

Microbial Risk Assessment tool for discharges near drinking water wells: Documentation Report

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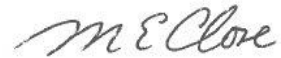
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CONTENTS

Glossary	8
1. Part 1 – Development of the Microbial Risk Assessment Tool ..	9
1.1 INTRODUCTION	9
1.2 WHAT IS THE ISSUE?.....	10
1.3 SCOPE OF THE MICROBIAL RISK ASSESSMENT TOOL.....	11
1.4 THE PROJECT TEAM.....	13
2. Part 2 – User Guide for the Microbial Risk Assessment Tool ..	15
2.1 SIDEBAR INFORMATION.....	15
2.2 INSTRUCTIONS.....	16
2.3 SOURCE PARAMETERS.....	17
2.4 FIGURES.....	18
2.5 PDF REPORT.....	19
2.6 EXAMPLE CASE STUDIES	20
2.6.1 Assessing the risk of norovirus contamination from a single OWMS20	
2.6.2 Comprehensive risk assessment from multiple contaminant sources	
24	
3. Part 3 – Technical Appendix for Microbial Risk Assessment	
Tool.....	35
3.1 OVERVIEW OF TECHNICAL APPENDIX	35
3.2 DESCRIPTION OF LAND-USE SCENARIOS	35
3.2.1 Multiple domestic on-site wastewater management systems	37
3.2.2 Community size on-site wastewater management systems.....	39
3.2.3 Dairy farming	40
3.2.4 Sheep and beef farming	41
3.2.5 Wildfowl.....	42
3.2.6 Stormwater systems.....	43
3.2.7 Animal effluent/manure application to land.....	44
3.3 SIMULATIONS OF WATER FLOW AND MICROBIAL TRANSPORT	45

3.3.1	Climate and Recharge estimates	45
3.3.2	Shedding Period	47
3.3.3	Water Supply Well Pumping Rate.....	48
3.3.4	Soil type and properties	49
3.3.5	Unsaturated (vadose) zone types and properties	50
3.3.6	Aquifer types and properties	51
3.3.7	Soil, vadose zone, and saturated zone thickness	56
3.3.8	Other assumptions and limitations of the flow scenarios	57
3.4	MICROBIAL LOADING AND REMOVAL RATES	58
3.4.1	Microbe selection for human related land-uses	58
3.4.2	Microbe selection for animal related land-uses.....	60
3.4.3	Microbe selection for stormwater systems.....	62
3.4.4	Summary of loading rates	63
3.5	TOLERABLE CONCENTRATIONS OF PATHOGENS IN DRINKING WATER	65
3.6	MODELLING APPROACH	68
3.6.1	Soil modelling	69
3.6.2	Vadose zone modelling	69
3.6.3	Saturated zone modelling	71
3.7	SUMMARY OF FEATURES	74

LIST OF TABLES

TABLE 1. RECHARGE RATES FOR 10 CLIMATIC REGIONS IN NZ, OBTAINED WITH THE IRRICALC MODEL BASED ON 44 YEARS OF DATA.	47
TABLE 2. ANNUAL AVERAGE AND 1-IN-10 YEAR 1-DAY RECHARGE RATES FOR 4 CLIMATE GROUPS BASED ON THE 10 CLIMATIC REGIONS IN NZ.	48
TABLE 3. SHEDDING PERIODS (DAYS) FOR EACH MICROBE IN RELATION TO FAECAL SOURCE/LAND USE.	48
TABLE 4. PUMPING RATE RANGES AND SCREEN DEPTHS PER AQUIFER TYPE. NUMBERS IN THE PARENTHESES ARE THE ASSUMED SCREEN DEPTHS IN METRES BELOW THE WATER TABLE (MBWT).....	49
TABLE 5. VIRUS AND BACTERIA REMOVAL RATES IN SPECIFIC AND GENERIC SOIL TYPES (PANG ET AL., 2008; SCHIJVEN ET AL., 2017; MCLEOD ET AL., 2008).	50
TABLE 6. VIRUS AND BACTERIA REMOVAL RATES IN DIFFERENT VADOSE ZONE MEDIA (MOORE ET AL., 2010; SCHIJVEN ET AL., 2017).	51
TABLE 7. SUMMARY OF VIRUS REMOVAL RATES IN GROUNDWATER AND ASSUMPTIONS OF THE LIKELY DISPERSION CONTRIBUTIONS TO THESE RATES THAT WERE ADOPTED IN THE MODELLING WORK (MOORE ET AL., 2010).	52
TABLE 8. THE EFFICIENCIES OF BACTERIAL REMOVAL IN DIFFERENT AQUIFER MEDIA (AFTER SCHIJVEN ET AL., 2017, TABLE 7).	53
TABLE 9. SUMMARY OF BACTERIAL REMOVAL RATES IN GROUNDWATER AND ASSUMPTIONS OF THE LIKELY DISPERSION CONTRIBUTIONS TO THESE RATES THAT WERE ADOPTED IN THE MODELLING WORK (SCHIJVEN ET AL., 2017; MOORE ET AL., 2010).....	54
TABLE 10. SUMMARY OF MEAN AQUIFER PROPERTIES ADOPTED IN THE MRA TOOL (FROM MOORE ET AL., 2010).	56
TABLE 11. SUMMARY OF THE EXPONENTIAL SEMI-VARIOGRAM PROPERTIES FOR HYDRAULIC CONDUCTIVITY USED TO REPRESENT THE SELECTED AQUIFER TYPES – SILL VALUES IN LOG10 (FROM MOORE ET AL., 2010).	56
TABLE 12: RAW (PRE STATISTICAL PROCESSING) LOADING RATES FOR <i>CAMPYLOBACTER</i> AND <i>E. COLI</i> IN VARIOUS LIVESTOCK AND IN WILDFOWL.	61
TABLE 13: RAW (PRE STATISTICAL PROCESSING) LOADING RATES FOR <i>CAMPYLOBACTER</i> , <i>E. COLI</i> , <i>GIARDIA</i> AND <i>CRYPTOSPORIDIUM</i> IN DAIRY FARM EFFLUENT	62
TABLE 14: RAW (PRE STATISTICAL PROCESSING) LOADING RATES FOR <i>CAMPYLOBACTER</i> , <i>E. COLI</i> , <i>GIARDIA</i> AND <i>CRYPTOSPORIDIUM</i> IN STORMWATER. .	63
TABLE 15: NON-CLIMATE DEPENDENT INITIAL CONCENTRATIONS AT THE SOURCE [MICROBE/L] FOR EACH MICROBE FOR THE HUMAN-RELATED LAND-USES.....	63
TABLE 16: PARAMETERS FOR CONVERTING LOADING RATES IN MPN/ANIMAL/DAY (OR CFU/ANIMAL/DAY) TO MPN/DAY (OR CFU/DAY).	64
TABLE 17: CLIMATE DEPENDENT INITIAL CONCENTRATIONS AT THE SOURCE [MICROBE/L] FOR EACH LAND USE AND MICROBE.	65

