was detected after 5 min and procedures to better control coagulation were implemented 10 min after the problem was detected. In this scenario, four additional hours passed until the chlorination system returned to normal conditions. It is assumed that after that, the plant relied only on the basic filtration credit of 3 log.

6.6.2.1 Analyzing the contributions of magnitude and duration of loss to risk in QMRA

The relationship between magnitude and duration of performance loss in the drinking water microbial risk context can be analyzed using scenarios 1 and 2, which have only two phases with different magnitudes and duration of failure. While scenario 2 presents a faster recovery, it provides a greater reduction in treatment performance in comparison to scenario 1 during the failure period. Using Equation 6.2, risk over the longest failure period of 12 h (measured as probability of infection per person over 12 h) is equal to 9.91×10^{-9} and 1.66×10^{-7} in scenarios 1 and 2, respectively, indicating that scenario 1 is less risky than scenario 2 despite its longer failure duration. If treatment were considered in a linear scale using Equation 6.1, the loss of performance over time of scenarios 1 and 2 would be $12 \log \cdot h$ ($1 \log \times 12 h$) and $6 \log \cdot h$ ($3 \log \times 2 h$), respectively. This would indicate that scenario 1 is less resilient than scenario 2, although it has approximately 17-fold more risk. Mathematically, handling treatment log-reduction values on a linear scale can potentially be misleading (Schmidt et al., 2020).

It is important to understand how the magnitude of failure and failure duration impact risk for a better description of resilience. In cases in which the probability of infection is much smaller than one and linearity of dose–response models can be assumed, it is simple to mathematically evaluate this relationship in the QMRA context. An increase in recovery time by a factor X is equivalent to a decrease in treatment log reduction of $\log_{10}(X)$ for the same effect on risk, as described in Appendix E Section E.1. As the recovery time increased 6-fold (12 h divided by 2 h) from scenario 2 to scenario 1 in this example, an equivalent failure of scenario 2 would be $4.22 \log$ ($5 - \log_{10} 6$). Because treatment in scenario 2 during the failure period was lower than $4.22 \log$, this scenario has a higher risk when compared to scenario 1. Due to the non-linearity of treatment log-reduction and time in the risk function, limiting the magnitude of failure is more relevant for risk reduction than decreasing the recovery time. In cases in which two scenarios with different magnitudes of loss and duration pose equivalent risk on average, it is also recommended to choose the one that has a lower magnitude of loss. This is because a higher treatment efficiency leads to a lower dose of pathogens, reducing the instantaneous risk. Lower risk spread out over a longer period may ease risk management by allowing more time for acquisition and application of resources. As this example with QMRA shows, resilience metrics can be substantially more complex than a simple addition or multiplication of the magnitude and duration of loss. A quantitative risk framework like QMRA can be a useful tool to link resilience and risk.

6.6.2.2 Prioritizing risk management strategies

Scenarios 2 and 3 represent different system responses to the same perturbation (i.e., a complete chlorination failure that decreased treatment of *Giardia* by 3 log). Similarly to the analyses conducted in Section 6.6.2.1, risks from these two operational strategies can be evaluated to define which one is less risky (and indirectly more resilient). The results show that the ozone system replacement (scenario 2) has a risk of 1.65×10^{-7} infections per person over 4.25 h, whereas quickly optimizing coagulation (scenario 3) has a risk of 5.37×10^{-8} infections per person over 4.25 h. Consistent with the previous result, this example shows the importance of reducing the magnitude of failure. In this case, a quick partial recovery substantially increases the resilience of the system despite the longer total recovery time. Notably, optimizing coagulation performance also seems operationally simpler than activating a whole new disinfection system. In a case in which two risk management strategies lead to similar risk, the simplicity or cost-effectiveness of different actions can also be considered in decision-making and resilience assessment.

6.6.3 Case study 3: Operational resilience contributes to better risk management

The efficiency of chlorine disinfection depends on temperature, thus the performance of the chlorination process in drinking water treatment can vary seasonally. For simplicity, it is assumed that a year can be described by only two seasons of equal length, in which 2 log inactivation of viruses is provided by chlorination during the cold season and 3 log during the warm season. An operational strategy is being considered to increase the disinfection performance by adding more chlorine during only one of the seasons. Assuming that the same incremental addition of chlorine can provide an additional 0.5 log inactivation during the cold season and 1 log during the warm season, as well as that viral contamination does not substantially vary throughout a year, guidance is needed to decide in which season it is more beneficial to implement this operational strategy. Figure 6.6 depicts these two alternative operational scenarios. The black line represents standard practice while the blue and pink lines represent application of the operational strategy in the cold and warm seasons, respectively.

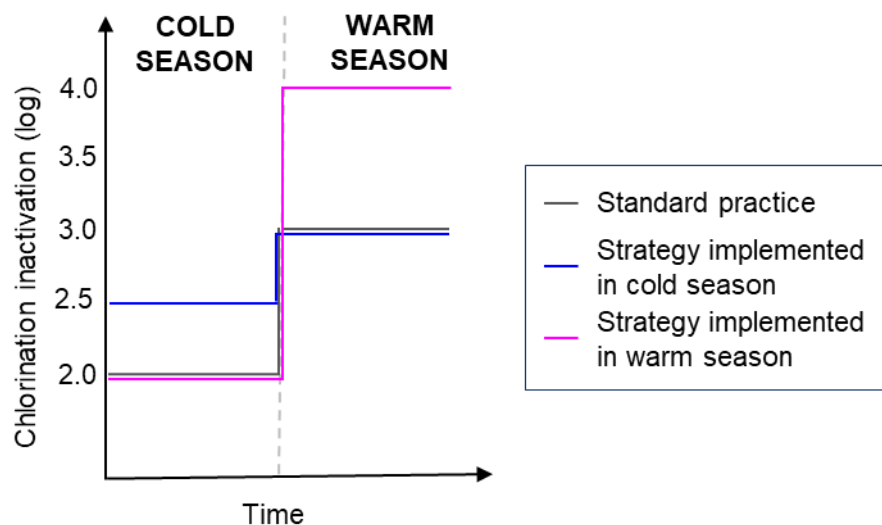


Figure 6.6: Scenarios described in case study 3

The effective log-reduction (Schmidt et al., 2020) can be used to compare the average performance over the two seasons of both operational strategies. Appendix E Section E.2 presents the calculations of results reported in this case study. Under the standard practice scenario, 2.26 log of inactivation of viruses is provided on average annually. Increasing the disinfectant dose during the cold season would increase the overall performance to 2.68 log while adding the same disinfectant dose increment in the warm season would lead to average performance of only 2.30 log. Therefore, it is better to implement the operational change in the cold season. This result may be counterintuitive because the increase in performance of adding the same dose in the warm season is higher. However, this example highlights the importance of *pushing the bottom up* (i.e., elevating performance when it is low) instead of focusing on providing more treatment during high performance periods. Due to the diminishing returns of equal incremental increases in log-reduction values (e.g., the difference between 1 log and 2 log is 9%, the difference between 2 log and 3 log is 0.9%), it is better to be “less bad” than “more good”. Other practical examples were reported in de Brito Cruz et al. (2023) (Chapter 4) for filtration in drinking water treatment, which is inherently a very dynamic process due to filter cycle variations. In one of the examples analyzed therein, increasing the removal during stable operation (the period of highest performance of the filter cycle) from 4.7 log to 7 log only increased the overall performance by 0.02 log if periods of lower performance were not changed, demonstrating that huge increments of performance may not always be as impactful as they seem to be. In case study 3, increasing the disinfection inactivation infinitely (i.e., removal of all pathogens) during the warm season still would

not result in a comparable effect on average treatment performance to increasing treatment by 0.5 log during the cold season, leading to only 2.30 log on average. This shows how low performance periods can drive overall treatment performance. Therefore, treatment can be affected by how infrastructure is operated and it is important to be strategic to obtain the best return on investment of any treatment change and ensure the provision of safe drinking water.

If considering the increment of performance over time linearly (i.e., adding 0.5 or 1 log over half of the year), implementing the operational change in the warm season would be erroneously evaluated as having a better effect in comparison to implementing the change in the cold season. However, treatment of microbial contaminants is measured on a logarithmic scale (i.e., non-linear). Consequently, the overall gain of performance must not be compared linearly. This case study is used here to show how operational resilience can be used to reduce risk. Notably, risk was not evaluated in case study 3 but, assuming that other factors influencing risk do not change in both situations, the risk associated with implementation of the operational strategy in the cold season will be lower than the corresponding risk for implementation in the hot season. Nevertheless, if these factors change in different seasons, it is important to evaluate its effects in conjunction with performance changes. As emphasized in case studies 1 and 2, the analysis of performance variations over time—even if considering the non-linear relationship between performance and time as in this case study—does not necessarily tell what the implications of increasing the treatment performance from 2.26 log to 2.30 log or 2.68 log are. It is desirable to know how much improvement (or less damage) resilience brings to a system. Risk considerations are critical to describe resilience, but other metrics can also be coupled with risk to understand the impacts of improved resilience (e.g., cost of operational strategies).

6.7 Limitations and research needs

This work presents a rationale for association between risk and resilience to enable practical implementation of resilience concepts in a drinking water safety context focusing on operational treatment resilience and microbial risks. However, one limitation of this approach to describe operational resilience is that it depends on data to characterize performance variations (or risk variations) over time. While it can be useful for post-incident assessment of resilience (i.e., after the system has been affected by a perturbation and its responses have been recorded), the applicability of analysis of performance variations over time for the development of resilience before a disruptive event

occurs depends on data or hypothetical scenarios to estimate how a system will behave when facing potential perturbations. Acknowledging this difficulty, other authors have argued that measuring resilience can only be done after a disturbance has ceased (Lake, 2013). A resilience metric was not proposed herein because the final performance (or risk) outcome depends not only on the resources a system has but also on how they are applied when an adverse event occurs. Two systems with the same infrastructure and operational capacity can be impacted differently by the same event because of one different decision. Nevertheless, scenario analyses can be used to compare and evaluate the usefulness of different alternatives for risk management, thus contributing to better operational responses.

As operational resilience is the capacity of a system to limit the risk consequences of insufficient treatment performance when adverse events perturb the system, describing these capacities through modelling or experimental work is important to advance operational resilience. Moreover, research is needed to better characterize the effects of sudden and impactful perturbations in water treatment, including cascading effects on a system level. The provision of safe water does not depend on *one* system that might fail in certain conditions. In fact, water treatment is composed of multiple individual and complex systems that are combined for achievement of multiple goals. Accounting for cascading effects and understanding the impact of dependencies on risk and resilience is critical for drinking water safety (de Brito Cruz et al., 2024 (Chapter 5)).

Additionally, risk assessment was used herein to indirectly measure the effects of resilience strategies. However, risk in QMRA is usually assessed on an annual basis, whereas many events that underscore the need for resilience in water systems are short-term events. The effects of these events can be averaged out if handled within long-term risk metrics, thus not indicating their potential criticality in the short-term. Therefore, new acceptable risk thresholds should be developed to better gauge resilience and enable better management of risks in different temporal scales.

This work focused on a specific aspect of operational resilience, considering only the effects of treatment performance variations over time. Operational resilience has a role for risk management that is often put in the background of big infrastructure investments. Instead of acquiring new resources to mitigate risks from potential adverse events, sometimes it can be simpler and less expensive to use existing resources as efficiently as possible for risk management. Notably, other factors influencing operations such as availability of material (e.g., chemical products) and human resources to implement operational changes (e.g., operators) can also contribute to operational resilience, and approaches to

describe these contributions need to be developed. There are several dimensions in which resilience can be described (e.g., social, technical, environmental) and, given the multiple concepts associated with resilience (e.g., anticipation of challenges, systems adaptation and transformation, recover), further research efforts are necessary to comprehensively describe resilience in the many types of water systems in which it can be studied. These efforts should go beyond existing theoretical frameworks to define resilience to more actionable frameworks, so that resilience is not only used as a trendy word but as a practically relevant tool in the water sector.

6.8 Conclusions

The need for building resilience as a risk management strategy has been increasingly discussed in the water sector, but risk is typically only considered as motivation for achieving resilience and not as an integral part of describing resilience. Achieving resilience requires prioritization of efforts to address the impacts of perturbations on a system and reduce risk, but without foundational risk concepts it is not possible to know the value of these efforts for risk management (e.g., by how much risk is reduced or what strategies should be prioritized). The main conclusions are as follows:

- It is critical to incorporate the risk concepts of probabilities of adverse events and consequences (quantitatively or not) into resilience descriptions to better assess the value of resilience strategies for risk management. This will better inform investments and decisions related to resilience, thus contributing to building and enhancing resilience in practice.
- Operational and design decisions affect treatment performance, and thus risk, sometimes in ways that are not immediately obvious. Operational resilience can be considered as the capacity of a system to limit the risk consequences of insufficient treatment performance when perturbed by adverse events and it can contribute to risk management by improving knowledge of a system and understanding of implications of different operational strategies on risk.
- In the drinking water QMRA context, limiting log-scale performance reductions after a perturbation is more important to resilience than reducing recovery times.

Beyond risk descriptors, frameworks are needed to explore, comprehensively describe and ultimately operationalize resilience in drinking water treatment. This is needed to ensure the continuous delivery

of safe drinking water and thus public health protection despite increasing threats in the water industry such as climate change, failing infrastructure and an aging workforce as well as the associated loss of institutional knowledge.

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Chapter 7

Conclusions, contributions and recommendations for future research

7.1 Conclusions

Conclusions specific to each objective are presented at the end of each Chapter. The major conclusions from this research can be summarized as follows:

- It is critical to tailor pathogen data collection during source water monitoring to best represent water entering the treatment plant so their use in risk assessment can better inform treatment decisions and maximize return on investment. While this may seem obvious, how to best represent system-specific attributes in monitoring design and implementation is often far from obvious. For example, ensuring that the water entering the treatment plant is accurately represented in big systems with multiple intakes can be challenging. Advantages and disadvantages of five methods were contrasted depending on the needs and capabilities of each water utility. Site-specific pathogen concentration variability affects the precision of computed treatment requirements, and this can be considered when determining sampling frequencies with a novel developed approach. Monitoring programs are costly and the treatment decisions based on them can have direct implications on public health protection. Nonetheless, data from other systems or the scientific literature are commonly used in drinking water risk assessment, ironically often at the expense of system-specific insight needed to accurately characterize risk and optimize treatment performance.
- When using risk assessment to determine treatment requirements, microorganism concentrations used in the model need to be consistent with the time frame over which risk is evaluated. Computing annual risk using an individual concentration value assumes that it is sustained all year round, which can substantially bias treatment requirements and misinform decisions. Temporal overrepresentation of concentration values occurs in practice due to conflation of instantaneous risk and an annual risk framework or due to the scarcity of data in drinking water risk assessment. Therefore, caution is needed when using such data.
- *Giardia* should be included along with *Cryptosporidium* in both protozoa monitoring programs and risk assessment for evaluation of treatment needs because *Giardia* cysts are often more abundant than *Cryptosporidium* oocysts and can therefore drive risk and treatment requirements, despite *Cryptosporidium* being more difficult to treat. Because Method 1623.1 allows for the concurrent analysis of both *Cryptosporidium* and *Giardia*, conducting risk assessment for both pathogens involves minimal additional effort.

- During short-term events in which water quality can rapidly deteriorate (e.g. accidental wastewater spills), case-specific data might not be available to estimate treatment needs. Conducting comprehensive and mathematically complex risk assessment is not practical when time-sensitive decisions are needed. Thus, scenario-based QMRA can be a useful tool for preliminary risk assessment and can potentially inform operational decisions to improve drinking water system response to adverse events.
- Plant-scale risk assessment is essential to microbial risk management because the collective and dynamic operation of multiple treatment units in parallel and/or in series is what ultimately determines risk. Current practice and regulatory guidance do not always acknowledge plant scale considerations (e.g., dynamic performance of parallel filters), thus missing opportunities for improved microbial risk management and public health protection.
- Periods of low performance have an amplified impact on overall treatment performance, especially because treatment performance of microbial contaminants is typically expressed using a logarithmic scale. Operational strategies should therefore prioritize improving performance when it is “low” rather than maximizing performance when it is already “high”. This conclusion challenges the intuitive notion that “more is always better”.
- Operational and design decisions (e.g., number of filters in operation, duration of stable operation and breakthrough, removal during stable operation and breakthrough, different backwashing schedules, filter-to-waste operation and coagulation optimization) affect plant-scale performance as shown with a newly developed model. The effects of these decisions are sometimes counterintuitive and should be characterized so that risk can be managed based on plant scale rather than individual process scale performance.
- Ignoring dependence among factors known to influence risk (e.g., source water quality, treatment efficiency) can lead to over- or underestimation of risk, sometimes substantially (e.g., more than an order of magnitude). Because these factors can be associated in practice, it is important to consider the effects of dependence on risk, or at least to explicitly acknowledge when independence is assumed; this has largely been absent in QMRA practice.
- Ideally, dependence can be evaluated using available mathematical approaches if QMRA input data (e.g., pathogen concentrations, treatment efficiency) are collected in a paired fashion. Recognizing that this is often not feasible in plant-scale water treatment, a newly developed

framework for analyzing the sensitivity of risk to dependence among model inputs can be used to describe the potential effect of dependence (i.e., how it could impact risk and by how much).