TABLE 18: CLIMATE DEPENDENT DAIRY LAND-USE INITIAL CONCENTRATIONS [MICROBE/L] PER ANIMAL. CONCENTRATIONS ARE THEN SCALED BY HERD SIZE TO OBTAIN INITIAL CONCENTRATION AT THE SOURCE [MICROBE/L].....	65
TABLE 19: DOSE RESPONSE CURVE PARAMETERS FOR NOROVIRUS AND <i>CAMPYLOBACTER</i> (TEUNIS ET AL., 2008; BLACK ET AL., 1988)	66
TABLE 20: NUMBER OF DAYS WITH RISK OF INFECTION PER YEAR (N), USED FOR CALCULATING THE TOLERABLE DAILY RATE OF INFECTION P_D	67
TABLE 21: MAXIMUM ACCEPTABLE CONCENTRATIONS GIVING RISE TO AN ANNUAL PROBABILITY OF INFECTION OF 1 IN 10,000 PER PERSON [MICROBE/L].....	68
TABLE 22: INPUT PARAMETER VALUES USED FOR VADOSE ZONE MODELLING (FROM MOORE ET AL., 2010).....	70

LIST OF FIGURES

FIGURE 1: SCHEMATIC FOR LAND-USE SCENARIOS	36
FIGURE 2: COMPONENTS OF MICROBIAL REMOVAL BETWEEN THE ON-SITE WASTEWATER MANAGEMENT SYSTEM (OWMS) AND GROUNDWATER ABSTRACTION POINT. 1) MICROBIAL REDUCTION WITHIN THE TREATMENT PLANT, 2) MICROBIAL REDUCTION WITHIN THE LAND APPLICATION SYSTEM (LAS), 3) MICROBIAL REDUCTION WITHIN THE UNSATURATED (VADOSE) ZONE, 4) MICROBIAL REDUCTION WITHIN THE SATURATED ZONE. NOTE: THE ABSTRACTION WELL IS DIRECTLY DOWN GRADIENT OF THE LAS. THE RED ARROWS GIVE THE DIRECTION OF FLOW AND PREDICTED REDUCTION IN MICROBIAL CONCENTRATION FROM THE OWMS TO THE ABSTRACTION WELL.....	37
FIGURE 3: MAP OF NEW ZEALAND CLIMATE REGIONS FROM THE NEW ZEALAND METEOROLOGICAL SERVICE DELINEATION (NEW ZEALAND METEOROLOGICAL SERVICE, 1983).....	46
FIGURE 4: ALGORITHM FOR CALCULATING THE TOLERABLE MICROBIAL CONCENTRATION IN WATER IN A WELL.	66
FIGURE 5: SINGLE REALISATION OF A 3D HETEROGENEOUS HYDRAULIC CONDUCTIVITY FIELD (DISTANCES IN M).	71
FIGURE 6: FORWARD AND INVERSE TRANSIENT TRANSPORT SOLUTIONS AT VARIOUS TIME STEPS (DISTANCE IN M AND TIME IN DAYS).	72
FIGURE 7: CUMULATIVE EFFECT OF MULTIPLE SOURCES (RIGHT SIDE) FROM A SINGLE INVERSE TRANSPORT SIMULATION (LEFT SIDE) USING THE SUPERPOSITION PRINCIPLE.....	73

GLOSSARY

AET: Actual evapotranspiration

CFU: colony forming units

CSO: Combined Sewer Overflows (CSO)

ECan: Environment Canterbury

ESR: Institute of Environmental Science and Research

FDE: Farming Dairy Effluent

FIB: Faecal indicator bacteria

FSL: Fundamental Soil Layer

GC: Gene copy

GNS: GNS Science

LAS: Land Application System

MRA: Microbial Risk Assessment

MPN: Most probable Number

OSET: On-Site Effluent Testing

OWMS: On-site Wastewater Management Systems

NA: Not available

NR: Not reported

PET: Potential Evapotranspiration

QMRA: Quantitative microbiological risk assessment

qPCR: quantitative Polymerase Chain Reaction

SSO: Sanitary Sewer Overflows

STEC: Shiga toxin-producing *Escherichia coli*

VCSN: Virtual Climate Station Network

1. Part 1 – Development of the Microbial Risk Assessment Tool

1.1 INTRODUCTION

The Microbial Risk Assessment (MRA) tool has been developed to address the need for councils and other organisations to make decisions about a range of activities near drinking water supply wells that have the potential to impact health risks to the drinking water.

The MRA tool builds upon previous work that estimated well separation distances from an Onsite Wastewater Management System (OWMS) carried out as an EnviroLink Tools project (Moore et al., 2010) as well as research into heterogeneity of New Zealand aquifer systems (Moore et al., 2019) and removal of microbes in various New Zealand groundwater systems (Close et al., 2008; Pang, 2009).

The 2010 guidelines were the best tool we had at the start of this project in 2019 but they have some major limitations. The MRA Tool makes two big improvements. Firstly, the 2010 guidelines only considered a single OWMS, whereas the new MRA Tool adds a number of other land uses, and also considers the impact of multiple OWMSs within an area together with the impact of water supply wells being pumped at different rates. Secondly, the 2010 guidelines were conservative and provided only the 95% confidence limits. This new MRA Tool provides additional information and allows visualisation of the uncertainty to assist the understanding of possible trade-offs (more certainty for health risks versus more constraints in land use activities) in risk with different separation distances and land use activities.

The documentation regarding the MRA Tool (this document) is in three parts.

- Part 1 – Provides background on why the MRA Tool has been developed, and an outline of how the MRA Tool has been developed.
- Part 2 – Gives guidance on the use of the MRA Tool and the User Interface: who might use it, and how to use it.
- Part 3 – Provides discussion on the technical details of the modelling and literature data that have been used in the development of the MRA Tool.

1.2 WHAT IS THE ISSUE?

Regional Councils need to be able to assist consent planners and rural and peri-urban communities making decisions about the management of a range of activities near drinking water supply wells. The MRA tool described here is one such approach that can be used in this context, focusing on the risk to human health from drinking-water where microbial pathogens are discharged onto or into land near a drinking water supply well. Some existing land use activities fall within designated drinking-water protection zones (often defined retrospectively after the activity commenced), which triggers the requirement for a resource consent. Councils need a defensible method to support any recommendations to grant or decline these consents based on quantitative risk modelling. The need for assessment of activities within drinking water protection zones has been signalled in the recent report *Essential Freshwater – Action for Healthy Waterways* (MfE, 2019). The initiatives detailed in Chapter 6 of the MfE report include strengthening the obligations on Regional Councils to “provide direction on setting source water risk protection area” and to “define the type of activities that must be assessed as potential risks to source waters within the source protection areas.” This MRA tool will assist Regional Council staff to carry out these obligations.

The need for this tool was identified from groundwater technical staff working within Regional Councils and has the support of the Groundwater Forum Special Interest Group. A scoping study in June 2018 to gauge support for this project confirmed this need (Tschrutter and Moriarty, 2018). The questionnaire that formed the basis of the scoping report was developed by ECan, ESR and GNS and was sent out to 17 councils and MfE. There were 20 responses (BoPRC and HBRC each had 2 staff complete the survey) with the scope and questions being widely supported by all the councils that responded. The scoping report also identified that a wide range of land use activities needed to be assessed and included within the tool, whereas the previous guidelines had only considered viral contamination from a single on-site wastewater management system. The agreed range of land use activities is described in the next section.

The benefits of having this MRA tool, underpinned by robust science include:

- Providing a more objective basis for decisions involving possible microbial contamination of groundwater supplies from activities within source protection zones that incorporates uncertainty analysis in a transparent manner.
- Providing greater guidance, and certainty to stakeholders throughout the country.
- Reducing variation in assessment quality.

- Assisting in consent processing of applications and indicating where additional mitigations or treatment may be required.
- Avoiding duplication of effort in development of methods by individual Regional Councils.

1.3 SCOPE OF THE MICROBIAL RISK ASSESSMENT TOOL

The MRA tool addresses a range of land use activities that might occur within a source protection zone of a drinking water well. The land-use/farming practices comprise:

- Multiple Onsite Wastewater Management Systems (OWMS)
- Community size OWMS
- Dairy farming
- Sheep and beef farming
- Wildfowl
- Stormwater systems
- Animal effluent/manure application.

Stockyards were originally included in the range of land uses, but it was decided to omit them from the MRA tool and treat them on a case-by-case basis as there are relatively few stockyards (< 60) in New Zealand and they vary widely in terms of size, number of sales, numbers of stock processed, and degree of effluent treatment.

Fluxes and flows of water transporting pathogens through the soil, vadose (unsaturated) and saturated groundwater zones are affected by hydrologic, hydrogeologic and anthropogenic factors. Infiltration rates and transport velocities are influenced primarily by the permeability of the media, topography, recharge rates, hydraulic gradient, and lithology. Therefore, a range of soil types, vadose zone types, and groundwater systems are included in the MRA tool to cover the conditions expected throughout New Zealand.

The rate and amount of transport of microbes increases exponentially as a soil nears saturation and most microbial transport occurs at saturated or near-saturated conditions (Close et al., 2008; 2010). Therefore, we have simulated microbial transport through the soil and unsaturated zones under these conditions. The IrriCalc daily soil water balance model was used to derive average recharge rates for various climate locations, as well as simulating a 1 in 10-year rainfall event as described in Section 3.3.1.

The climate regions were taken from the New Zealand Meteorological Service delineation (New Zealand Meteorological Service, 1983) and modified by excluding the mountainous, high rainfall areas as they are not directly relevant to groundwater systems. The regions were combined, resulting in a total of 10 modified climate regions for simulation, which were categorised further into 4 main climate groups.

For the MRA tool, loading rates for each microbe were estimated for each land use and their transport was simulated through a selected soil layer (if applicable), a selected vadose zone media, and into and through a groundwater system. The options that cover New Zealand conditions are described more fully in sections 3.3.4, 3.3.5 and 3.3.6, for soils, vadose zone media and aquifer types, respectively. Three pumping rates were simulated for the water supply well to represent a domestic household, a small town and a large city (see Section 3.3.3).

Microbial removal and transport through different aquifer types for various land-use activities is simulated. Only unconfined aquifers are considered as within scope for this tools project as the inclusion of variable confinement status introduces significant complexity and requires individualised site information. For the groundwater simulations, only boundary conditions of fixed groundwater levels and/or no flow conditions are simulated within this project.

Norovirus was chosen as the most suitable viral pathogen for the MRA tool with regards to the human related land-use scenarios (further discussed in Section 3.4.1). *Campylobacter* was considered the most appropriate organism to be used for agriculture related land-use scenarios due to its widespread prevalence in animals, and the high rate of infections within the New Zealand population (further discussed in Section 3.4.2). *E. coli* was included for all land-use scenarios as an indicator of faecal contamination and because of its use in regulatory standards.

The risk assessment focuses on the three main source–pathway-receptor components: (i) the spatial and temporal distribution of numbers of pathogen contaminants released from the specific land use activities under consideration; (ii) the probabilities of removal and attenuation of these pathogens as they are transported in the subsurface; (iii) the infection probability rates associated with exposure to pathogens in drinking water. A key aspect that is included in the tool is the uncertainty associated with the assessment, and how this relates to quantitative risks to human health. Users can view the complete uncertainty range at once rather than selecting a specific level of uncertainty (such as the expected value of 50%, 90% confidence level, or an even more conservative level such as 99% confidence). In this way, the entire spectrum from risk averse to risk tolerant solutions can be considered.

1.4 THE PROJECT TEAM

The project team consisted of members who together brought to the project expertise in the areas of groundwater science, groundwater modelling, drinking water quality, planning, and the needs and workings of regional councils.

Murray Close (ESR) has 44 years of experience in groundwater quality research. His current interests are the assessment and modelling of groundwater contamination, regional and national assessments of groundwater quality, vadose zone processes, groundwater ecosystems, and the impact of land use on groundwater quality.