- A water supply system's capacity to limit risk consequences of insufficient treatment performance when adverse events perturb it can be defined as its operational resilience. It is important to consider and characterize this capacity (i.e., which strategies can be implemented, how they can be used and what their effects on risk are) because operations and design decisions affect treatment performance, and thus risk, sometimes in ways that are not immediately obvious.
- Resilience description must reflect risk to be an actionable tool for risk management because achieving resilience requires prioritization of efforts to address the impacts of perturbations on a system; this can only be done if the probabilities of adverse events and the magnitudes of their consequences—foundational risk concepts—are included. Beyond risk descriptors, frameworks are needed to explore, comprehensively describe and ultimately operationalize resilience in drinking water treatment. This is needed to ensure the continuous delivery of safe drinking water and thus public health protection despite increasing threats in the water industry such as climate change, failing infrastructure and an aging workforce as well as the associated loss of institutional knowledge.

7.2 Key contributions

Managing acute risks from microbial contaminants is an everlasting goal of the water industry. Integrating knowledge of system operations with risk represents an important step to ensure this goal is achieved given old and new microbial challenges that the water industry faces. The aforementioned conclusions provide original contributions to advance science or practice in the following areas:

7.2.1 Water treatment decision-making

Drinking water utilities can be confronted with insufficient guidance on what level of treatment is needed to control microbial risks when experiencing changes in source water quality, adjusting to regulatory updates or having to respond to events affecting their raw water or routine operations. Sole reliance on generic rules provided in drinking water regulations might render treatment insufficient even in typical conditions because different systems may have different needs. The water industry is

especially known for being risk averse because it is intrinsically related to public health protection, but huge costs associated with always implementing *more* infrastructure and technologies are not affordable in many places. Therefore, water supply systems need to ensure drinking water safety while preventing expending unnecessary resources when making treatment decisions.

Treatment needs depend on knowledge of raw water quality (input of the treatment system) as well as targets for treated water quality (output of the treatment system) in various conditions. While the definition of acceptable risk targets for drinking water has opportunities for development identified (but not addressed) in this research (i.e., in cases of short-term events), contributions were provided to improve knowledge of raw water quality and define treatment goals during typical conditions and to support treatment decisions as best as possible when source water quality information is not available. **In Chapter 2, comprehensive guidance for development of routine pathogen monitoring programs** was proposed including planning (sampling location and frequency), execution (procedures for sample collection and analysis, data recording and storage), data analysis (estimation of contaminant concentration, evaluation of treatment needs) and decision support (assessment of treatment sufficiency). These routine monitoring programs not only support treatment decisions during typical operations but also provide information about baseline conditions. During challenging short-term disruptions (e.g., sudden water quality variations caused by climate-change-related disturbances, treatment deficiencies, aging infrastructure failures), it is also important to have good characterization of baseline water quality because regulatory compliance in drinking water is usually defined in terms of annualized (long-term) acceptable risk targets. This was demonstrated in Chapter 3, in which a simple modeling framework using deterministic and scenario-based QMRA was developed to support treatment response after short-term events. **This framework can be adapted by water utilities for rapid treatment decision-making when data availability is limited or time-sensitive decisions are needed.**

7.2.2 Water treatment operations

The role of treatment operations to support management of microbial risk is broadly recognized and was emphasized in this research. While operations are usually in the background when compared to “having” treatment infrastructure in the water industry, it is worth referring to a perhaps very different industry that clearly illustrates the potential of operations for performance. Formula 1[®] fans can well understand that what defines a champion is not the best car or the best driver, but the best balance of

both. **A remarkable contribution of this research to how operational practices are viewed in water treatment is that it cannot be analyzed in silos. This research demonstrated that optimized performance of individual units does not reflect plant-scale performance.** It is critical to analyze water treatment with a systems perspective and evaluate plant-scale performance because risk depends on the quality of treated water that exits a plant and this quality is a result of several complex and not always independent processes.

The common belief that “more is always better” was also refuted in the context of treatment of microbial contaminants. As demonstrated in Chapters 4 and 6, operational strategies should prioritize improving performance when it is low rather than maximizing performance when it is already high because treatment of microbial contaminants is usually assessed in a logarithmic scale. Additionally, understanding and applying appropriate operational changes is arguably cheaper than implementing new infrastructure in the water industry. Advancing this topic, **several novel contributions were reported in Chapter 4 in the context of conventional filtration regarding the effects on plant-scale performance of different operational decisions such as number of filters in operation, backwash staggering schedules and filter-to-waste operation. An adaptable model was developed to evaluate the effects of several design and operational changes on plant-scale filtration performance and to identify strategies to increase treatment resilience to microbial risks.** In Chapter 6, the concept of operational resilience was defined and illustrative case studies showed how the integration of fundamental risk concepts into resilience descriptions is critical for practical implementation of resilience as a risk management tool.

7.2.3 Quantitative microbial risk assessment

QMRA is an established modelling framework that supports microbial risk management in drinking water. As with any modeling approach, QMRA often relies on simplifying assumptions to enable estimation of health risks. This work investigated the effect of a commonly overlooked assumption when risk is evaluated using Monte Carlo simulations in drinking water QMRA: the independence among model inputs. Drinking water is a product of several complex processes from the source to the tap that can be associated in some circumstances. Dependence between pathogen concentrations and treatment efficiency is especially concerning if deteriorated water quality occurs concurrently with reduced treatment performance, which results in higher risk. This research showed that ignoring dependence can have an impact on risk profiles (either under- or overestimating risk) and consequently

impact decision-making to control microbial risk in drinking water (Chapter 5). **Acknowledging that data scarcity is usually a big limitation to assessing dependence in this field, a framework is provided to characterize the potential for assumed independence to bias interpretation when it is not valid.**

Notably, data availability is a general limitation in several QMRA applications due to the difficulties of estimating microbial concentrations and characterizing exposure. It is common to conduct risk assessments with assumed values from literature or available data that were not necessarily collected for the intended purpose of the risk assessment. In this context, **another contribution of this research was to establish criteria for the collection of data in pathogen monitoring programs to match their use in QMRA for evaluation of treatment needs (Chapter 2).**

The connection between QMRA and resilience was also explored in this research. While resilience has been an intensively debated topic in many areas, there are not many frameworks for practical implementation of this concept in water treatment. **By allowing measurement of the benefits of resilience, the contribution of QMRA to operational resilience in drinking water was presented in this research, opening a path forward to evolving resilience assessments in practice (Chapter 6).**

7.2.4 Monitoring policy

Although policy development was not the main focus of this research, some contributions can be highlighted, especially regarding pathogen monitoring programs. Drinking water policies tend to prescribe rules or provide guidance generically to cover as many situations as possible. However, there are multiple possibilities for provision of drinking water (e.g., types of water source, treatment systems, human and financial resources available) and water systems have recently been stressed by changes such as emerging contaminants, extreme events and increasing demand. These factors increasingly make it difficult to apply *one-size-fits-all* rules to all systems, which underscore the need for specific guidance.

It is important to know the quality of raw water to efficiently treat it, but implementing a pathogen monitoring program is costly. When it is done, monitoring should be conducted strategically to maximize return on investments and better inform decision-making because the treatment decisions based on monitoring can also be costly and, more importantly, are intrinsically related to public health protection. Thus, monitoring cannot be viewed as one single tool able to support the multiple objectives

needed for the provision of safe drinking water. For instance, monitoring water quality for source water protection is different than monitoring for evaluation of treatment needs which in turn is different than monitoring for detection of treatment failures. A monitoring program that is designed to characterize average source water quality may not be informative enough to determine treatment decisions about the water entering the plant and to ensure the provision of safe drinking water not just on average but all the time. The purpose of monitoring programs must be clear, so specific guidelines developed to target monitoring goals are not misinterpreted by water practitioners.

Expanding what is presented in current water policies regarding the development of monitoring protocols to inform treatment decisions, specific guidance was provided in this research. **To better support the choice of sampling locations, additional approaches were added to the ones recommended in guidance following the United States Environmental Protection Agency's (U.S. EPA) Surface Water Treatment Rules along with a discussion of their advantages and disadvantages. A novel approach was also proposed to determine the frequency of sampling to better represent a system's needs in terms of its water quality,** instead of what is instructed in regulations in the United States and the Netherlands that use the size of a system to prescribe sampling frequency requirements. Increased variability in pathogen concentrations leads to more imprecise risk estimates, thus more data may be needed to increase confidence in the accuracy of estimated treatment requirements. Alternatively, a sampling protocol linked to source water quality instead of a system size can save costs if the variability of pathogen concentrations is low.

This work also provided evidence to support inclusion of *Giardia* in protozoa monitoring programs in addition to monitoring of *Cryptosporidium*, as *Giardia* can drive treatment needs in some systems due to its increased concentrations compared to *Cryptosporidium*. Currently, the United States only requires monitoring of *Cryptosporidium* for establishment of treatment requirements, and this consideration should be included in the ongoing potential revisions of the Microbial and Disinfection Byproducts Rules of the U.S. EPA.

This work also identified the need for establishing fixed-magnitude safety factors when determining compliance rules. The sufficiency of treatment can be consistently evaluated across systems with fixed thresholds (e.g., a maximum 0.3 log difference between treatment achieved and required) instead of ratios that can become more lenient as treatment needs are greater (e.g., 90% of treatment required, as 90% of 3.0-log is 2.7-log, 90% of 4.0-log is 3.6-log, and so on).

Multiple thresholds could be set to trigger different risk management strategies (e.g., operational changes, regulator notification, boil water advisory, interruption of supply).

7.3 Recommendations for future research

Safe drinking water is an irreplaceable human need and controlling risks from microbial contaminants is a key focus to ensure this need is fulfilled and to support progress toward the United Nations' Sustainable Development Goal 6 (i.e., ensure availability and sustainable management of water and sanitation for all). This research contributed to addressing some gaps in this context, but opportunities for advancing microbial risk management through integration of risk assessment and water supply operations still exist and are expected to emerge as new microbial water challenges arise and water systems capacities to deal with them continue to evolve. Potential research topics for further investigation are:

- Guidance for event-based pathogen monitoring: Similarly to the guidance provided in Chapter 2 for routine pathogen monitoring programs, protocols for event-based monitoring can be developed to characterize events and potentially inform treatment responses.
- Description of non-stationarity in risk assessment: As non-stationary has been indicated as one of the drivers of change in how risks are managed in water systems, it is worth investigating the scope of non-stationarity regarding pathogen concentrations in water, how it can be modelled and what potential implications there are for risk management.
- Development of new risk references: As discussed in Chapter 3, common long-term acceptable risk references to assess risks in QMRA may not meaningfully support immediate risk management of short-term events. Research is needed to propose new risk references appropriate to address different risk situations.
- Enhancing risk management for *de facto* reuse: Given the widespread implementation of *de facto* reuse (i.e., reuse of wastewater discharged upstream of a drinking water intake), policies should be developed to integrate water and wastewater systems via guidance to manage risk from wastewater spill events.

- Investigation of autocorrelation in drinking water QMRA: The effects of dependence among different model inputs in drinking water QMRA were explored in Chapter 5, but evidence and potential effects of autocorrelation (i.e., temporal dependence between values of one input) remain unexamined in this field.
- Resilience in water systems: While this research focused on operational resilience, resilience is a broad concept that can be applied to many areas in drinking water (e.g., infrastructure, logistics, governance, source water protection) and frameworks to operationalize the application of resilience can be developed.

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Appendix A

Supplementary information for Chapter 2

A.1 Derivation of equation for assessment of log reduction required

Equation 2.1 for assessment of log-reduction required (LR_{req}) can be derived given the daily source water (oo)cyst concentration (C_{daily}) in (oo)cysts/100 L, parameter of the dose–response model (A), daily volume of unboiled tap water consumed in litres (B), fraction of infections leading to illness (C), disability-adjusted life years (DALYs) per case (D) and maximum acceptable risk (E).

Using an exponential dose–response model, the daily probability of infection is given by

$$P_{inf,daily} = 1 - e^{-A \times \frac{B}{100} \times 10^{-LR_{req}} \times C_{daily}} \quad (A1)$$

The annual probability of infection can be then evaluated from

$$P_{inf,a} = 1 - \prod_{i=1}^{365} (1 - P_{inf,daily}) \quad (A2)$$

Replacing (A1) in (A2):

$$P_{inf,a} = 1 - \prod_{i=1}^{365} \left(1 - \left(1 - e^{-A \times \frac{B}{100} \times 10^{-LR_{req}} \times C_{daily}} \right) \right) = 1 - \prod_{i=1}^{365} \left(e^{-A \times \frac{B}{100} \times 10^{-LR_{req}} \times C_{daily}} \right) \quad (A3)$$

Equation A3 can be simplified to

$$P_{inf,a} = 1 - e^{-A \times \frac{B}{100} \times 10^{-LR_{req}} \times \sum_{i=1}^{365} C_{daily}} \quad (A4)$$

The sum of daily concentrations can be expressed using the average source water concentration in a year (C_{raw})

$$C_{raw} = \frac{\sum_{i=1}^{365} C_{daily}}{365} \quad (A5)$$

Using (A5) in (A4)

$$P_{inf,a} = 1 - e^{-A \times \frac{B}{100} \times 10^{-LR_{req}} \times (365 \times C_{raw})} \quad (A6)$$

The annual DALYs (E) can be calculated from the annual probability of infection using the fraction of infections leading to illness (C) and DALYs per illness (D) factors as in

$$E = P_{inf,a} \times C \times D = (1 - e^{-A \times \frac{B}{100} \times 10^{-LR_{req}} \times (365 \times C_{raw})}) \times C \times D \quad (A7)$$

Replacing the values of E (10^{-6} DALYs/person/year), C (0.4 for *Giardia* and 0.7 for *Cryptosporidium*) and D (1.67×10^{-3}) used in this study in Equation A7, the factor $A \times \frac{B}{100} \times 10^{-LR_{req}} \times (365 \times C_{raw})$ is equal to 0.001498 and 0.000856 for *Giardia* and *Cryptosporidium*, respectively. Because this factor is small in both cases, the limit $1 - e^{-x} \approx x$ as $x \rightarrow 0$ can be used with an error of $< 1\%$. Accordingly, the annual DALYs can be simplified to

$$E \approx A \times \frac{B}{100} \times 10^{-LR_{req}} \times (365 \times C_{raw}) \times C \times D \quad (A8)$$

Applying a base-10 logarithm on both sides of Equation A8:

$$\log(E) \approx \log(A) + \log\left(\frac{B}{100}\right) - LR_{req} + \log(365 \times C_{raw}) + \log(C) + \log(D) \quad (A9)$$

The log-reduction required can be back-calculated rearranging Equation A9:

$$LR_{req} \approx \log(365 \times C_{raw}) + \log(A) + \log\left(\frac{B}{100}\right) + \log(C) + \log(D) - \log(E)$$

A.2 Reassessment of sampling strategy in Calgary

In the framework implemented in Calgary in 2021, additional sampling of the river intake of the Bearspaw treatment plant was included and the method chosen to represent the water entering the plant was to adjust the number of samples per intake based on their average proportional flow contribution. The framework was reassessed after two years of implementation to evaluate the impact of adding this new sampling point and possibly adjust the number of samples at each intake, if needed, because these average contributions can vary over time. Data from May 2021 to Apr 2023 about the contribution of each intake was analysed and 66% of the water comes from the dam intake on average. As a result, it was recommended to maintain the previously recommended numbers of samples per intake. To analyze the effect of the addition of a new sampling point, monthly concentrations of *Cryptosporidium* and *Giardia* considering both intakes individually as well as collectively are shown in Figure A.1. Except for a higher *Cryptosporidium* concentration in the river intake in October 2021, the concentrations in the two intakes do not differ substantially, which may allow sampling only at the dam intake or less frequent sampling of the river intake if the monitoring program needs to be simplified.

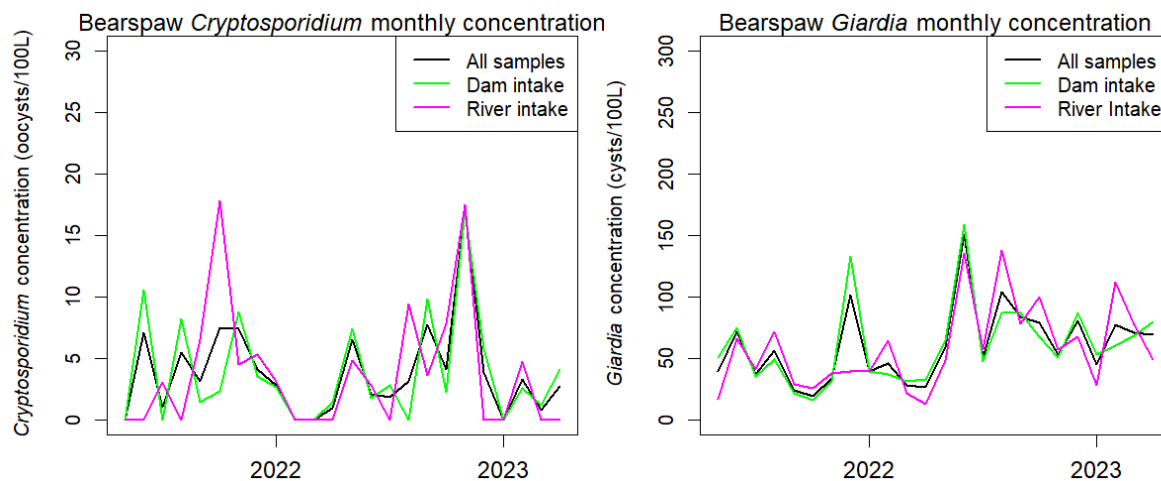


Figure A.1: *Cryptosporidium* and *Giardia* concentrations at the intakes of the Bearspaw treatment plant from May 2021 to April 2023.