Theo Sarris (ESR) has 25 years' experience in groundwater modelling in the United States, Europe and New Zealand, across research, government and engineering consulting. His expertise lies in modelling the transport of contaminants and pathogens in heterogeneous environments and quantification of modelling predictions uncertainties. His research interests include the development of theory and methodologies for transport modelling, environmental risk analysis, quantification of uncertainty in groundwater resources and optimisation of environmental systems.

Allanah Kenny (ESR) is a groundwater modeller with a Masters in Mathematics and a PhD in Mechanical Engineering. Her current research focuses on a range of topics including contaminant transport modelling, source protection zone delineation, and visualisation of groundwater flow for the improvement of public awareness.

Megan Devane (ESR) is an environmental microbiologist with a Masters in Microbiology and a PhD in Water Resource Management. She has twenty years of experience working at ESR advising councils and iwi about faecal contamination issues in their waterways and the transmission of pathogens through the environment.

Bronwyn Humphries (ESR) has 20 years' experience in the water sector as a consultant, in a regional council and as a researcher. She currently researches groundwater quality issues, with a particular focus on wastewater, and the impact on environmental and human health.

Catherine Moore (GNS) has more than 30 years of experience in groundwater modelling as a researcher and groundwater consultant, and from a regional council perspective (Environment Canterbury). She leads the groundwater modelling team at GNS and has expertise in the incorporation of uncertainty analysis into groundwater modelling and its implication for groundwater management. She has given keynote addresses and has taken

workshops on incorporating uncertainty approaches into groundwater management in New Zealand.

Brioch Hemmings (GNS) has more than 10 years of numerical modelling experience with application to geophysics, volcanology, volcano hydrogeology and now, specifically, groundwater modelling at GNS. His particular interest and expertise are in quantifying numerical model uncertainty to support decision making. He is a lead contributor to the pyEMU library which aims to facilitate the uptake of uncertainty analyses in numerical modelling studies.

Conny Tschritter (GNS) is a groundwater scientist with 13 years of experience in New Zealand and is leading the Groundwater Strategic Science Investment Funding research programme at GNS. Her main research interests include hydrogeological and geological data analysis, 3D geological modelling and visualisation; machine learning; and remote sensing for hydrogeological applications.

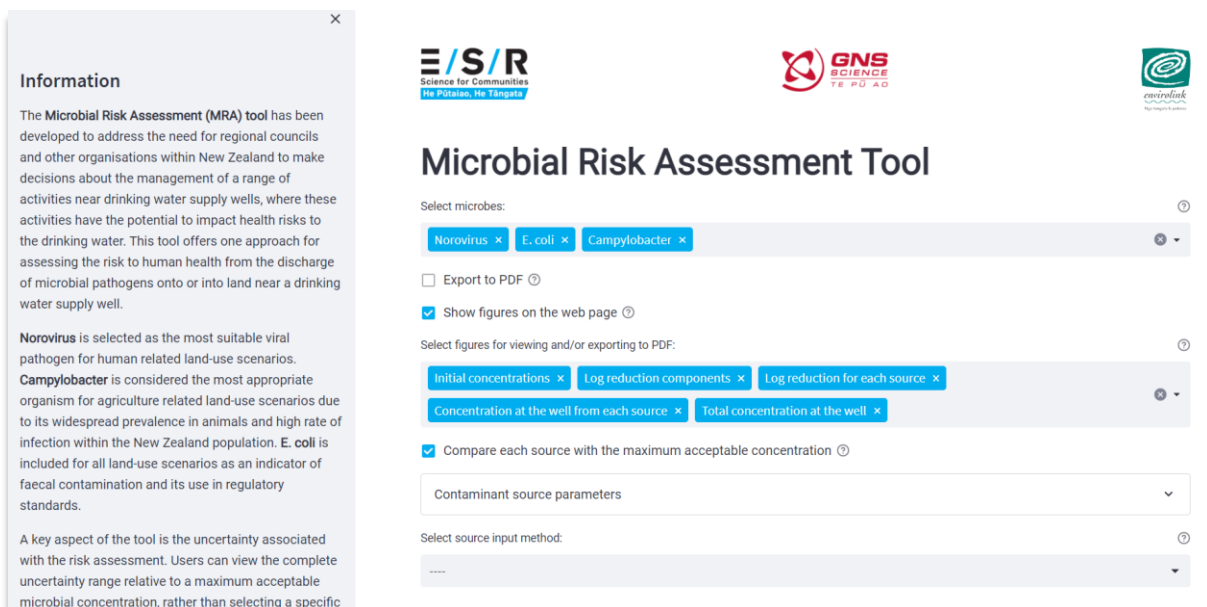
Lisa Scott (Environment Canterbury) is a groundwater management specialist and joined the team as the regional councils' champion to assist in maintaining the linkage between the project and councils. Her project role was to ensure regular and effective contact with regional council personnel and delivery of a product with a council-friendly format.

Stephen Collins (Horizons regional council) and **Susie Osbaldiston** (Northland Regional Council) supported the project as champions and sponsors for the associated EnviroLink Large Advice Grants.

2. Part 2 – User Guide for the Microbial Risk Assessment Tool

This user guide provides a comprehensive explanation of how to navigate the MRA tool, understand its functionalities, and interpret the outputs it generates. Two case studies are included to provide examples of how the MRA tool can be used.

The tool is accessed through an interactive web application located at <https://mra-tool-nz.streamlit.app/>. It utilizes a python script developed with Streamlit, an open-source framework for creating web apps, and is hosted on Streamlit's Community Cloud.



2.1 SIDEBAR INFORMATION

Upon accessing the user interface, the sidebar will be visible on the left side of the screen (the sidebar can be hidden by pushing the X or made visible by pushing the > icon). The sidebar provides important information about the tool, including its purpose, the selection of suitable pathogens for different land-use scenarios, and details about the maximum acceptable concentrations for each pathogen. It also provides instructions on how to use the tool effectively, explains the interactive figures, and introduces the option to save a PDF report as detailed below.

2.2 INSTRUCTIONS

The Instructions section serves as a guide to using the tool. It explains the process of selecting specific microbes for risk assessment, exporting results to a PDF report, and viewing interactive figures on the web page. It also outlines the different methods for selecting input sources and provides information on error messages and warnings.

Here is an overview of the instructions provided in the sidebar:

- Select specific microbes for risk assessment using the **Select microbes** option. Selected microbes are displayed in blue on the selection bar and can be toggled into the non-selected area below the bar.
- To export results to a PDF report, check the **Export to PDF** box and (optionally) provide a name and affiliation. To enable interactive figures on the web page, check the **Show figures on the web page** box. By default, this option is already selected. If either option is selected, the user can **Select figures** to view/export to PDF.
- The **Contaminant source parameters** dropdown menu provides detailed information on the available input parameters.
- Select the input sources in 3 ways: **Selection boxes** (the most straightforward method), **Text input**, or import from **Text file**. The text input and text file options allow for adding multiple sources at once. Note that the text options require sources to be in a specific format; some placeholder sources are given in the **Text input** box as an example.
- The user is able to add sources using different input methods: selecting **Add source/sources** will add to the existing list of sources without overwriting.
- If there are no issues, the chosen sources will be added successfully. If there are errors or inconsistencies, an error message will be displayed and the incorrect source/sources will not be added. Any warnings will also be displayed in the **View warnings** dropdown menu (though these can be ignored if necessary). Please be aware that there are limited options available when the number of sources exceeds 12 (see section 2.4), and the maximum number of sources is 100.
- The user can either **Overwrite existing sources** or **Remove all sources** to start again. All currently added sources can be viewed in the dropdown menu **View sources**, or the chosen sources can be saved in a text file for later use by selecting **Download source text file**.

- Sources are shown on the **Source locations** figure with their position relative to the pumping well. Hovering over a source will show the relevant source information. Labels can be removed by unchecking the **show labels** checkbox and adjusting the aspect ratio with the **fixed aspect ratio** checkbox.
- Select **Run tool** to calculate the risks for each selected microbe, generate the selected figures, and/or export to PDF. If the user needs to stop the execution midway, select **Stop running**. If **Export to PDF** is selected, a download link will appear below the progress bar when complete.
- Results are divided into four tabs: **Norovirus**, **E. coli**, **Campylobacter**, and **Summary** and are primarily presented as interactive figures, described in section 2.4. The final output for each selected microbe is a probability of exceeding the maximum acceptable concentration at the pumping well.
- If there is any lag experienced due to a high number of figures on the web page, this issue can be resolved by selecting **Remove results**. Please note that selecting any other buttons/checkboxes will also refresh the page and remove the results, though all selected options and sources will remain. To view results again, simply select **Run tool**.

2.3 SOURCE PARAMETERS

The **Contaminant source parameters** dropdown menu on the main page of the user interface provides detailed information on the full scope of the tool, including all available options for the pumping well and microbial contaminant sources. This expandable section contains the following tabs:

- Climate
- Land use
- Soil
- Vadose zone
- Aquifer
- Source location
- Pumping scenario
- Treatment (OWMS only)

- Herd size (Dairy only)

Each tab provides a brief overview of the relevant information (e.g. average recharge rates for each climate option, average removal rates for each soil material, etc.). Each tab also presents the available input options when adding contaminant sources to the tool.

Contaminant source parameters ^

Climate Land use Soil Vadose zone Aquifer Source location Pumping scenario Treatment (OWMS only) Herd size (Dairy only)

The treatment parameter is applicable only to the **OWMS** (On-site Wastewater Management System) and **Community OWMS** land use scenarios.

Based on studies it has been observed that approximately 30% of systems experience some level of failure. To account for this, the simulations allow for a lower level of treatment in a proportion of OWMS scenarios. Specifically, in 30% of the simulations, the log reduction is reduced by a factor of 0.5 log removal.

OWMS treatment system	Description	Log reduction
Primary	e.g. solids settling tank	0.6
Secondary	e.g. aerobic biological processing and settling/filtering of effluent received from a primary treatment unit	1.6
Advanced secondary	e.g. sand filter, a packed bed filter, or a textile bed reactor, where effluent trickles through the bed material containing micro-organisms	2.6

Parameter options:

- *Primary*
- *Secondary*
- *Advanced secondary*
- *None*

2.4 FIGURES

The tool generates several figures for each selected microbe, which can be viewed interactively on the webpage and/or exported to a PDF. The figures are presented as box and whisker plots due to uncertainty incorporated at each stage of the tool.

When displayed on the webpage these figures are interactive; using the controls that appear at the top right of the figure the user is able to zoom, pan, autoscale to the data range, enlarge to full screen, or download as a .png image file. In addition, hovering over a figure will show the minimum, median, maximum, and quartile data. Note that figures displaying concentration distributions are presented on a logarithmic scale.

The available figures are listed below:

- **Initial concentrations:** distribution range of initial concentrations for each microbial source.
- **Log reduction components:** distribution of the log reduction in concentration for each component of each microbial source. The components are labelled as follows:
 - **treatment** (for wastewater management system land-use scenarios)
 - **soil** (for remaining land-use scenarios)
 - **vadose** (unsaturated) zone
 - **transport** through the aquifer (saturated zone)
 - **filtration** through the aquifer (saturated zone)
- **Log reduction for each source:** distribution of the total log reduction for each microbial source.
- **Concentration at the well from each source:** distribution of the resulting concentration at the well from each microbial source (if there are multiple sources). The user can also choose to **compare each source with the maximum acceptable concentration** - this checkbox will appear under the figure selection box.
- **Total concentration at the well:** distribution of the total concentration at the well from all microbial sources, compared to the maximum acceptable concentration. Also displays the concentration values for a range of percentiles below the figure.

Please be aware that when the number of sources exceeds 12, there are limited options available for displaying or exporting figures to PDF for performance and display reasons. Only the figures showing source locations and/or total concentration at the well can be displayed or exported.

2.5 PDF REPORT

The MRA tool allows the user to export the results as a PDF report. By checking the **Export to PDF** box and optionally providing a name and affiliation, a download link will be available below the progress bar once the export is complete.

The PDF report contains the following information:

- Name and affiliation of the user (if provided) and the date the report was generated.
- A brief overview of the tool.

- The microbes selected for risk analysis.
- The number of microbial contaminant sources and a figure showing their locations relative to the pumping well.
- A list of the microbial contaminant sources with their input parameters.
- The selected figures and percentile tables (if applicable) for each selected microbe.
- A brief summary detailing the contributing sources and the overall probability of exceeding the maximum acceptable concentration for each selected microbe.

2.6 EXAMPLE CASE STUDIES

To demonstrate the functionality of the MRA tool, two example case studies are provided below.