A.3 Analysis to determine frequency of sampling

To determine the sampling frequency in Calgary, historical pathogen concentration data from January 2016 to June 2020 were analyzed for the development of the framework in 2021 (Table A.1). After two years of implementation, the framework was revised, and two analyses were conducted: one included only two years of data after the implementation of the framework (Table A.2) and the last analysis includes all data collected since 2016 (Table A.3). Five different numbers of samples taken during a year (n) were considered (4, 6, 12, 24 and 48) and 1000 simulations were conducted for each to compare the precision on estimated yearly treatment requirements.

Precision is described in terms of under- and overestimation of treatment, in which overestimation is measured by the difference between the 97.5th percentile of the 10,000 values simulated and the treatment required using all historical data (herein called true treatment) and underestimation is represented by the difference between the true treatment and 2.5th percentile.

The zero values in Table A.1, Table A.2 and Table A.3 are explained by the low concentrations of *Cryptosporidium* oocysts in both plants, which mostly led to the minimum treatment requirement of 3 log. These analyses show that the sampling approach implemented in Calgary, in which samples are taken twice a month in each water treatment plant (WTP), is sufficient to estimate log-reduction requirements with an error of less than 0.3 log.

Table A.1: Precision of yearly treatment requirements based on 10,000 simulations using data from January 2016 to June 2020

Number of samples per year	Bears paw WTP				Glenmore WTP			
	<i>Cryptosporidium</i>		<i>Giardia</i>		<i>Cryptosporidium</i>		<i>Giardia</i>	
	True treatment - 2.5 th Percentile	97.5 th percentile True treatment	True treatment - 2.5 th percentile	97.5 th percentile True treatment	True treatment - 2.5 th Percentile	97.5 th percentile True treatment	True treatment - 2.5 th percentile	97.5 th percentile True treatment
4	0.00	0.18	0.48	0.33	0.00	0.00	0.00	0.44
6	0.00	0.07	0.37	0.28	0.00	0.00	0.00	0.36
12	0.00	0.00	0.25	0.19	0.00	0.00	0.00	0.25
24	0.00	0.00	0.16	0.13	0.00	0.00	0.00	0.16
48	0.00	0.00	0.10	0.08	0.00	0.00	0.00	0.08

Table A.2: Precision of yearly treatment requirements based on 10,000 simulations using data from May 2021 to April 2023

Number of samples per year	Bears paw WTP				Glenmore WTP			
	<i>Cryptosporidium</i>		<i>Giardia</i>		<i>Cryptosporidium</i>		<i>Giardia</i>	
	True treatment - 2.5 th Percentile	97.5 th percentile True treatment	True treatment - 2.5 th Percentile	97.5 th percentile True treatment	True treatment - 2.5 th Percentile	97.5 th percentile True treatment	True treatment - 2.5 th Percentile	97.5 th percentile True treatment
4	0.00	0.01	0.31	0.26	0.00	0.00	0.05	0.44
6	0.00	0.00	0.25	0.21	0.00	0.00	0.05	0.36
12	0.00	0.00	0.17	0.15	0.00	0.00	0.05	0.25
24	0.00	0.00	0.11	0.09	0.00	0.00	0.05	0.14
48	0.00	0.00	0.06	0.04	0.00	0.00	0.00	0.00

Table A.3: Precision of yearly treatment requirements based on 10,000 simulations using data from January 2016 to April 2023

Number of samples per year	Bears paw WTP				Glenmore WTP			
	<i>Cryptosporidium</i>		<i>Giardia</i>		<i>Cryptosporidium</i>		<i>Giardia</i>	
	True treatment -	97.5 th percentile	True treatment -	97.5 th percentile	True treatment -	97.5 th percentile	True treatment -	97.5 th percentile
	2.5 th Percentile	True treatment	2.5 th Percentile	True treatment	2.5 th Percentile	True treatment	2.5 th Percentile	True treatment
4	0.01	0.15	0.42	0.30	0.00	0.00	0.14	0.58
6	0.00	0.06	0.33	0.26	0.00	0.00	0.14	0.49
12	0.00	0.00	0.22	0.18	0.00	0.00	0.14	0.37
24	0.00	0.00	0.15	0.13	0.00	0.00	0.14	0.27
48	0.00	0.00	0.10	0.08	0.00	0.00	0.14	0.18

A.4 Data management

To ensure that the data used to evaluate required log-reduction or for exploratory analyses are reliable, it is necessary to have a carefully developed protocol for data management. Historical data collected in the monitoring program since 2012 were analyzed during the development of the framework. This analysis identified opportunities for improvement of the data management approach conducted in Calgary, which were subsequently implemented.

If possible, the use of spreadsheets should be avoided because they are (1) prone to errors in data entry and inconsistent formatting, (2) difficult to protect from changes and manage version control and (3) laborious to update continuously. In particular, spreadsheets are often organized to facilitate specific computations and plotting rather than as a sortable database that is ready for upload into other software. Protocols should be developed for the maintenance and archiving of bench sheets, the recording of pertinent details in a Laboratory Information Management System (LIMS) and verification of correct and complete data entry. Despite using a LIMS for storing reportable data, the City of Calgary used to store part of the non reportable monitoring data (e.g., analytical recovery) only in spreadsheets used for quality control charting. Challenges with the use of spreadsheets such as the ones mentioned above motivated transition to use of a LIMS for all data storage. However, LIMS can be a “black-box” that only trained personnel can operate. Because of this, spreadsheets are still used for training staff on the calculations incorporated in the system, exploratory analysis and troubleshooting.

Regarding the type of data that should be recorded, documentation of the following details is suggested for every raw water sample: sample identification number, sample location, sample date and time, number of filters used, number of IMS tubes used, volume filtered, number of seeded (oo)cysts and numbers of seeded and indigenous (oo)cysts observed. When multiple filters and/or multiple IMS tubes are used, data specific to each one should be recorded in the bench sheets but the cumulated data are sufficient for recording in the LIMS database. Other important details that can be included for quality control are laboratory material lot numbers and dates, technician identification for specific steps in the sample collection and analysis processes and other important water quality parameters such as indicators of high pathogen concentrations or diminished pathogen removal (e.g., turbidity).

It is also important to document any special remark about unexpected incidents or samples collected outside the scope of the routine monitoring program. For example, if a sample is not fully analyzed or is rejected (e.g., due to low recovery or a research purpose outside of compliance monitoring), all

available data should be recorded in a way that easily allows their exclusion from compliance reporting and determination of required treatment. In cases when 1) samples were incompletely analyzed or rejected, 2) additional samples were included in calculations used for compliance and/or 3) samples were not included in calculations used for compliance, it is important to document the corresponding reasons in a readily accessible location, though not necessarily as part of the LIMS database.

A.5 Limitations of monitoring and risks analysis approaches

The methodology used to evaluate treatment needs from monitoring data has several limitations. Table A.4 provides a summary of simplifying assumptions or known sources of error as well as their likely effects on the computation of required log-reduction.

Table A.4: Limitations of monitoring and risk analysis approaches

Assumption or known source of error	Likely effect
Error in estimating the average protozoa concentrations from collected grab samples	Unknown, but analysis of recommended sampling plan shows that error is below 0.3-log
Non-random sample scheduling	Unknown, but presumed to be small
Reduced sample volumes during high source water turbidity events	Unknown, but no clear evidence of atypical concentrations in previous data
Assumed representativeness of internal seed recovery	Unknown relationship to recovery of indigenous (oo)cysts
Statistical error in simplified calculation of recovery-adjusted concentration estimate	Slight overestimation of concentration and required log-reduction (Schmidt et al., 2013)
Statistical error in unweighted calculation of annual concentration estimate	Unknown, but small given almost equal number of days per month
Assumed representativeness of daily unboiled tap water consumption value	Unknown, but value higher than Health Canada's increases calculated required log-reduction by 0.16 log
Assumed representativeness of dose-response models, probability of illness given infection and DALYs per case for naturally occurring (oo)cysts and population in Calgary	Unknown, but based on Health Canada's assessment of the best available science
Assumption that all observed (oo)cysts are pathogenic and viable	Substantial overestimation of log-reduction required is likely (approximately 1 log in Lapen et al. (2016))

Appendix B

Supplementary information for Chapter 3

B.1 Bow River flow

Figure B.1 presents monthly streamflow in the Bow River near Cochrane (station number: 05BH005) calculated from daily reported data extracted from the Environment and Climate Change Canada Historical Hydrometric Data web site (Water Office, 2025) on April 16, 2025. Data are not usually reported from November to February because ice conditions affect the measurement of water levels and discharge.

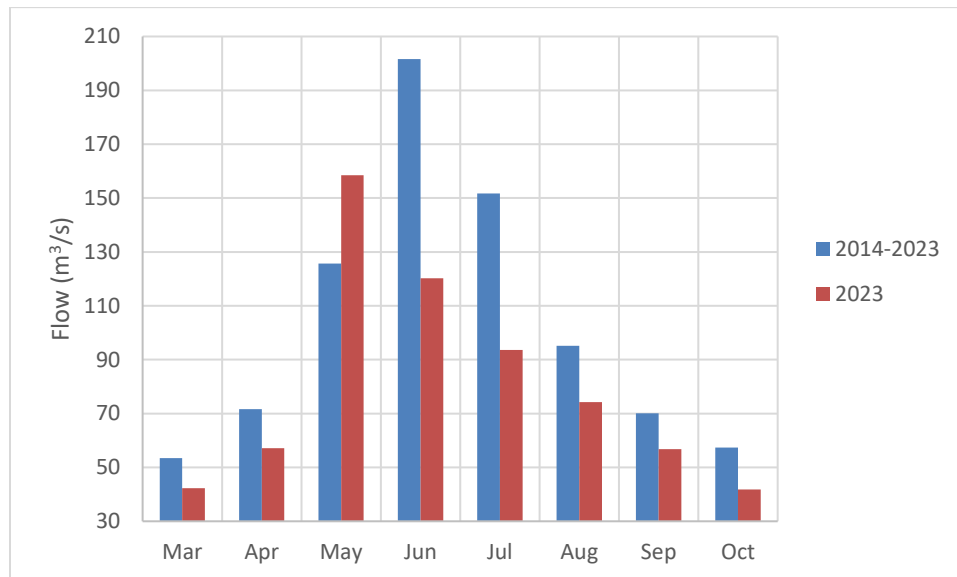


Figure B.1: Average monthly flow in the Bow River from 2014 to 2023 and in 2023

B.2 Examples of applications of Equation 3.6

This section presents some applications of the generalized model provided in Equation 3.6 of Chapter 3 to guide emergency preparedness of drinking water treatment utilities. The following examples consider the same context of the study (i.e., the risk arisen from ingestion of drinking water contaminated with rotavirus). Equation B1 presents the dose of pathogens ingested as a function of pathogen concentration (C), treatment log-reduction (LR) and daily volume of water consumption (V). A fixed volume of 1.45 L per person per day will be used here. Equation B2 represents the daily probability of infection using the dose of Equation B1 and the exact beta-Poisson dose–response model ($\alpha = 0.167$ and $\beta = 0.191$) from Teunis & Havelaar (2000). Equation B3 is the annual probability of infection considering an event of duration t that can change the concentration of pathogens or treatment log-reduction. The indices 0 and f represent baseline and event conditions, respectively. The annual risk reference of 10^{-4} infections per person is used here as an acceptable annual risk.

$$D(C, LR) = C \times 10^{-LR} \times V \quad (B1)$$

$$P(C, LR) = 1 - {}_1F_1(\alpha, \alpha + \beta; -D(C, LR)) \quad (B2)$$

$$P_{inf}(C_0, C_f, LR_0, LR_f, t) = 1 - \left((1 - P(C_0, LR_0))^{T_{max} - t} (1 - P(C_f, LR_f))^t \right) \quad (B3)$$

Example 1: What would be the maximum duration of an event that can be sustained without exceeding the annual risk reference given a baseline concentration of 0.01 units/L, a fixed level of treatment of 6 log and an event concentration of 3000 units/L?

In this example, $C_0 = 0.01$ units/L, $C_f = 3000$ units/L, $LR_0 = LR_f = 6$, $V = 1.45$ L, $P_{inf} = 10^{-4}$, $T_{max} = 365$ days and t is the only unknown variable. Using Equations B1, B2 and B3, t is calculated to be 0.0481 days or approximately 69 minutes.

Example 2: If the event of Example 1 lasts for 2 days, what is the maximum event concentration acceptable?

Here, $C_0 = 0.01$ units/L, $LR_0 = LR_f = 6$, $V = 1.45$ L, $P_{inf} = 10^{-4}$, $T_{max} = 365$ days, $t = 2$ days and C_f is the only unknown variable. Using Equations B1, B2 and B3, C_f is calculated to be approximately 72 units/L.

Example 3: If the event of Example 1 lasts for 9 hours, what is the minimum treatment required to counteract the event concentration of 3000 units/L?

Here, $C_0 = 0.01$ units/L, $C_f = 3000$ units/L, $LR_0 = 6$, $V = 1.45$ L, $P_{inf} = 10^{-4}$, $T_{max} = 365$ days, $t = 0.375$ day and LR_f is the only unknown variable. Using Equations B1, B2 and B3, LR_f is approximately 6.9 log (i.e., additional 1 log treatment reduction should be provided to ensure drinking water safety).

Example 4: A problem in the disinfectant dosing system made the treatment log-reduction reduce from 9 to 2 log during 5 hours in a year. What would be the maximum average source water concentration so the annual risk is acceptable?

Here, $LR_0 = 9$, $LR_f = 2$, $V = 1.45$ L, $P_{inf} = 10^{-4}$, $T_{max} = 365$ days, $t = 0.208\bar{3}$ day and C_0 and C_f are equal and unknown. Using Equations B1, B2 and B3, the maximum average concentration should be approximately 0.07 units/L.

Appendix C

Supplementary information for Chapter 4

C.1 Constant flow, variable production model

The model presented in this work assumed that when a filter is backwashed, the influent flow is redistributed among the operating filters, so the volume of treated water produced is constant over time (variable flow-constant production, VF-CP). Here this model was adapted for the situation where the flow does not change in operating filters during backwashing, leading to a production of less water during these periods (constant flow-variable production, CF-VP).

To explain the difference in results between these two models, generalized forms of the equations of the combined plant-scale log-reduction (Equation 4.1) and overall log-reduction over a full filter cycle (Equation 4.2) are needed. They are presented in Equations C1 and C2, where n is the number of filters, Q_t is the combined effluent flow of the set of filters at each time, and $Q_{i,t}$, $LR_{i,t}$ and $Op_{i,t}$, are, respectively, the influent flow, the log-reduction and the status of each individual filter in time ($Op_{i,t} = 0$ for backwashing and $Op_{i,t} = 1$ for all the other phases).

$$LR_{combined,t} = -\log_{10} \left(\frac{\sum_{i=1}^n Q_{i,t} \times 10^{-LR_{i,t} \times Op_{i,t}}}{\sum_{i=1}^n Q_{i,t} \times Op_{i,t}} \right) \quad (C1)$$

$$LR_{overall} = -\log_{10} \left(\frac{\sum_{t=1}^T Q_t \times 10^{-LR_{combined,t}}}{\sum_{t=1}^T Q_t} \right) \quad (C2)$$

In both the VF-CP and CF-VP models, Equation C1 can be simplified to Equation 1 when flow is equal among all operating filters, so the combined log-reduction pattern over time is the same in both models. Likewise, Equation C2 can be simplified to Equation 2 in the VF-CP model because combined flow (Q_t) is constant over time. However, the CF-VP model has variable combined flow because the production of water is reduced during backwashing. Thereby, the combined log-reduction during backwashing carries a lower weight in comparison with periods when more water is produced. Hence, a difference in overall log-reduction between these two sets of model assumptions is expected.

Most of the analyses in the paper considered backwashes that are evenly staggered such that the other filters were usually in stable operation during backwashing. The emphasis that the VF-CP model gives

to the combined pathogen removal during backwashing in comparison to the CF-VP model is not enough to produce substantial impacts on the overall log-reduction. This is because there are periods of much lower log-reduction driving the overall performance, as reflected in the conclusions of Section 4.4.3. Thus, the overall log-reduction varies in some cases only in the second decimal place, as illustrated in Figure C.1, which replicates the analysis of the effect of the duration of stable operation (Section 4.4.2) under the CF-VP model.