2.6.1 Assessing the risk of norovirus contamination from a single OWMS

In this hypothetical case study, we will evaluate the risk of norovirus contamination from a single on-site wastewater management system (OWMS) located directly upstream from a small community pumping well. You can do this case study on the website as you work through the example.

The vadose and aquifer media consist of alluvial gravel and the climate is categorised as group “G1”. The vadose zone has a depth of 10 m to the groundwater table. The OWMS has a secondary treatment system, such as aerobic biological processing and settling/filtering of effluent received from a primary treatment unit. As the OWMS by design discharges below the soil layer, the soil material is assigned ‘None’.

We next look at the log reduction components (i.e. treatment, vadose, aquifer transport and aquifer filtration) and the resulting total concentration at the pumping well in relation to the maximum acceptable concentration. For this case study example, the figures will be displayed on the webpage rather than exporting to a PDF report.

- Step 1: Select microbes

From the "Select microbes" option, choose "Norovirus" for the risk assessment.

- Step 2: Select figures

Select "Show figures on the web page" and ensure "Export to PDF" is not selected. From the "Select figures" option, choose "Log reduction components" and "Total concentration at the well".

Select microbes: ?

Norovirus x

Export to PDF ?

Show figures on the web page ?

Select figures for viewing and/or exporting to PDF: ?

Log reduction components x Total concentration at the well x

- Step 3: Add the contaminant source

Select the source input method as "Selection boxes". Choose the various source parameters from the boxes provided and use the "Add source" option to add the contaminant source.

Select source input method: ?

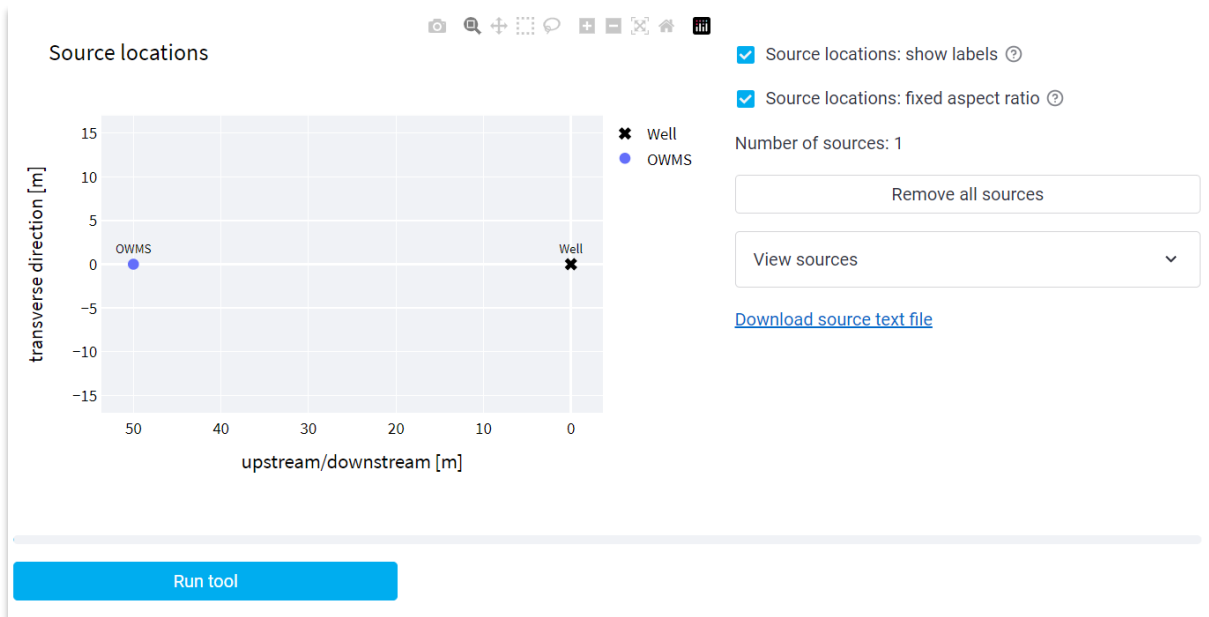
Selection boxes v

Climate	Pumping scenario	Source distance upstream [m]
G1 (lowest recharge rate) v	Small community (SC) v	50.0 - +
Land use	Aquifer material	Source distance transverse direction [m]
OWMS v	Alluvial gravel (AlGr) v	0.0 - +
Soil material	Vadose material	Herd size (Dairy only)
None v	Alluvial gravel (AlGr) v	0 - +
Soil depth [m]	Vadose depth [m]	Treatment (OWMS only)
0.0 - +	10 0 80	Secondary v

Add source

- Step 4: Review Sources and Run Tool

Verify the added source in the source locations figure and the "View sources" dropdown menu. If everything appears correct, select "Run tool" to initiate the risk assessment calculations.



- Step 5: Analyse Results

Switch to the "Norovirus" tab to explore the figures related to the norovirus risk assessment. Review the interactive figures for the log reduction components and total concentration at the well compared to the maximum acceptable concentration for norovirus.

In this case study, transport through the alluvial gravel aquifer exhibits the highest median log reduction and arguably provides the greatest contribution to overall log reduction as the contaminant travels from the OWMS source to the pumping well. The aquifer filtration component has the lowest median log reduction but the greatest maximum, indicating a high level of uncertainty in filtration through the alluvial gravel aquifer.

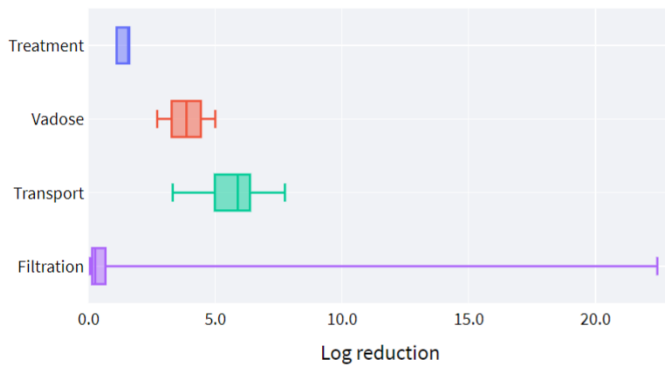
The resulting concentration of norovirus at the pumping well covers a large range from 1.0×10^{-20} to 3.7×10^2 per L. In this case the probability of the concentration exceeding the maximum acceptable concentration is 96%, where the maximum acceptable concentration is 3×10^{-6} per L (the concentration expected to result in the tolerable annual infection probability of 1 in 10,000 per year).