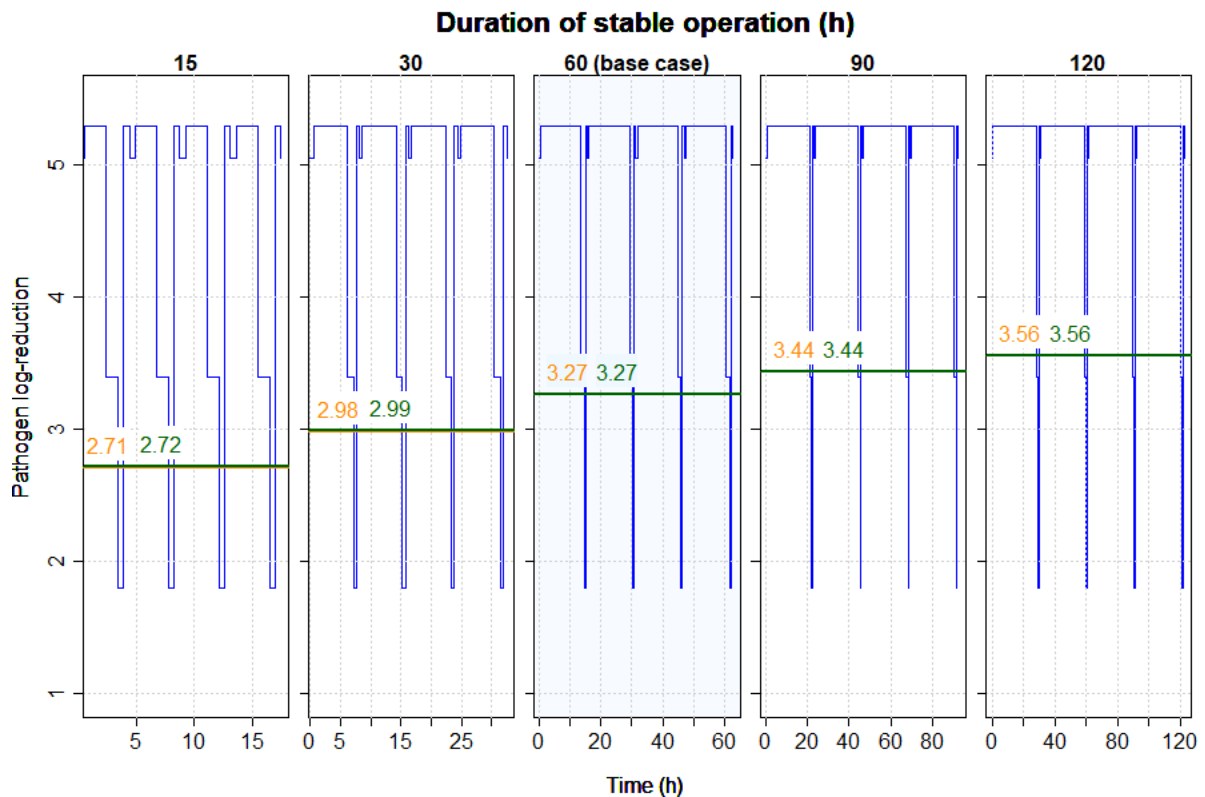


Figure C.1: Replication of the analysis of the effect of the duration stable operation considering the constant flow-variable production (CF-VP) model (orange line)

However, in the backwash staggering analysis, there are scenarios in which the overall pathogen removal is reduced because other filters are in the breakthrough phase during backwashing. In these cases, a difference between models is clearer, as presented in Figure C.2 that reproduces the backwash staggering analysis (Section 4.4.6) under the CF-VP model. Here, the overall log-reduction is greater in some cases because the periods of poor removal during backwashing have diminished influence due to the production of less water. Specifically, the overall log-reduction is the same in all scenarios of backwash staggering in the CF-VP model because there are no changes in flow to accentuate the impact

of performance of the other filters during backwashing and all filter cycle attributes are unchanged. Just rearranging the moment that each filter goes through each of the phases of a filter cycle will only affect the combined log-reduction (instantaneous), not the overall log-reduction (average performance). The constant flow-variable production procedure is more robust to the reduction of performance caused by overlapping of poor removal phases during backwashing. This procedure is also beneficial because it avoids hydraulic surges caused by flow variations, which are known to compromise treatment performance (Han et al., 2009; Edzwald, 2011).

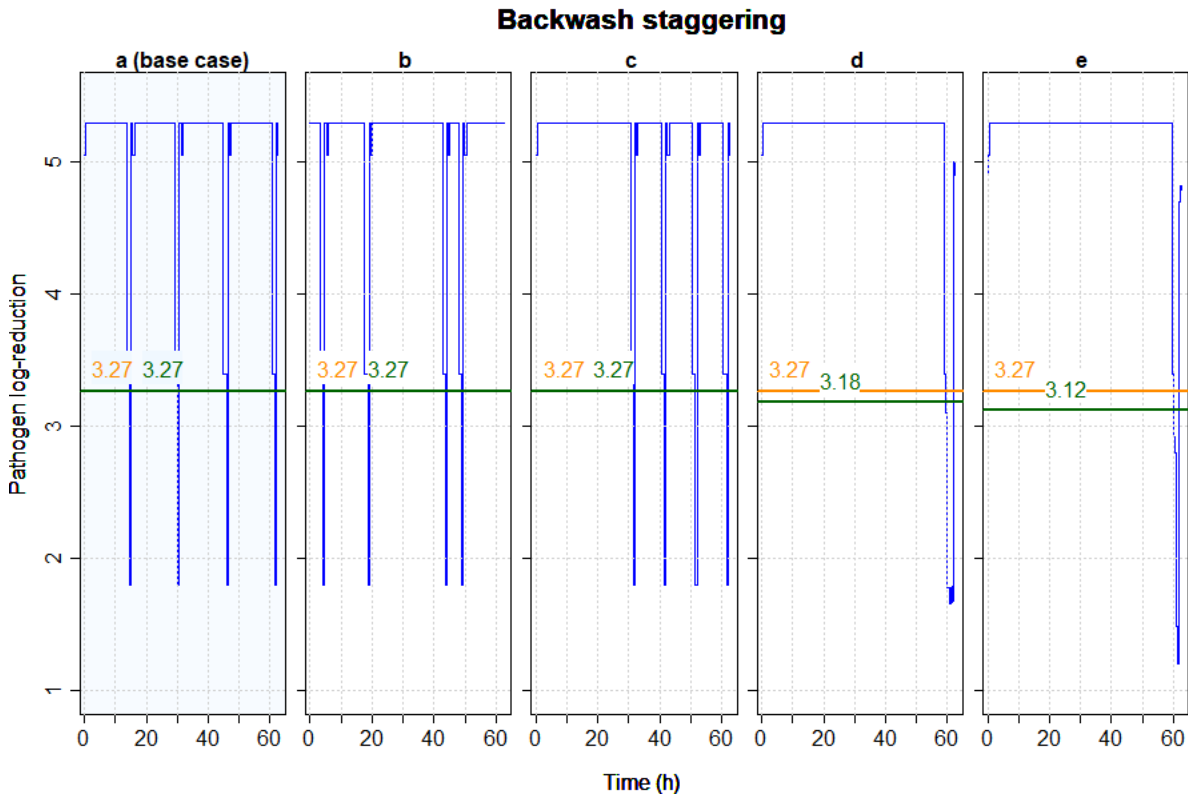


Figure C.2: Replication of the analysis of backwash staggering considering the constant flow-variable production (CF-VP) model (orange line). Case a: base case, case b: random backwash staggering, case c: backwashes spaced by 10 h, case d: backwashes spaced by 0.5 h and case e: backwashes spaced by 0.25 h

C.2 R code used to perform the analyses presented in the paper

```
# This code is built to perform the calculations presented in the paper "Filter
# Operation Effects on Plant-Scale Microbial Risk: Opportunities for Enhanced
# Treatment Performance". It is not optimized for use as a package.
# It is divided in three main sections: the model inputs are specified in part 1,
# a main function receiving the model inputs and returning a figure presenting
# the combined and overall log-reduction for all cases tested in a specific analysis
# is shown in part 2, and part 3 calls the main function of part 2 according to one of
# the eight analyses presented in the paper.
#
# Dafne de Brito Cruz, M.Sc.
# July 28, 2023

##### PART 1 - INPUTS #####

# FILTER CYCLE PARAMETERS
#Specification of duration and log-reduction for filter cycle phases in five
#different cases to be tested (including the base case). The coagulation
#analysis has three cases, and the log-reductions during ripening and early
#breakthrough are adjusted to not be greater than the removal during stable
#operation.

# Durations of filter cycle phases (in hour)
d_r <- c(0.5,1.5,2.5,3.5,4.5) # ripening
d_so <- c(15,30,60,90,120) # stable operation
d_eb <- c(1,1,1,0.5,0) # early breakthrough
d_lb <- c(0.5,0.25,0,0,0) # late breakthrough
d_bw <- c(0,0.25,0.5,0.75,1) # backwash

# Log-reduction of filter cycle phases
LR_r <- c(4.7, 3.3, 2.0, 1.2) # ripening
LR_so <- c(4.7,5.0,5.3,6.0,7.0) # stable operation
LR_eb <- c(rep(c(2.8),5)) # early breakthrough
LR_lb <- c(0,0.6,1.2,2.0,2.8) #late breakthrough

# Adjusting log-reductions in different coagulation conditions
LR_so_coag <- c(1.4,3.1,5.3) # stable operation
LR_r_coag <- c(1.4,3.1,4.7) # ripening
LR_eb_coag <- c(1.4, 2.8, 2.8) # early breakthrough

#-----#

# SYSTEM PARAMETERS
#Definition of number of filters (five cases), total duration of the
#analysis (in seconds) and influent flow for the set of filters.

nf <- c(2,4,8,20,50) # number of filters
DA <- 62.5*3600 # duration of analysis (s)
q_t <- 100 # influent flow rate (set of all filters)

#-----#

# Auxiliary variables to use the same main function

# Number of filters in the base case is in the second position of nf
nf_fixed <- rep(c(nf[2]),5)
# Duration of ripening in the base case is in the first position of d_r
d_r_fixed <- rep(c(d_r[1]),5)
# Duration of stable operation in the base case is in the third position of d_so
d_so_fixed <- rep(c(d_so[3]),5)
```

```

# Duration of early breakthrough in the base case is in the first position of d_eb
d_eb_fixed <- rep(c(d_eb[1]),5)
# Duration of late breakthrough in the base case is in the first position of d_lb
d_lb_fixed <- rep(c(d_lb[1]),5)
# Duration of backwashing in the base case is in the third position of d_bw
d_bw_fixed <- rep(c(d_bw[3]),5)
# Removal during ripening in the base case is in the first position of LR_r
LR_r_fixed <- rep(c(LR_r[1]),5)
# Removal during stable operation in the base case is in the third position of LR_so
LR_so_fixed <- rep(c(LR_so[3]),5)
# Removal during late breakthrough in the base case is in the third position of LR_lb
LR_lb_fixed <- rep(c(LR_lb[3]),5)
# Titles of the five backwash staggering cases, also used to refer to this analysis
stg <- c("a","b","c","d","e")
# Title of the first case of filter-to-waste analysis, also used to refer to this case
ftw <- c("Ripening-to-waste")

##### PART 2 - MAIN FUNCTION #####
# This function returns a plot with combined and overall log-removal for all
# cases given:
# MODEL: type of model (VFCEP: variable flow, constant production
#           or CFVP: constant flow, variable production)
# ANALYSIS: type of analysis (e.g., number of filters, backwash staggering)
# NF: number of filters in all cases
# T: duration of analysis (in seconds)
# Q_t: influent flow for the set of filters
# D_R, D_SO, D_EB, D_LB, D_BW: durations of ripening, stable operation,
#   early breakthrough, late breakthrough and backwashing, respectively,
#   for all cases (in hour).
# LR_R, LR_SO, LR_EB, LR_LB: log-reductions during ripening, stable operation,
#   early breakthrough and late breakthrough, respectively, for all cases.

MainFunction <- function (MODEL, ANALYSIS, NF, T, Q_t, D_R, D_SO, D_EB, D_LB, D_BW,
                          LR_R, LR_SO, LR_EB, LR_LB){

  for(case in 1:NROW(ANALYSIS)){

    # Duration of filter cycle (in seconds)
    D <- (D_R[case]+D_SO[case]+D_EB[case]+D_LB[case]+D_BW[case])*3600

    #-----#

    # Initializing matrices of log-reduction
    LR_ti <- matrix(, nrow=T, ncol=NF[case]) #instantaneous log-reduction of each filter
    status_ti <- matrix(, nrow=T, ncol=NF[case]) #instantaneous status (active or not) of
each filter
    phase_ti <- matrix(, nrow=T, ncol=NF[case]) #instantaneous phase of each filter
    LR_t <- c() # instantaneous log-reduction of set of filters (combined logreduction)

    #-----#

    # Startup condition for each filter (time within the filter cycle in s)

    # For evenly staggered 2,4,8,20,40 filters
    t0_1 <- c(1*2/D,1+1*2/D)*D/2
    t0_2 <- c(1*4/D,1:3+1*4/D)*D/4
    t0_3 <- c(1*8/D,1:7+1*8/D)*D/8
    t0_4 <- c(1*20/D,1:19+1*20/D)*D/20
    t0_5 <- c(1*50/D,1:49+1*50/D)*D/50

    # For backwash staggering analysis
    set.seed(5)

```

```

# Case a - even
t0_e <- c(1/3600,15.625+1/3600,31.25+1/3600,46.875+1/3600)*3600
# Case b - random
t0_ne1 <- runif(4,1,62.5*3600)
# Case c - Cycles staggered by 10 h
t0_ne2 <- c(1/3600,10+1/3600,20+1/3600,30+1/3600)*3600
# Case d - sequential backwash, cycles staggered by 30 min
t0_ne3 <- c(1/3600,0.5+1/3600,1+1/3600,1.5+1/3600)*3600
# Case e - overlap backwash and poor, cycles staggered by 15 min
t0_ne4 <- c(1/3600,0.25+1/3600,0.50+1/3600,0.75+1/3600)*3600

if (identical(ANALYSIS, nf)){
  t0 <- cbind(t0_1, t0_2, t0_3, t0_4, t0_5)}
else if (identical(ANALYSIS, stg)){
  t0 <- cbind(t0_e, t0_ne1,t0_ne2,t0_ne3,t0_ne4)}
else {t0 <- cbind(t0_2,t0_2,t0_2,t0_2,t0_2)}

#-----#

# Determining phase, status and log-reduction of each filter at each time step
# LR_ti: instantaneous log-reduction
# status_ti: 1(active), 0 (inactive or backwashing)
# phase_ti: R (ripening), SO (stable operaiton), EB (early breakthrough),
#           LB (late breakthrough, B (backwashing).

for (i in 1:NF[case]){
  nt=1
  for (t in t0[i,case]:(t0[i,case]+D-1)){
    if ((t%D) <= D_R[case]*3600){
      LR_ti[nt,i] <- LR_R[case]
      status_ti[nt,i] <- 1
      phase_ti[nt,i] <- "R"}
    else if ((t%D) > D_R[case]*3600 & (t%D) <= (D_R[case]+D_SO[case])*3600){
      LR_ti[nt,i] <- LR_SO[case]
      status_ti[nt,i] <- 1
      phase_ti[nt,i] <- "SO"}
    else if ((t%D) > (D_R[case]+D_SO[case])*3600 &
              (t%D) <= (D_R[case]+D_SO[case]+D_EB[case])*3600){
      LR_ti[nt,i] <- LR_EB[case]
      status_ti[nt,i] <- 1
      phase_ti[nt,i] <- "EB"}
    else if ((t%D) > (D_R[case]+D_SO[case]+D_EB[case])*3600 &
              (t%D) <= (D_R[case]+D_SO[case]+D_EB[case]+D_LB[case])*3600){
      LR_ti[nt,i] <- LR_LB[case]
      status_ti[nt,i] <- 1
      phase_ti[nt,i] <- "LB"}
    else if ((t%D) > (D_R[case]+D_SO[case]+D_EB[case]+D_LB[case])*3600 &
              (t%D) <=
              (D_R[case]+D_SO[case]+D_EB[case]+D_LB[case]+D_BW[case])*3600){
      LR_ti[nt,i]= 0
      status_ti[nt,i] <- 0
      phase_ti[nt,i] <- "B"}
    nt<-nt+1
  }
}

#-----#

# Calculating combined and overall log-reduction

#Number of filters active (not in backwash) at each time step

```

```

active <- rowSums(status_ti)
# Eliminates the ripening phase in the filter-to-waste analysis
if (identical(ANALYSIS,ftw)){status_ti[which(phase_ti=="R")]<-0}
# Flow at each filter
if (identical(MODEL,"VFCP")){
  Q_ti <- status_ti*(Q_t/active)}
else if(identical(MODEL,"CFVP")){
  Q_ti <- status_ti*(Q_t/NF[case])}
R_ti <- 10^(-LR_ti)
# Overall log-reduction
LR_t <- -log10(cumsum(rowSums(Q_ti*R_ti))/cumsum(rowSums(Q_ti)))
# Combined log-reduction
LR_t2 <- -log10(rowSums(Q_ti*R_ti)/rowSums(Q_ti))

#-----#

# PLOTS

t <- c(1:T)/3600

#Number of filters plot
if (identical(ANALYSIS, nf)){
  plot(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),type="l",
    col = c("blue"), cex.axis=1.5, yaxt='n', cex.main=1.5,
    main= if (case == 2){paste(ANALYSIS[case], "(base case)")}
      else {paste(ANALYSIS[case])})

  if (case == 2){
    adjustcolor("aliceblue",alpha.f = 0.3)
    rect(par("usr")[1],par("usr")[3],par("usr")[2],par("usr")[4],col = "aliceblue")
    lines(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),col = c("blue"))}
  title("Number of filters", outer = TRUE, line = 1, cex.main=2)}

# Duration of stable operation plot
else if (identical(ANALYSIS, d_so)){
  plot(t, LR_t2, xlim=c(3600,D)/3600, ylim=c(1,5.5),type="l",
    col = c("blue"), cex.axis=1.5, yaxt='n', cex.main=1.5,
    main= if (case == 3){paste(ANALYSIS[case], "(base case)")}
      else {paste(ANALYSIS[case])})

  if (case == 3){
    adjustcolor("aliceblue",alpha.f = 0.3)
    rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], col = "aliceblue")
    lines(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),col = c("blue"))}
  title("Duration of stable operation (h)", outer = TRUE, line = 1, cex.main=2)}

# Removal during stable operation plot
else if (identical(ANALYSIS, LR_so)){
  plot(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,7),type="l",
    col = c("blue"), cex.axis=1.5, yaxt='n', cex.main=1.5,
    main= if (case == 3){paste(formatC(ANALYSIS[case],format ="f",digits=1),"(base
case)")}
      else {paste(formatC(ANALYSIS[case], format = "f", digits=1), "")})

  if (case == 3){
    adjustcolor("aliceblue",alpha.f = 0.3)
    rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], col = "aliceblue")
    lines(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),col = c("blue"))}
  title("Removal during stable operation", outer = TRUE, line = 1, cex.main=2)}

# Duration of early and late breakthrough plot
else if (identical(ANALYSIS, d_eb)){