Norovirus

Norovirus: 1 source (OWMS)

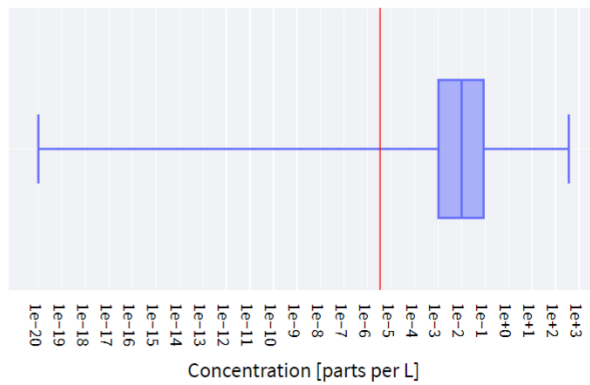
P(above max acceptable concentration of 3e-06) = 96%

Norovirus, OWMS: Log reduction components



Norovirus: Total concentration at the well

P(above max acceptable conc of 3e-06) = 96%



View percentiles

Percentile	Concentration [parts per L]
0%	< 1.0e-20
1%	1.6e-09
2%	1.4e-07
5%	1.2e-05
10%	9.7e-05
20%	5.9e-04
25%	1.1e-03
50%	1.0e-02
75%	8.7e-02
80%	1.5e-01
90%	5.7e-01
95%	1.6e+00
98%	4.6e+00
99%	9.1e+00
100%	3.7e+02

2.6.2 Comprehensive risk assessment from multiple contaminant sources

In the second hypothetical case study we will assess the risk of norovirus, *E. coli*, and *Campylobacter* contamination from two OWMS sources and a Dairy source located near a pumping well for a single dwelling.

The vadose and aquifer media consist of alluvial sand and the climate is categorised as group “G3” (Table 2). The vadose zone will have a depth of 5 m to the groundwater table. The OWMS will have primary treatment systems such as a solids settling tank. The Dairy source will have a herd size of 200 animals, soil depth of 1 m, and soil material of clay loam (the OWMS sources discharge below the soil layer so their soil material is ‘None’).

We will export all available figures and results to a PDF report.

- Step 1: Select microbes

From the "Select microbes" option, choose "Norovirus", "*E. coli*" and "*Campylobacter*" for the risk assessment.

- Step 2: Select figures

Select “Export to PDF” and deselect “Show figures on the web page”. Add a name and affiliation. From the “Select figures” option, choose all available options.

The screenshot shows a web-based interface for selecting microbes and figures. At the top, under 'Select microbes:', there are three blue buttons with white text: 'Norovirus x', 'E. coli x', and 'Campylobacter x'. Below this is a checked checkbox for 'Export to PDF'. The 'Name of User:' section has two input fields: 'User Name' and 'Company'. The 'User Affiliation:' section has a 'Company' input field. There is an unchecked checkbox for 'Show figures on the web page'. The 'Select figures for viewing and/or exporting to PDF:' section has five blue buttons with white text: 'Initial concentrations x', 'Log reduction components x', 'Log reduction for each source x', 'Concentration at the well from each source x', and 'Total concentration at the well x'. At the bottom, there is a checked checkbox for 'Compare each source with the maximum acceptable concentration'.

- Step 3: Add the contaminant sources

Select the source input method as “Text input”. The “Text input” and “Text file” options are preferable when dealing with multiple sources at once. Enter the various source parameters in the correct format (refer to the “Contaminant source parameters” dropdown menu for assistance) and use the "Add sources" option to add the contaminant sources.

Select source input method: ?

Text input

Enter source details in the format:

climate, land use, soil material, soil depth, vadose material, vadose depth, aquifer material, source upstream, source transverse, pumping scenario, treatment, herd size (separating sources with a semicolon)

```
G3, OWMS, None, 0, ALSa, 5, ALSa, 90, 40, SD, Primary, None;
G3, OWMS, None, 0, ALSa, 5, ALSa, 50, 60, SD, Primary, None;
G3, Dairy, Clay loam, 1, ALSa, 5, ALSa, 200, -25, SD, None, 200
```

Add sources

- **Step 4: Review Sources and Run Tool**

Verify the added sources in the source locations figure and the "View sources" dropdown menu. If everything appears correct, select "Run tool" to initiate the risk assessment calculations.



- **Step 5: Analyse Results**

Switch to the "Summary" tab to view a brief summary of the final results. Download the PDF report from the link that appears below the progress bar.

Operation complete

[Download PDF report](#)

Run tool

Remove displayed results

Norovirus E. coli Campylobacter [Summary](#)

Summary

Norovirus: 2 sources (OWMS 1, OWMS 2)

P(above max acceptable concentration of 3e-06) = 60%

E. coli: 3 sources (OWMS 1, OWMS 2, Dairy)

P(above max acceptable concentration of 5e+00) = 0.02%

Campylobacter: 1 source (Dairy)

P(above max acceptable concentration of 5e-04) = 0%

The PDF report contains the risk assessment for all three microbes and all figures selected in Step 2. The first page contains a brief overview of the tool, the selected microbes, the number of contaminant sources, and the figure displaying the source locations relative to the pumping well. The second page contains the list of contaminant sources with their input parameters.

Microbial Risk Assessment Tool: Output Report

Prepared by User Name (Company) on 29/05/2023

The tool is available online at <https://mra-tool-nz.streamlit.app/>

The Microbial Risk Assessment (MRA) tool allows users to make decisions about the management of activities near drinking water supply wells that have the potential to impact health risks to the drinking water. Users can view the complete uncertainty range relative to a maximum acceptable microbial concentration, rather than selecting a specific level of uncertainty.