```

```

plot(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),type="l",
     col = c("blue"), cex.axis=1.5, yaxt='n', cex.main=1.5,
     main= if (case == 1){paste(ANALYSIS[case], " / ",d_lb[case], " (base case)")}
     else {paste(ANALYSIS[case], " / ",d_lb[case])})

if (case == 1){
  adjustcolor("aliceblue",alpha.f = 0.3)
  rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], col = "aliceblue")
  lines(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),col = c("blue"))}
title("Duration of early / late breakthrough (h)", outer = TRUE, line = 1, cex.main=2))

# Removal during late breakthrough plot
else if (identical(ANALYSIS, LR_lb)){
  plot(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(0,5.5),type="l",
       col = c("blue"), cex.axis=1.5, yaxt='n', cex.main=1.5,
       main= if (case == 3){paste(formatC(ANALYSIS[case],format = "f",digits=1),"(base
case)")}
       else {paste(formatC(ANALYSIS[case], format = "f", digits=1), "")})

  if (case == 3){
    adjustcolor("aliceblue",alpha.f = 0.3)
    rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], col = "aliceblue")
    lines(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),col = c("blue"))}
  title("Removal during late breakthrough", outer = TRUE,line = 1, cex.main=2))

# Backwash staggering plot
else if (identical(ANALYSIS, stg)){
  plot(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),type="l",
       col = c("blue"), cex.axis=1.5, yaxt='n', cex.main=1.5,
       main= if (case == 1){paste(ANALYSIS[case], "(base case)")}
       else {paste(ANALYSIS[case], "")})

  if (case == 1){
    adjustcolor("aliceblue",alpha.f = 0.3)
    rect(par("usr")[1],par("usr")[3],par("usr")[2],par("usr")[4],col = "aliceblue")
    lines(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),col = c("blue"))}
  title("Backwash staggering cases", outer = TRUE, line = 1, cex.main=2))

# Coagulation plot
else if (identical(ANALYSIS, LR_so_coag)){
  plot(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),type="l",
       col = c("blue"), cex.axis=1.5, yaxt='n', cex.main=1.5,
       main= if(case==1){c("Sub-optimal coagulation case I")}
       else if (case==2){c("Sub-optimal coagulation case II")}
       else{c("Optimal coagulation (base case)")}

  if (case == 3){
    adjustcolor("aliceblue",alpha.f = 0.3)
    rect(par("usr")[1],par("usr")[3],par("usr")[2],par("usr")[4],col = "aliceblue")
    lines(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),col = c("blue"))}

# Filter-to-waste plot
else if (identical(ANALYSIS, ftw)){
  plot(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),type="l",
       col = c("blue"), cex.axis=1.5, yaxt='n', cex.main=1.5,
       main= if (case == 1){paste(ANALYSIS[case], "")}
       else {paste(ANALYSIS[case], "")})
  title("Removal during ripening", outer = TRUE, line = 1, cex.main=2))
else if (identical(ANALYSIS, LR_r)){
  plot(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),type="l",
       col = c("blue"), cex.axis=1.5, yaxt='n', cex.main=1.5,

```

```

main= if (case == 1){paste(formatC(ANALYSIS[case],format = "f",digits=1),"(base
case)")}
      else {paste(formatC(ANALYSIS[case], format = "f", digits=1), "")}}

if (case == 1){
  adjustcolor("aliceblue",alpha.f = 0.3)
  rect(par("usr")[1],par("usr")[3],par("usr")[2],par("usr")[4],col = "aliceblue")
  lines(t, LR_t2, xlim=c(3600,T)/3600, ylim=c(1,5.5),col = c("blue"))}

# Title
title(xlab="Time (h)",ylab="Pathogen log-reduction",cex.lab=1.5, outer = TRUE,line = 3)

# Grid
grid(nx = NULL, ny = NULL, col = "lightgray", lty = 3)

# Boxes with overall log-reduction
if (identical(ANALYSIS, ftw)|identical(ANALYSIS, LR_r)){
  xx <- c(D/25,0.35*D,0.35*D,D/25)/3600
  yy <- c(LR_t[D]+0.05,LR_t[D]+0.05,LR_t[D]+0.3,LR_t[D]+0.3)
  polygon(xx, yy, col="white", border=FALSE)
  text(x=D/(3600*5), y=LR_t[D]+0.175,
       labels=paste(formatC(LR_t[D],format = "f",digits = 2)),
       las=2, mgp=c(3,0.35,0), cex=1.5, col="darkgreen")}
else{
  xx <- c(D/25,D/4,D/4,D/25)/3600
  yy <- c(LR_t[D]+0.05,LR_t[D]+0.05,LR_t[D]+0.3,LR_t[D]+0.3)
  polygon(xx, yy, col="white", border=FALSE)
  text(x=3*D/(3600*20), y=LR_t[D]+0.175,
       labels=paste(formatC(LR_t[D],format = "f",digits = 2)),
       las=2, mgp=c(3,0.35,0), cex=1.5, col="darkgreen")}

# Tick marks on the y-axis
if (identical(ANALYSIS, LR_so)){
  axis(side=2, at=1:7,labels = if (case == 1) {1:7}
       else FALSE, cex.axis=1.5)}
else if (identical(ANALYSIS, LR_r)){
  axis(side=2, at=1:5.5,labels = if (case == 1) {1:5.5}
       else FALSE, cex.axis=1.5)}

# Line representing the value of overall log-reduction
abline(h=LR_t[D], col="darkgreen", lty=1, lwd=2)
}
}

##### PART 3 - ANALYSIS #####

# 1. Number of filters
par(mfrow = c(1,NROW(nf)), oma = c(4,4,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)
MainFunction("VFPC",nf, nf, DA, q_t, d_r_fixed, d_so_fixed, d_eb_fixed, d_lb_fixed,
            d_bw_fixed, LR_r_fixed, LR_so_fixed,LR_eb, LR_lb_fixed)

# 2. Length of stable operation
par(mfrow = c(1,NROW(d_so)), oma = c(4,4,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)
MainFunction("VFPC",d_so, nf_fixed, DA, q_t, d_r_fixed, d_so, d_eb_fixed, d_lb_fixed,
            d_bw_fixed, LR_r_fixed, LR_so_fixed, LR_eb, LR_lb_fixed)

# 3. Removal of stable operation
par(mfrow = c(1,NROW(LR_so)), oma = c(4,4,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)
MainFunction("VFPC",LR_so, nf_fixed, DA, q_t, d_r_fixed, d_so_fixed, d_eb_fixed,
            d_lb_fixed, d_bw_fixed, LR_r_fixed, LR_so,LR_eb, LR_lb_fixed)

# 4. Length of Breakthrough

```

```

par(mfrow = c(1,NROW(d_eb)), oma = c(4,4,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)
MainFunction("VFCEP",d_eb, nf_fixed, DA, q_t, d_r_fixed, d_so_fixed, d_eb, d_lb,
  d_bw_fixed, LR_r_fixed, LR_so_fixed, LR_eb, LR_lb_fixed)

# 5. Removal of late breakthrough
par(mfrow = c(1,NROW(LR_lb)), oma = c(4,4,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)
MainFunction("VFCEP",LR_lb, nf_fixed, DA, q_t, d_r_fixed, d_so_fixed, d_eb_fixed,
  d_lb_fixed, d_bw_fixed, LR_r_fixed, LR_so_fixed, LR_eb, LR_lb)

# 6. Backwash staggering
par(mfrow = c(1,NROW(stg)), oma = c(4,4,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)
MainFunction("VFCEP",stg, nf_fixed, DA, q_t, d_r_fixed, d_so_fixed, d_eb_fixed,
  d_lb_fixed, d_bw_fixed, LR_r_fixed, LR_so_fixed, LR_eb, LR_lb_fixed)

# 7. Coagulation
par(mfrow = c(1,NROW(LR_so_coag)), oma = c(4,4,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)
MainFunction("VFCEP",LR_so_coag, nf_fixed, DA, q_t, d_r_fixed, d_so_fixed, d_eb_fixed,
  d_lb_fixed, d_bw_fixed, LR_r_coag, LR_so_coag, LR_eb_coag, LR_lb_fixed)

# 8. Ripening to waste
par(mfrow = c(1,NROW(LR_r)+1), oma = c(4,4,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)
MainFunction("VFCEP",ftw, nf_fixed, DA, q_t, d_r_fixed, d_so_fixed, d_eb_fixed,
  d_lb_fixed, d_bw_fixed, LR_r, LR_so_fixed, LR_eb, LR_lb_fixed)
MainFunction("VFCEP",LR_r, nf_fixed, DA, q_t, d_r_fixed, d_so_fixed, d_eb_fixed,
  d_lb_fixed,d_bw_fixed, LR_r, LR_so_fixed, LR_eb, LR_lb_fixed)

```

Appendix D

Supplementary information for Chapter 5

D.1 Modeling correlation between two lognormal distributions using the bivariate normal distribution

Here, the bivariate normal distribution is used to sample correlated lognormal variables. Transforming a normal distribution into a lognormal distribution is common knowledge.

Let X and Y be lognormal random variables: $X \sim \text{LogNormal}(\lambda_X, \zeta_X^2)$, $Y \sim \text{LogNormal}(\lambda_Y, \zeta_Y^2)$

Then, $U = \ln(X)$ and $V = \ln(Y)$ are normal: $U \sim \text{Normal}(\mu_U, \sigma_U^2)$, $V \sim \text{Normal}(\mu_V, \sigma_V^2)$, with means $\mu_U = \lambda_X$, $\mu_V = \lambda_Y$ and standard deviations $\sigma_U = \zeta_X$ and $\sigma_V = \zeta_Y$.

Accordingly, the means of the lognormal distributions are:

$$\mu_X = e^{\mu_U + \frac{1}{2}\sigma_U^2} \quad (\text{D1})$$

and

$$\mu_Y = e^{\mu_V + \frac{1}{2}\sigma_V^2} \quad (\text{D2})$$

However, a transformation is not enough to ensure that the lognormal distributions are correlated in the same way that the normal distributions are. To know the correlation coefficient between the sampled correlated lognormal distributions, it is necessary to find the link between the covariance of two normal variables with the covariance of the corresponding lognormal variables.

Assuming that the covariance of X and Y , $\text{Cov}(X, Y)$, is known, what is the covariance of U and V , $\text{Cov}(U, V)$?

Define $W = U + V$ so that $XY = e^U e^V = e^{U+V} = e^W$

Given that U and V are normally distributed, $W = U + V$ is also normally distributed with $\mu_W = \mu_U + \mu_V$ and $\sigma_W = \sqrt{\sigma_U^2 + \sigma_V^2 + 2\text{Cov}(U, V)}$. Then, $XY = e^W$ is lognormal: $XY \sim \text{LogNormal}(\mu_W, \sigma_W^2)$. Therefore, the mean of XY is

$$E[XY] = e^{\mu_W + \frac{1}{2}\sigma_W^2} \quad (\text{D3})$$

Using the identity $\text{Cov}(X, Y) = E[XY] - E[X]E[Y]$ and Equation D3:

$$Cov(X, Y) = e^{\mu_W + \frac{1}{2}\sigma_W^2} - \mu_X\mu_Y \quad (D4)$$

Replacing $\mu_W = \mu_U + \mu_V$ and $\sigma_W = \sqrt{\sigma_U^2 + \sigma_V^2 + 2Cov(U, V)}$ in Equation D4:

$$Cov(X, Y) = e^{\mu_U + \mu_V + \frac{1}{2}(\sigma_U^2 + \sigma_V^2 + 2Cov(U, V))} - \mu_X\mu_Y = e^{\mu_U + \frac{1}{2}\sigma_U^2} e^{\mu_V + \frac{1}{2}\sigma_V^2} e^{Cov(U, V)} - \mu_X\mu_Y \quad (D5)$$

Substituting Equations D1 and D2 in D5:

$$Cov(X, Y) = \mu_X\mu_Y e^{Cov(U, V)} - \mu_X\mu_Y = \mu_X\mu_Y (e^{Cov(U, V)} - 1)$$

Rearranging for $Cov(U, V)$:

$$Cov(U, V) = \ln \left(1 + \frac{Cov(X, Y)}{\mu_X\mu_Y} \right)$$

Using the formulas for Pearson's correlation coefficient $\rho_{U, V} = \frac{Cov(U, V)}{\sigma_U\sigma_V}$ and $\rho_{X, Y} = \frac{Cov(X, Y)}{\sigma_X\sigma_Y}$, with σ_X and σ_Y being the standard deviations of the variables X and Y , respectively,

$$\rho_{U, V}\sigma_U\sigma_V = \ln \left(1 + \frac{\rho_{X, Y}\sigma_X\sigma_Y}{\mu_X\mu_Y} \right)$$

This equation allows finding the correlation coefficient between the correlated lognormal variables ($\rho_{X, Y}$) given the correlation established between their corresponding normal variables with the bivariate normal distribution.

D.2 Possible values of the correlation coefficient between two lognormal distributions correlated through their corresponding normal distributions

For a multivariate normal distribution to have a density, it must be a non-degenerate case (i.e., each random variable part of the multivariate distribution cannot be described by a linear function of the others). A multivariate normal distribution is non-degenerate when the covariance matrix (UV) is positive definite, which occurs if all its eigenvalues are positive.

Given an $n \times n$ matrix UV , an eigenvalue (λ_e) of UV is a scalar for which there are some non-zero vectors $X_e \in \mathbb{C}^n$ so that $UV \times X_e = \lambda_e \times X$. If $UV \times X_e = \lambda_e \times X$, then:

$$UV \times X_e - \lambda_e \times X = 0$$

$$(UV - \lambda_e I) \times X_e = 0, \text{ where } I \text{ is the identity matrix.}$$

It can be proved that the matrix $UV - \lambda_e I$ is not invertible. Hence, a way to find the eigenvalues of UV is solving the expression $\det(UV - \lambda_e I) = 0$, where $\det(UV - \lambda_e I)$ is the determinant of this matrix.

$$\text{Finding } \lambda_e: \det(UV - \lambda_e I) = 0$$

$$UV - \lambda_e I = \begin{pmatrix} \sigma_U^2 & \text{Cov}(U, V) \\ \text{Cov}(U, V) & \sigma_V^2 \end{pmatrix} - \lambda_e \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} = \begin{pmatrix} \sigma_U^2 - \lambda_e & \text{Cov}(U, V) \\ \text{Cov}(U, V) & \sigma_V^2 - \lambda_e \end{pmatrix}$$

$$\det(UV - \lambda_e I) = (\sigma_U^2 - \lambda_e) \times (\sigma_V^2 - \lambda_e) - \text{Cov}(U, V)^2 = 0$$

$$\lambda_e^2 - \lambda_e(\sigma_U^2 + \sigma_V^2) + \sigma_U^2 \sigma_V^2 - \text{Cov}(U, V)^2 = 0$$

Solving for λ_e :

$$\lambda_e = \frac{(\sigma_U^2 + \sigma_V^2) \pm \sqrt{(\sigma_U^2 + \sigma_V^2)^2 - 4(\sigma_U^2 \sigma_V^2 - \text{Cov}(U, V)^2)}}{2}$$

$$\lambda_e = \frac{(\sigma_U^2 + \sigma_V^2) \pm \sqrt{\sigma_U^4 + \sigma_V^4 + 2\sigma_U^2 \sigma_V^2 - 4\sigma_U^2 \sigma_V^2 + 4 \text{Cov}(U, V)^2}}{2}$$

$$\lambda_e = \frac{(\sigma_U^2 + \sigma_V^2) \pm \sqrt{(\sigma_U^2 - \sigma_V^2)^2 + 4 \text{Cov}(U, V)^2}}{2}$$

We want all $\lambda_e > 0$, so that $\text{Cov}(UV)$ is positive definite.

$$(\sigma_U^2 + \sigma_V^2) + \sqrt{(\sigma_U^2 - \sigma_V^2)^2 + 4Cov(U, V)^2} > 0 \text{ ok!}$$

$$(\sigma_U^2 + \sigma_V^2) - \sqrt{(\sigma_U^2 - \sigma_V^2)^2 + 4Cov(U, V)^2} > 0$$

$$(\sigma_U^2 + \sigma_V^2) > \sqrt{(\sigma_U^2 - \sigma_V^2)^2 + 4Cov(U, V)^2}$$

$$(\sigma_U^2 + \sigma_V^2)^2 > (\sigma_U^2 - \sigma_V^2)^2 + 4Cov(U, V)^2$$

$$\sigma_U^4 + \sigma_V^4 + 2\sigma_U^2\sigma_V^2 > \sigma_U^4 + \sigma_V^4 - 2\sigma_U^2\sigma_V^2 + 4Cov(U, V)^2$$

$$4\sigma_U^2\sigma_V^2 > 4Cov(U, V)^2$$

$$\sigma_U^2\sigma_V^2 > Cov(U, V)^2$$

$$-\sigma_U\sigma_V < Cov(U, V) < \sigma_U\sigma_V \text{ (I)}$$

Solving the second part of inequality (I), $Cov(U, V) < \sigma_U\sigma_V$:

Using the expression for $Cov(U, V)$ found in Appendix D Section D.1:

$$\ln\left(1 + \frac{\rho\sigma_X\sigma_Y}{\mu_X\mu_Y}\right) < \sigma_U\sigma_V$$

$$1 + \frac{\rho\sigma_X\sigma_Y}{\mu_X\mu_Y} < e^{\sigma_U\sigma_V}$$

$$\rho < (e^{\sigma_U\sigma_V} - 1) \frac{\mu_X\mu_Y}{\sigma_X\sigma_Y}$$

This expression gives an upper limit to ρ . Denoting it by ρ_{MAX} ,

$$\boxed{\rho_{MAX} = \frac{\mu_X\mu_Y}{\sigma_X\sigma_Y}(e^{\sigma_U\sigma_V} - 1)}$$

Solving the first part of inequality (I), $Cov(U, V) > -\sigma_U\sigma_V$:

Using the expression for $Cov(U, V)$ found in Appendix D Section D.1:

$$\ln\left(1 + \frac{\rho\sigma_X\sigma_Y}{\mu_X\mu_Y}\right) > -\sigma_U\sigma_V$$

$$1 + \frac{\rho\sigma_X\sigma_Y}{\mu_X\mu_Y} > e^{-\sigma_U\sigma_V}$$

$$\frac{\rho\sigma_X\sigma_Y}{\mu_X\mu_Y} > (e^{-\sigma_U\sigma_V} - 1)$$

In our cases, μ_X, μ_Y, σ_X and σ_Y are necessarily greater than 0.

$$\rho > \frac{\mu_X \mu_Y}{\sigma_X \sigma_Y} (e^{-\sigma_U \sigma_V} - 1)$$

This is a lower limit for ρ . Denoting it by ρ_{MIN_1} , $\rho_{MIN_1} = \frac{\mu_X \mu_Y}{\sigma_X \sigma_Y} (e^{-\sigma_U \sigma_V} - 1)$

The conditions of a logarithm also need to be satisfied so $Cov(UV) = \ln \left(1 + \frac{\rho \sigma_X \sigma_Y}{\mu_X \mu_Y} \right)$, as given by Appendix D Section D.1, exists. This requires $1 + \frac{\rho \sigma_X \sigma_Y}{\mu_X \mu_Y} > 0$:

$$\rho > -\frac{\mu_X \mu_Y}{\sigma_X \sigma_Y}$$

Another lower limit for ρ was found. $\rho_{MIN_2} = -\frac{\mu_X \mu_Y}{\sigma_X \sigma_Y}$.

To check which lower limit is more restrictive, calculate $\rho_{MIN_1} - \rho_{MIN_2}$:

$$\rho_{MIN_1} - \rho_{MIN_2} = \frac{\mu_X \mu_Y}{\sigma_X \sigma_Y} (e^{-\sigma_U \sigma_V} - 1) - \left(-\frac{\mu_X \mu_Y}{\sigma_X \sigma_Y} \right)$$

$$\rho_{MIN_1} - \rho_{MIN_2} = \frac{\mu_X \mu_Y}{\sigma_X \sigma_Y} e^{-\sigma_U \sigma_V}$$

Because $\sigma_U \sigma_V > 0$, $0 < e^{-\sigma_U \sigma_V} < 1$, then $\rho_{MIN_1} - \rho_{MIN_2} > 0$ and $\rho_{MIN_1} > \rho_{MIN_2}$.

This means ρ_{MIN_1} is more restrictive than ρ_{MIN_2} .

Therefore, $\rho_{MIN} = \frac{\mu_X \mu_Y}{\sigma_X \sigma_Y} (e^{-\sigma_U \sigma_V} - 1)$

Then, possible correlation coefficient values for two lognormal distributions correlated through their corresponding normal distributions are

$$\frac{\mu_X \mu_Y}{\sigma_X \sigma_Y} (e^{-\sigma_U \sigma_V} - 1) < \rho < \frac{\mu_X \mu_Y}{\sigma_X \sigma_Y} (e^{\sigma_U \sigma_V} - 1)$$

D.3 R code used to perform the analyses of scenarios 1 and 2

```
# This code is built to perform the analyses of scenarios 1 and 2 presented in
# the paper "Drinking water QMRA and decision-making: Sensitivity of risk to
# dependence among inputs". It is not optimized for use as a package.
#
# Dafne de Brito Cruz, M.Sc.
# January 17, 2024

#Importing libraries
library(MASS)

#Setting seed
set.seed(16)

##### SCENARIO 1 #####

# MAIN VARIABLES
# Influent pathogen concentration is represented by  $X \sim \text{Normal}(\mu_X, \text{var}_X)$ 
# Treatment log-reduction is represented by  $Y \sim \text{Normal}(\mu_Y, \text{var}_Y)$ 
# X and Y are joint normally distributed

#Distributions X and Y: setting parameters
mu_X <- 0.75
var_X <- 0.17^2
sd_X <- sqrt(var_X)
mu_Y <- 3
var_Y <- 0.35^2
sd_Y <- sqrt(var_Y)

#Correlation coefficient (X and Y)
rho <- c(-1,-0.5,0,0.5,1)
#Covariance(X,Y)
cov_XY <- sqrt(var_X)*sqrt(var_Y)*rho

#Setting up plotting area
par(mfrow = c(1,5), oma = c(4,5.5,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)

#Evaluating risk
for (rho_i in 1:5){
  Pi <- list() # list with annual probability of infection for several years
  for (k in 1:1000){
    #Simulating values from the joint normal distribution X,Y
    XY <- as.data.frame(mvrnorm(n=365,mu=c(mu_X, mu_Y),
                                     Sigma=matrix(c(var_X, cov_XY[rho_i],
                                                         cov_XY[rho_i], var_Y),2,2)))

    colnames(XY) <- c('X','Y')

    #Calculating concentration after treatment (C_eff)
    C_eff <- as.data.frame((XY$X)*10^(-XY$Y))

    #Calculating risk
    Pi_d <- as.data.frame(1-exp(-0.018*C_eff*0.0145)) #daily probability of
infection
    Pnoti_d <- as.data.frame(1-Pi_d) #daily probability of not infection
    Pi_a <- 1 - prod(Pnoti_d) #annual probability of infection
    Pi <- append(Pi, Pi_a)
  }
}
```

```

#Risk plots
plot(unlist(Pi),ylim=c(0.00007, 0.00016), log='y', main = bquote(rho ==
.(rho[rho_i])),
      cex.main=2, cex.axis=1.7, yaxt='n', xaxt='n', cex=1.5)
title(ylab="Annual probability of infection \n",cex.lab=2, outer = TRUE, line = 2)
axis(side=2, at=c(0.00007, 0.00009, 0.00011, 0.00013, 0.00015),
      labels = if (rho_i == 1) {c(0.00007, 0.00009, 0.00011, 0.00013, 0.00015)}
      else FALSE, cex.axis=1.5)
mean_Pi <- mean(unlist(Pi))
var_Pi <- var(unlist(Pi))
lb_95 <- quantile(unlist(Pi),0.05)
ub_95 <- quantile(unlist(Pi),0.95)
print(mean_Pi)
abline(h=mean_Pi, col="blue", lwd=3)
abline(h=lb_95, col='magenta', lwd=3,lty=2)
abline(h= ub_95, col='magenta', lwd=3,lty=2)
text(x = 500, y = 0.00016,
      paste("mean = ", formatC(mean_Pi,format = "e", digits = 2)),
col="blue",cex=1.5)
text(x = 500, y = 0.000155,
      paste("COV = ", formatC(sqrt(var_Pi)/mean_Pi,format = "e", digits = 2)),
col="darkgreen",cex=1.5)
}

##### SCENARIO 2 #####
#Setting seed
set.seed(16)

# MAIN VARIABLES
# Influent pathogen concentration is represented by  $X \sim \text{LogNormal}(\lambda_X, \zeta_X)$ 
# Treatment log-reduction is represented by  $Y \sim \text{LogNormal}(\lambda_Y, \zeta_Y)$ 
#  $U = \ln(X)$  is normal
#  $V = \ln(Y)$  is normal
#  $U$  and  $V$  are joint normally distributed

#Distributions  $X$  and  $Y$ : setting parameters and calculating mean and variance
lambda_X <- -3.15
zeta_X <- 2.19
lambda_Y <- 1.2
zeta_Y <- 0.3

mu_X <- exp(lambda_X+zeta_X^2/2)
var_X <- (exp(zeta_X^2)-1)*exp(2*lambda_X+zeta_X^2)
mu_Y <- exp(lambda_Y+zeta_Y^2/2)
var_Y <- (exp(zeta_Y^2)-1)*exp(2*lambda_Y+zeta_Y^2)

#Calculating parameters of  $U$  and  $V$ 
var_U <- log(1+var_X/mu_X^2)
mu_U <- log(mu_X)-0.5*var_U
var_V <- log(1+var_Y/mu_Y^2)
mu_V <- log(mu_Y)-0.5*var_V

#Calculating possible rho values, so that the covariance matrix is positive definite
rho_max <- ((mu_X*mu_Y)/(sqrt(var_X)*sqrt(var_Y)))*(exp(sqrt(var_U)*sqrt(var_V))-1)
rho_min <- ((mu_X*mu_Y)/(sqrt(var_X)*sqrt(var_Y)))*(exp(-sqrt(var_U)*sqrt(var_V))-1)

#Correlation coefficients ( $X$  and  $Y$ )

```

```

rho <- c(rho_min,rho_min/2,0,rho_max/2,rho_max)
#Covariance(X,Y)
cov_XY <- sqrt(var_X)*sqrt(var_Y)*rho
#Covariance(U,V)
cov_UV <- log(1+cov_XY/(mu_X*mu_Y))

#Setting up plotting area
par(mfrow = c(1,5), oma = c(4,5.5,3,0) + 0.1, mar = c(0.5,0,1.5,1) + 0.1)

#Evaluating risk
for (rho_i in 1:5){
  Pi <- list() #list with annual probability of infection for several years
  for (k in 1:1000){
    #Simulating values from the joint normal distribution U,V
    UV <- as.data.frame(mvrnorm(n=365,mu=c(mu_U, mu_V),
                                     Sigma=matrix(c(var_U, cov_UV[rho_i], cov_UV[rho_i],
var_V),2,2)))
    colnames(UV) <- c('U','V')

    #Calculating concentration after treatment (C_eff)
    C_eff <- as.data.frame(exp(UV$U)*10^(-exp(UV$V)))

    #Calculating risk
    Pi_d <- as.data.frame(1-exp(-0.018*C_eff*0.0145)) #daily risk of infection
    Pnoti_d <- as.data.frame(1-Pi_d) #daily probability of not infection
    Pi_a <- 1 - prod(Pnoti_d) #annual probability of infection
    Pi <- append(Pi, Pi_a)
  }

#Risk plots
  plot(unlist(Pi),log='y', main = bquote(rho == .(round(rho[rho_i], digits=2))),
ylim=c(0.000001, 0.1),
      cex.main=2, cex.axis=1.7, cex=1.5, yaxt='n',xaxt='n')
  title(ylab = "Annual probability of infection \n",cex.lab=2,outer = TRUE, line =
2)
  axis(side=2, at=c(0.000001,0.00001, 0.0001, 0.001, 0.01, 0.1),
      labels = if (rho_i == 1) {c(0.000001,0.00001, 0.0001, 0.001, 0.01, 0.1)} else
FALSE, cex.axis=1.5)

  mean_Pi <- mean(unlist(Pi))
  var_Pi <- var(unlist(Pi))
  lb_95 <- quantile(unlist(Pi),0.05)
  ub_95 <- quantile(unlist(Pi),0.95)
  abline(h=lb_95, col='magenta', lwd=3,lty=2)
  abline(h= ub_95, col='magenta', lwd=3,lty=2)
  abline(h=mean_Pi, col="blue", lwd=3)
  text(x = 500, y = 0.1,
      paste("mean =", formatC(mean_Pi, format = "e", digits = 2)),
col="blue",cex=1.5)
  text(x = 500, y = 0.06,
      paste("COV =", formatC(sqrt(var_Pi)/mean_Pi, format = "e", digits = 2)),
col="darkgreen",cex=1.5)
}

```

D.4 Calgary case study: treatment and concentration plots

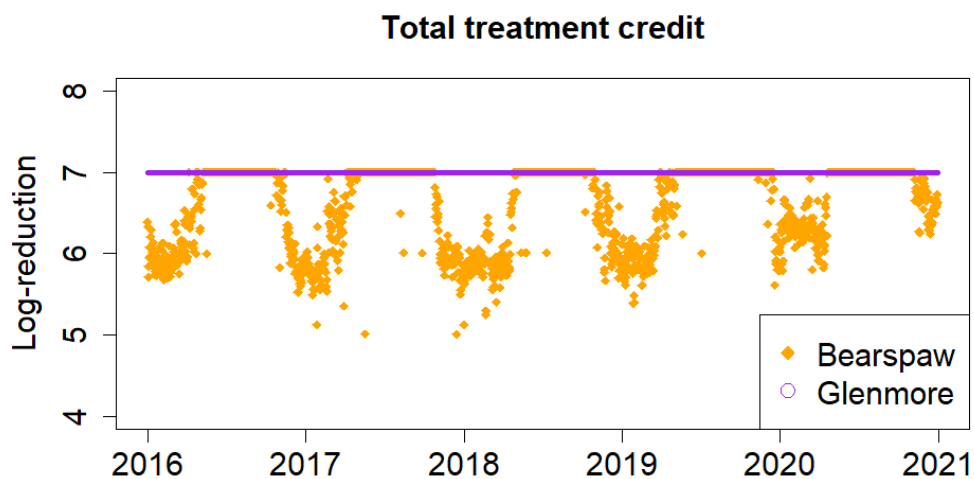


Figure D.1: Total treatment credit (filtration and disinfection) at Bears paw and Glenmore water treatment plants from 2016 to 2020

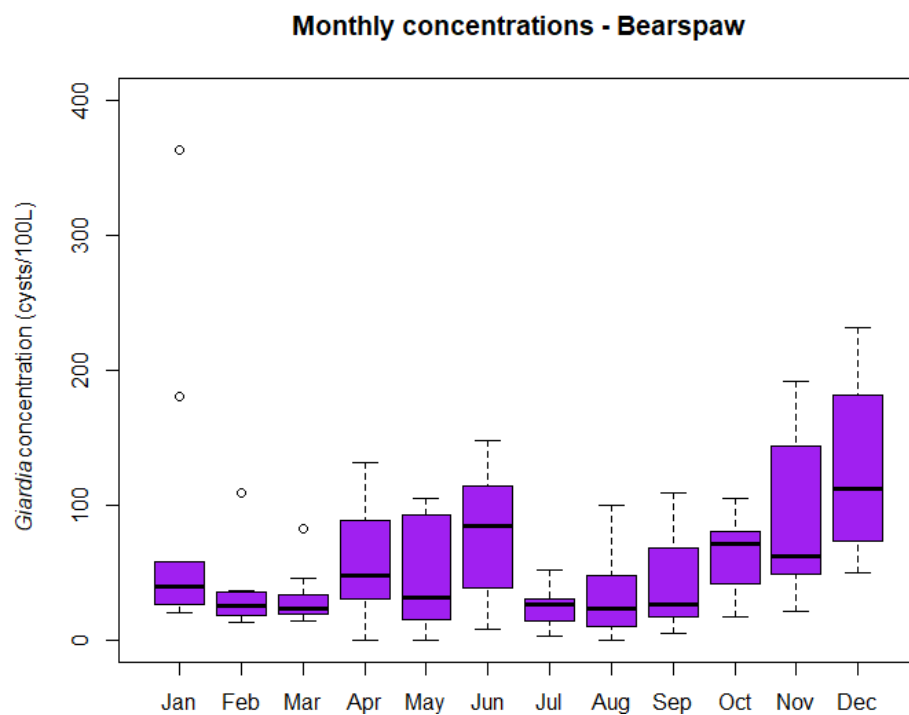


Figure D.2: Monthly Giardia cyst concentration at Bears paw raw water from 2016 to 2020

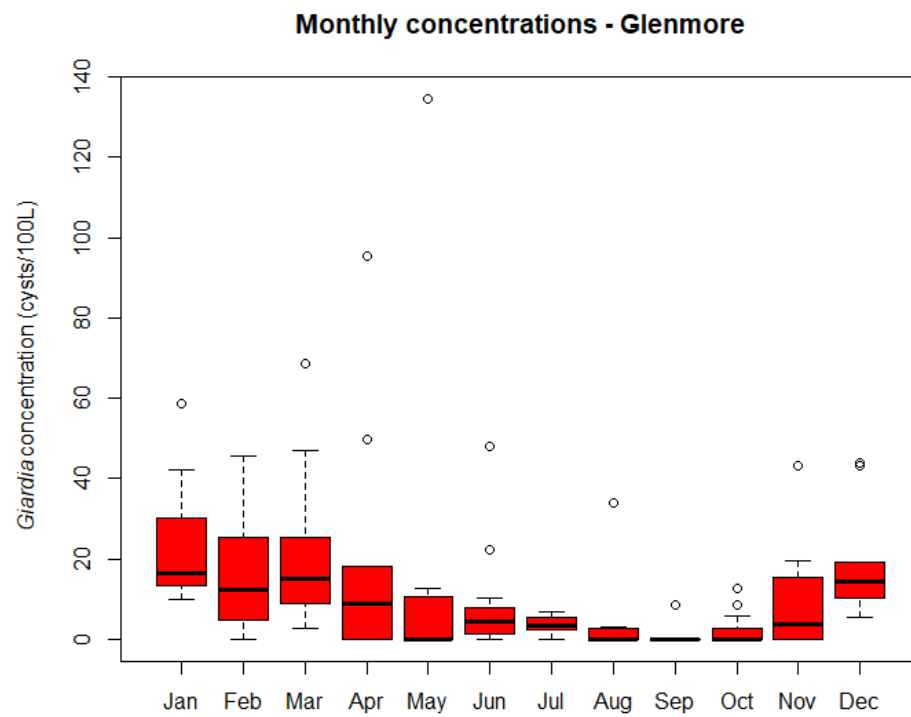


Figure D.3: Monthly Giardia cyst concentrations at Glenmore raw water from 2016 to 2020

D.5 Empirical cumulative distribution functions of annual probability of infection

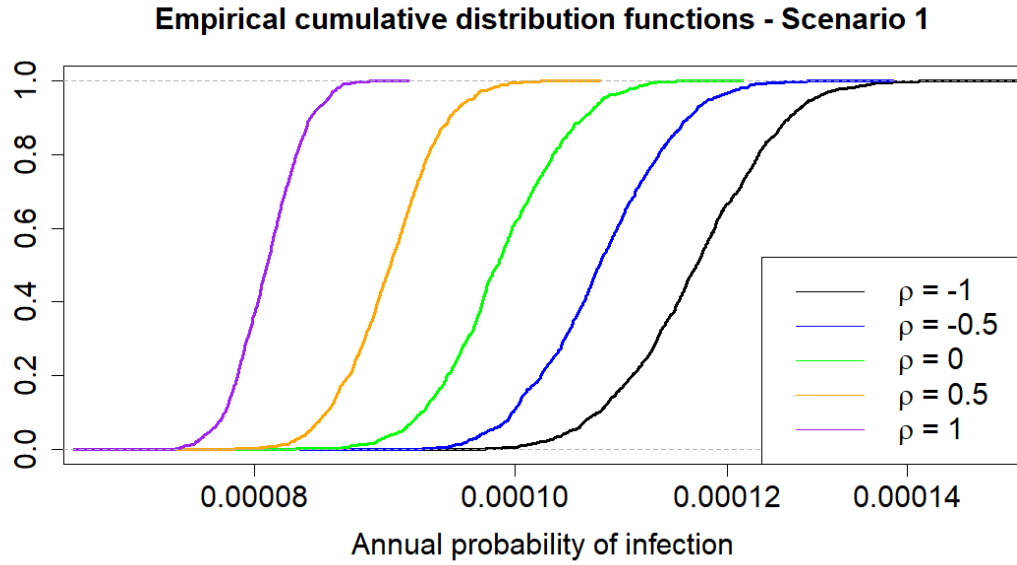


Figure D.4: Empirical cumulative distribution functions of annual probability of infection given different correlation coefficients between normally distributed concentration and treatment log-reduction (Scenario 1)

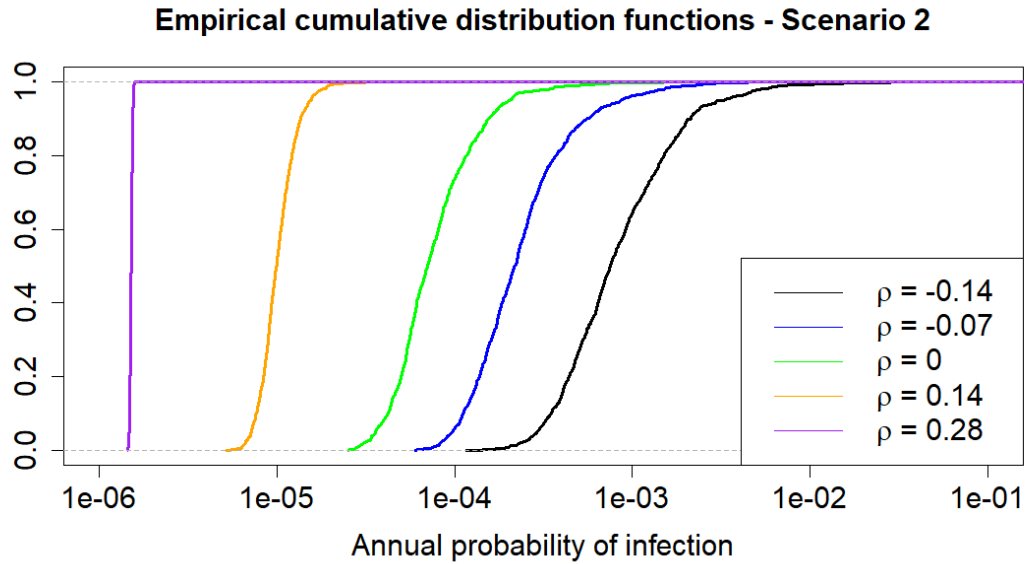


Figure D.5: Empirical cumulative distribution functions of annual probability of infection given different correlation coefficients between lognormally distributed concentration and treatment log-reduction (Scenario 2)

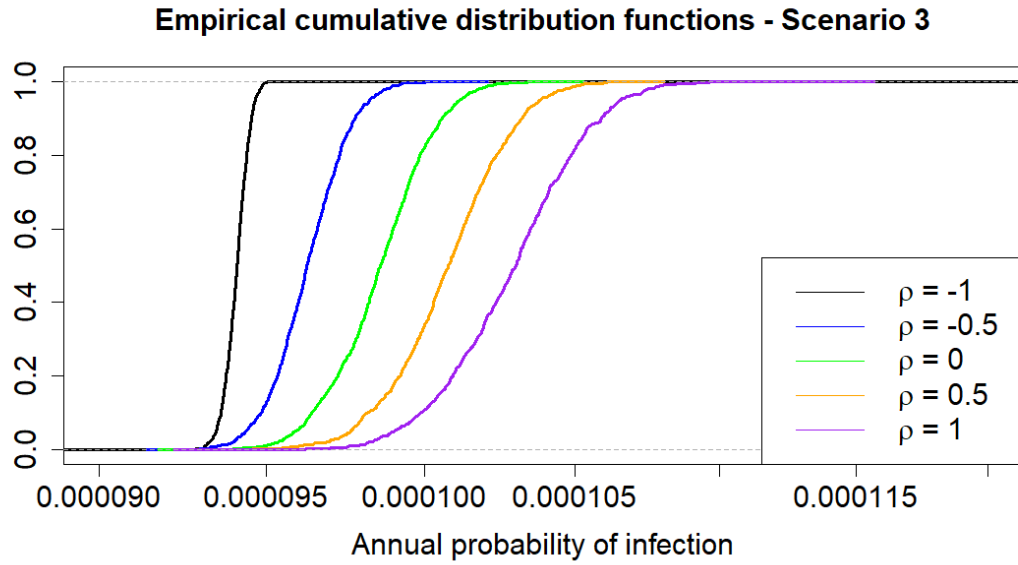


Figure D.6: Empirical cumulative distribution functions of annual probability of infection given different correlation coefficients between normally distributed concentration and volume of treated water consumed (Scenario 3)

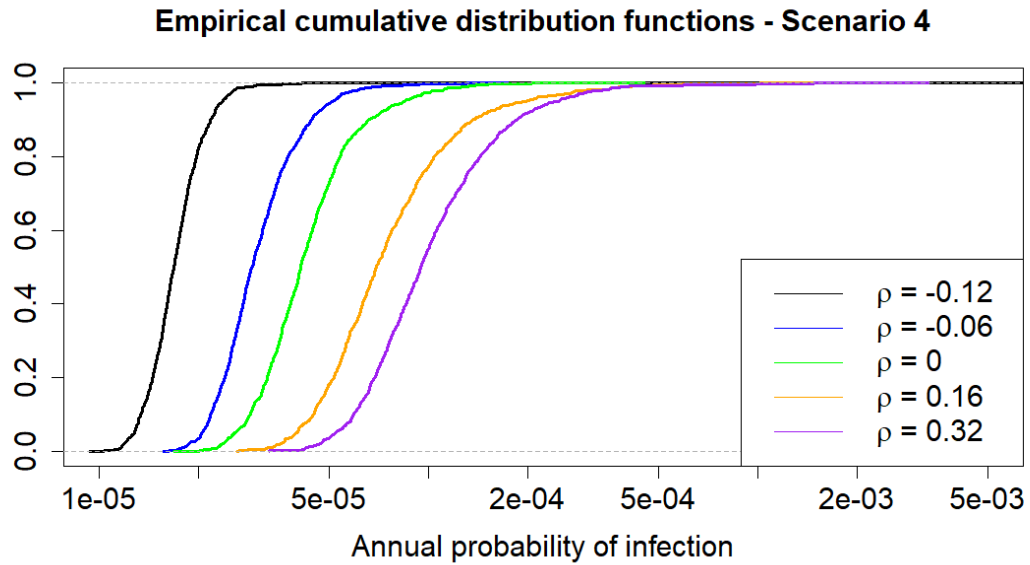


Figure D.7: Empirical cumulative distribution functions of annual probability of infection given different correlation coefficients between lognormally distributed concentration and volume of treated water consumed (Scenario 4)

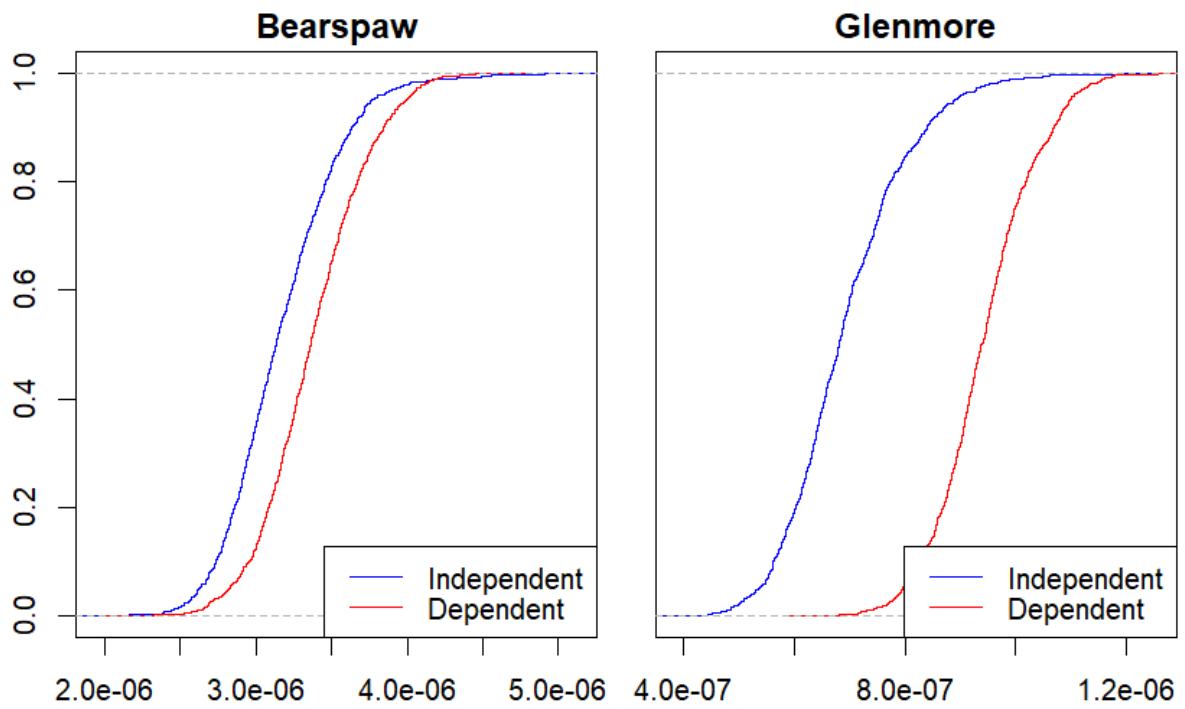


Figure D.8: Empirical cumulative distribution functions of annual probability of infection in the independent and dependent scenarios considering *Giardia* concentrations at Bears paw and Glenmore water treatment plants

D.6 Extra scenario run to test the different in results between scenarios 1 and 2

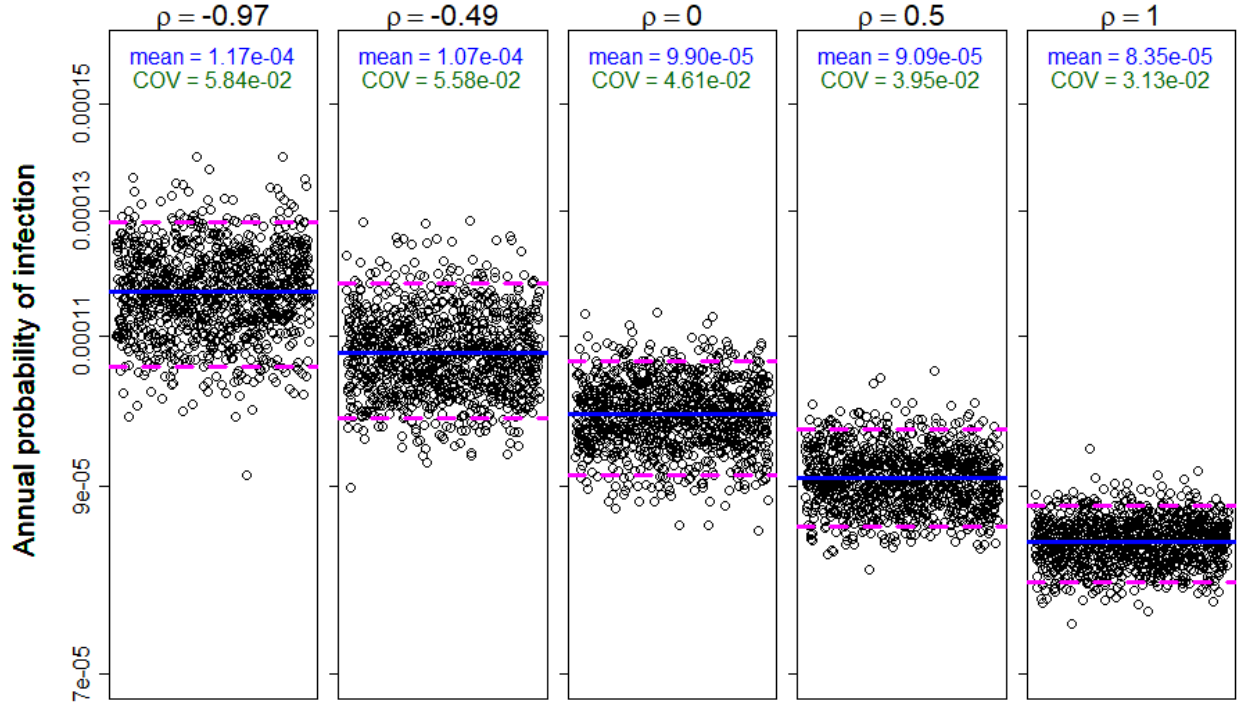


Figure D.9: Annual probability of infection in each of 1000 simulated years given different correlation coefficients between lognormally distributed concentration and treatment log-reduction, $C \sim \text{LogNormal}(-0.31, 0.22)$ and $LR \sim \text{LogNormal}(1.09, 0.12)$. The blue line indicates the mean value and COV represents the sample coefficient of variation. The pink dashed lines indicate the 5th and 95th percentiles

D.7 A brief introduction to copulas and their use to model dependence

Copulas are a common way to characterize multivariate distributions. By definition, a copula is a multivariate distribution function with uniform marginals. What makes the use of copulas convenient to represent multivariate distributions is the property that every continuous random variable X can be transformed into a uniform distribution using the cumulative distribution function $F(x)$, as illustrated in Figure D.10. Hence, using the uniform marginals of a copula, the structure of dependence of this copula can be applied without restriction on the distribution of any individual input.

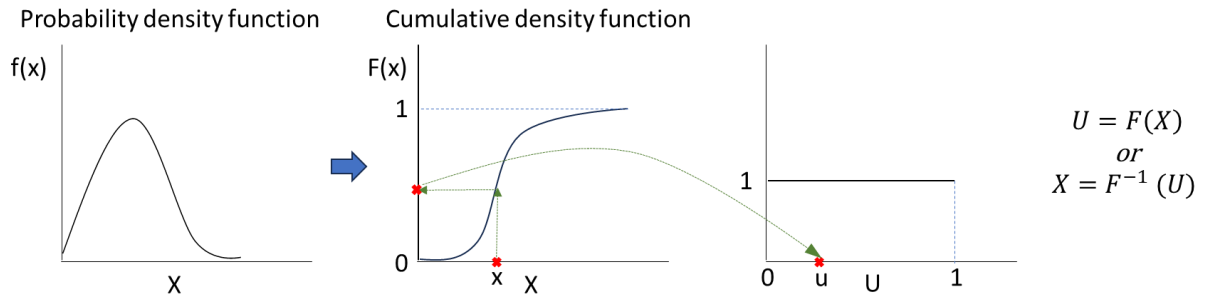


Figure D.10: Transformation of a random variable X into a uniform distribution

To give an example of how copulas can be used to represent a structure of dependence between two distributions, consider the multivariate distributions obtained from the random variables $X \sim \text{Lognormal}(4,10)$ and $Y \sim \text{Exponential}(5)$ using both the independent and Frank copulas. The independent copula, representing two independent random variables is given by $C_{\text{indep}}(u_1, u_2) = u_1 u_2$, while the Frank copula is represented by $C_{\text{Frank}}(u_1, u_2; \theta) = -\frac{1}{\theta} \log \left(1 + \frac{(e^{-\theta u_1} - 1)(e^{-\theta u_2} - 1)}{e^{-\theta} - 1} \right)$. Using the library *copula* in R, 1000 samples were generated from each of these copulas according to the following R code. The parameter used for the Frank copula was $\theta = 10$. These samples can be visualized in Figure D.11.

```
library("copula")

set.seed(16)

#Building a bivariate distribution with the independent and Frank copula with uniform
margins
Indep <- mvdc(indepCopula(dim=2), margins = c("unif","unif"),
              paramMargins = list(list(min = 0, max = 1), list(min = 0, max = 1)))

Frank <- mvdc(frankCopula(param = 10, dim = 2), margins = c("unif","unif"),
              paramMargins = list(list(min = 0, max = 1), list(min = 0, max = 1)))
```

```
#Sampling 1000 random values from each bivariate distribution
rIndep <- rMvdc(1000, Indep)
rFrank <- rMvdc(1000, Frank)

#Plotting the pair of values sampled
plot(rIndep[,1], rIndep[,2], xlab=c("Uniform(0,1)"), ylab=c("Uniform(0,1)"),
     main=expression(paste("Independent copula")))
plot(rFrank[,1], rFrank[,2], xlab=c("Uniform(0,1)"), ylab=c("Uniform(0,1)"),
     main= expression(paste("Frank copula ", theta, "=10")))
```

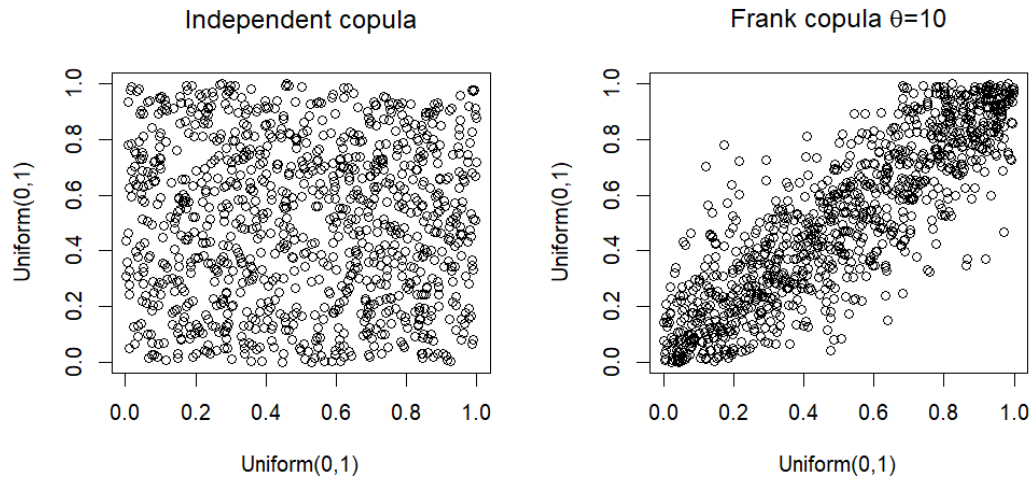


Figure D.11: A thousand random samples from the independent and Frank copulas with uniform marginal distributions

Figure D.11 shows how these two bivariate distributions have different dependence structures. Because every probability distribution can be transformed into a uniform distribution and vice-versa (Figure D.10), it is possible to transfer the structure of dependence to any marginal distribution. To do that, the values from uniform distributions sampled using these copulas will be transformed to the distributions of interest ($X \sim \text{Lognormal}(4, 0.1)$ and $Y \sim \text{Exponential}(5)$) using the inverse cumulative density function (CDF) of these distributions. Figure D.12 shows how these distributions are linked with the independent and Frank copulas, and the R code to impose this dependence follows.

```
Ind.LN <- qlnorm(rIndep[,1], meanlog=4, sdlog=0.1)
Ind.EXP <- qexp(rIndep[,2], rate=5)
plot(Ind.LN, Ind.EXP, xlab=c("Lognormal(4,0.1)"), ylab=c("Exponential(5)"),
     main=expression(paste("Independent copula")), xlim=c(40,80), ylim=c(0,2))

Dep.LN <- qlnorm(rFrank[,1], meanlog=4, sdlog=0.1)
Dep.EXP <- qexp(rFrank[,2], rate=5)
plot(Dep.LN, Dep.EXP, xlab=c("Lognormal(4,0.1)"), ylab=c("Exponential(5)"), main=
expression(paste("Frank copula ", theta, "=10")), xlim=c(40,80), ylim=c(0,2))
```

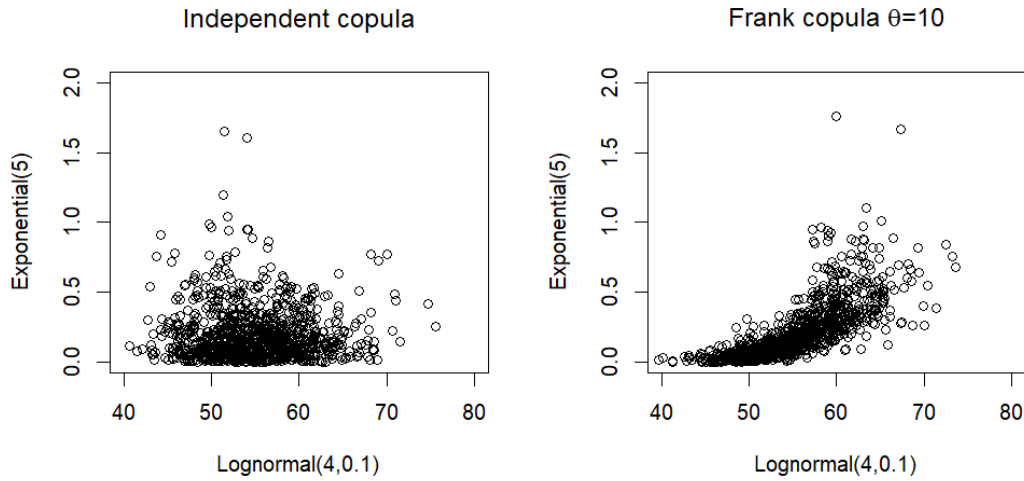


Figure D.12: A thousand random samples from the independent and Frank copulas with $\text{Lognormal}(4, 0.1)$ and $\text{Exponential}(5)$ as marginal distributions

Generating bivariate samples from the chosen lognormal and exponential distribution could be done directly using the *mvdc* function above, directly specifying the marginals as these two distributions (not as uniform distributions). However, this process was done in more steps here to explain why the fact of copulas having uniform marginals is important for characterizing multivariate distributions.

The copula theory is based on Sklar's theorem (Sklar, 1959), which states that any multivariate distribution can be represented by a copula and univariate marginal distributions (i.e., distributions for one variable at a time irrespective of the value of other dependent variables). Conversely, given some univariate distributions and a copula, a multivariate distribution can be derived. This theory allows treatment of multivariate distributions to be divided into two simpler steps: (1) fitting univariate marginals, as done to fit a distribution to one variable at a time, and (2) selecting a copula to establish the dependence structure and link the marginals. There are several families of easy-to-use parametric copulas that can represent different types of dependence, and programming tools like R allow simple manipulation of these mathematical functions.

To give an example of how copulas can be used to characterize the multivariate distribution of a given dataset, data from the Eric D. Soulis weather station in 2020 (Seglenieks, 2024) is analyzed here. To investigate a potential dependence between temperature and water content in the air, a scatterplot is shown in Figure D.13.

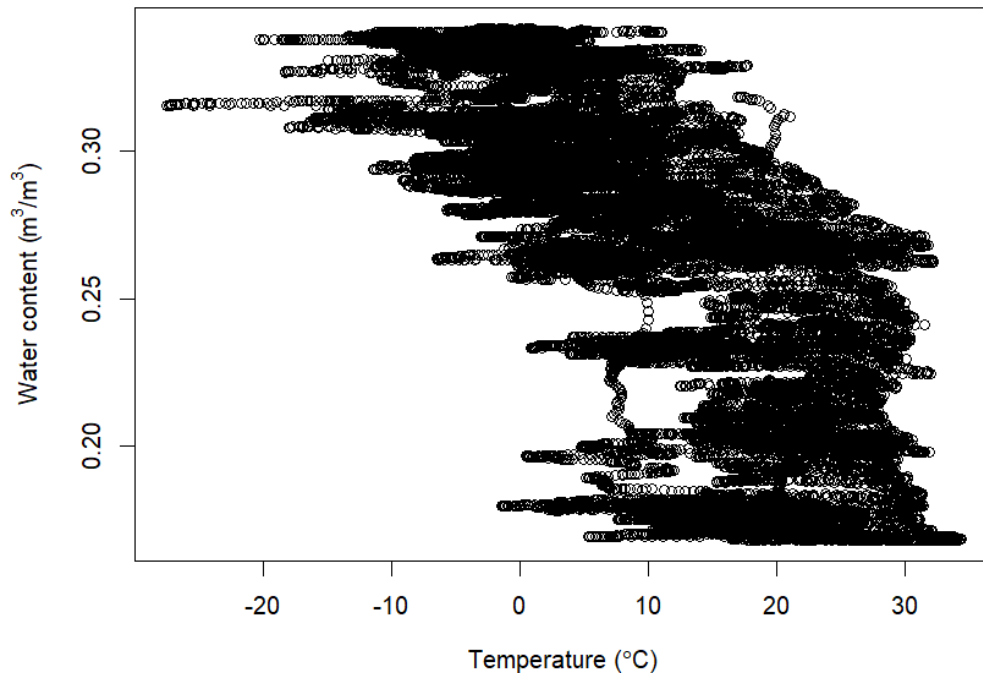


Figure D.13: Water content and temperature data at the Eric D. Soulis weather station in 2020

Figure D.13 shows an expected tendency of decreasing water content with increasing temperature. The Spearman correlation coefficient between these two variables is -0.75. Supposing that these variables were to be used in simulations in a model, it would be more appropriate to consider this dependence when sampling values from their distributions.

Using the *VineCopula* package in R, it is possible to choose a family of copulas that better describes this dataset as well as to determine the parameter of the chosen copula. First, the *pobs* function can be used to compute the pseudo-observations (i.e., the cumulative relative frequency) for each value of the dataset and then the *BiCopSelect* function selects an appropriate bivariate copula family and estimates the corresponding parameters using maximum likelihood estimation. A pseudo code executing the aforementioned steps is shown below.

```
install.packages("VineCopula")

library("readxl")
library("VineCopula")

#Reading Excel file with data
df <- read_excel("Document path")

#Removing cells with incomplete data
df <- na.omit(df)
```

```

#Scatterplot of temperature and water content
plot(df$Temperature, df$`Water Content`, xlab=c("Temperature"),
      ylab=c("Water content"))

#Calculating Spearman correlation coefficient between temperature
#and water content. The columns 2 and 3 of the dataframe represent
#temperature and water content, respectively.
cor(df[,2:3], method="spearman")

#Computing pseudo-observations
var_a <- pobs(df)[,2]
var_b <- pobs(df)[,3]

#Selecting copula
copula <- BiCopSelect(var_a, var_b, familyset = NA)

copula$family
copula$par

```

This code outputs the Frank Copula (family 5) with a parameter of -5.934 as the best fit to this data. The *VineCopula* package also allows fitting a specific type of copula, performing goodness of fit methods to compare different fits and generating random samples from the copula chosen. Other packages in R (e.g., *copula*) or in other programming languages (e.g., package *Copulas* in Python) are also available to work with copulas.

Appendix E

Supplementary information for Chapter 6

E.1 Assessing risk during an event period

This supplementary material presents an equation to evaluate risk in an interval of time in the drinking water QMRA context. If the raw water pathogen concentration (C), treatment log-reduction (LR) and volume of drinking water consumed (V) can be described as functions of time, the instantaneous dose of pathogens consumed via drinking water (D) is represented in Equation E1, where t represents time.

$$D(t) = C(t) \times 10^{-LR(t)} \times V(t) \quad (E1)$$

Given a dose–response function $g(D(t); \theta)$, where θ is the set of parameters of a dose–response model, the instantaneous probability of infection is:

$$P_{inf}(t) = g(D(t); \theta) \quad (E2)$$

Risk over an event period (Δt) can be evaluated by taking n independent time intervals Δt_i associated with a probability of infection $P_i(t)$, where $\sum_{i=1}^n \Delta t_i = \Delta t$, as illustrated in Figure E.1.

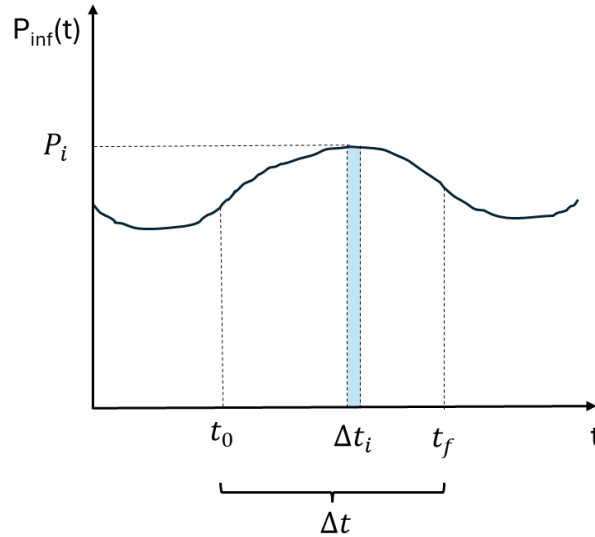


Figure E.1: Instantaneous probability of infection

The probability of infection in the event period ($P_{\Delta t}$) is:

$$P_{\Delta t} = 1 - \prod_{i=1}^n (1 - P_i(t))^{\Delta t_i}$$

Let's denote $A = \prod_{i=1}^n (1 - P_i(t))^{\Delta t_i}$

$$\text{Then, } P_{\Delta t} = 1 - A \quad (\text{E3})$$

$$\ln(A) = \ln\left(\prod_{i=1}^n (1 - P_i(t))^{\Delta t_i}\right) = \sum_{i=1}^n \ln(1 - P_i(t))^{\Delta t_i} = \sum_{i=1}^n \Delta t_i \ln(1 - P_i(t)) \quad (\text{E4})$$

As $n \rightarrow \infty$, the sum $\sum_{i=1}^n \Delta t_i \ln(1 - P_i(t))$ converges to the integral $\int_{t_0}^{t_f} \ln(1 - P_{inf}(t)) dt$, where t_0 and t_f represent the times when the event starts and ends, respectively ($t_f - t_0 = \Delta t$). The integral $\int_{t_0}^{t_f} \ln(1 - P_{inf}(t)) dt$ represents the area under the function $\ln(1 - P_{inf}(t))$ during the event period.

From (E4), $\ln(A) = \int_{t_0}^{t_f} \ln(1 - P_{inf}(t)) dt$

$$\text{Then } A = e^{\int_{t_0}^{t_f} \ln(1 - P_{inf}(t)) dt} \quad (\text{E5})$$

Substituting (E5) into (E3):

$$P_{\Delta t} = 1 - e^{\int_{t_0}^{t_f} \ln(1 - P_{inf}(t)) dt} \quad (\text{E6})$$

Approximation 1:

If $P_{inf}(t) \ll 1$, $\ln(1 - P_{inf}(t)) \approx -P_{inf}(t)$.

Then, Equation E6 can be simplified to $P_{\Delta t} = 1 - e^{-\int_{t_0}^{t_f} P_{inf}(t) dt}$

Approximation 2:

Considering linearity of dose-response models at low doses, $P_{inf}(t) \approx kD(t)$, where k is constant.

Then, Equation E6 can be further simplified to $P_{\Delta t} = 1 - e^{-k \int_{t_0}^{t_f} D(t) dt}$.

Comparing the risk of two events only depends on how the dose of pathogens vary over time. Using this approximation and the assumption that only treatment changes over time (e.g., in treatment failure

scenarios), risk only depends on $\int_{t_0}^{t_f} \mathbf{10}^{-LR(t)} dt$. Thus, an increase in recovery time by a factor X is equivalent to a decrease in treatment log reduction of $\log_{10}(X)$ for the same effect on risk.

E.2 Case study 3 calculations

The effective log-reduction (LR_{eff}) is presented in Equation E7 (Schmidt et al., 2020), in which LR_i representd the log-reduction in each i phase in a total of n phases.

$$LR_{eff} = -\log\left(\frac{\sum_{i=1}^n 10^{-LR_i}}{n}\right) \quad (E7)$$

In the two seasons described in case study 3, Equation E7 can be simplified to Equation E8.

$$LR_{eff} = -\log\left(\frac{10^{-LR_{cold}} + 10^{-LR_{warm}}}{2}\right) \quad (E8)$$

Then, under standard practice:

$$LR_{eff_{standard}} = -\log\left(\frac{10^{-2} + 10^{-3}}{2}\right) = 2.26$$

If the risk management strategy is applied in the cold season:

$$LR_{eff_{cold}} = -\log\left(\frac{10^{-2.5} + 10^{-3}}{2}\right) = 2.68$$

If the risk management strategy is applied in the warm season:

$$LR_{eff_{warm}} = -\log\left(\frac{10^{-2} + 10^{-4}}{2}\right) = 2.30$$

Finally, if all pathogens are removed during the warm season, $10^{-LR_{warm}} = 0$:

$$LR_{eff} = -\log\left(\frac{10^{-2}}{2}\right) = 2.30$$