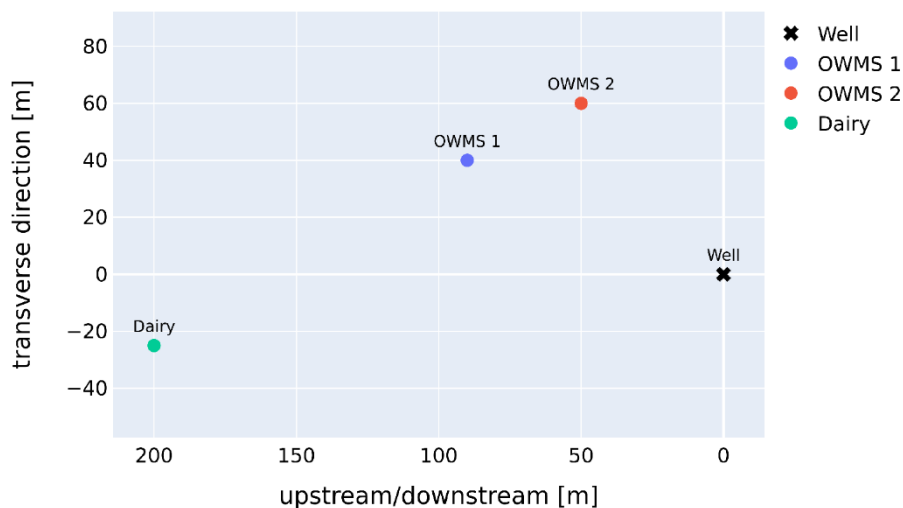
Microbes selected for risk assessment: Norovirus, E. coli, Campylobacter.

Norovirus is selected as the most suitable viral pathogen for human related land-use scenarios. E. coli is included for all land-use scenarios as an indicator of faecal contamination and its use in regulatory standards. Campylobacter is considered the most appropriate organism for agriculture related land-use scenarios due to its widespread prevalence in animals and high rate of infection within the New Zealand population.

For Norovirus and Campylobacter, the maximum acceptable concentration is the concentration expected to result in the tolerable annual infection probability (1 in 10,000 per year). For the indicator microbe E. coli, a drinking water standard of < 1 per 100 mL has been set by the Ministry of Health, therefore 5 per L has been used as the maximum acceptable concentration.

Number of microbial contaminant sources: 3

Source locations



List of contaminant sources

Universal parameters:

Pumping scenario: Single dwelling (SD)
Climate: G3
Vadose zone material: Alluvial sand (AlSa) | Vadose zone depth: 5m
Aquifer material: Alluvial sand (AlSa)

Source OWMS 1:

Land use: OWMS | Treatment: Primary
Soil material: None | Soil depth: 0m
Distance upstream: 90.0m | Transverse distance: 40.0m
Distance from well: 98.5m

Source OWMS 2:

Land use: OWMS | Treatment: Primary
Soil material: None | Soil depth: 0m
Distance upstream: 50.0m | Transverse distance: 60.0m
Distance from well: 78.1m

Source Dairy:

Land use: Dairy | Herd size: 200
Soil material: Clay loam | Soil depth: 1.0m
Distance upstream: 200.0m | Transverse distance: -25.0m
Distance from well: 201.6m

Subsequent pages present the selected figures for the norovirus risk assessment. In this case the two OWMS sources contribute to norovirus while the Dairy source does not contribute. The first figure displays the distributions for the initial concentration at the two OWMS sources. These distributions are identical due to their matching land-use scenario.

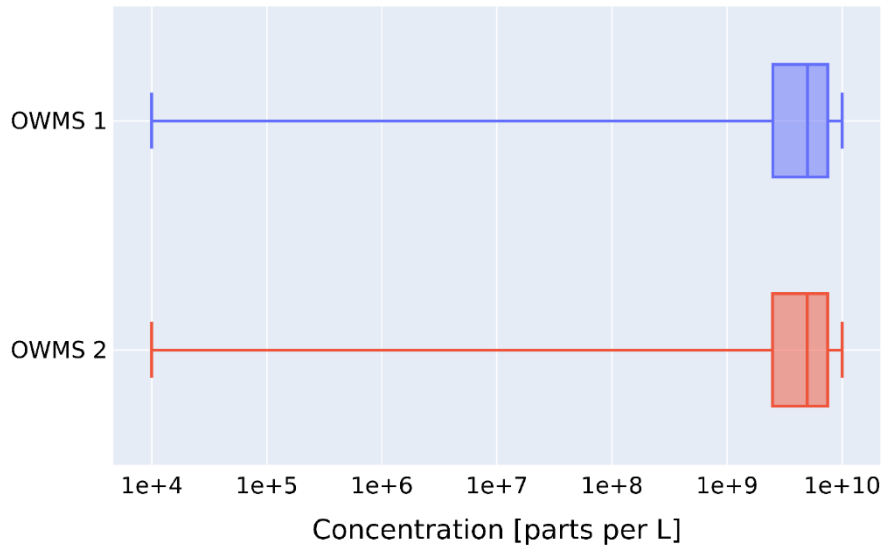
The second figure displays the log reduction components for each source. For both sources the log reduction from treatment at the source is minimal, and the log reduction through the vadose zone is identical for both sources.

The first source (OWMS 1) is positioned closer to being directly upstream of the pumping well compared to OWMS 2. As a result, the log reduction from transport through the aquifer is slightly lower for OWMS 1. However, OWMS 1 is a greater overall distance from the well (98.5 m vs. 78.1 m for OWMS 2), therefore the filtration component for OWMS 1 is greater than for OWMS 2.

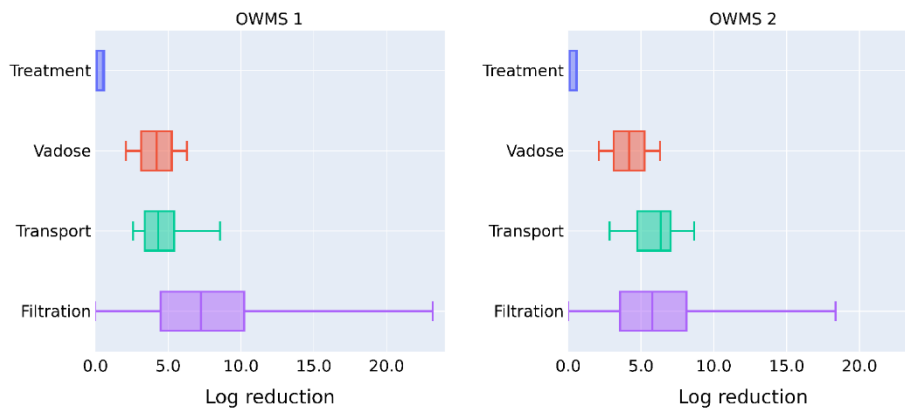
The third and fourth figures display the overall log reduction and total resulting concentration at the pumping well for each source. In this case the log reduction and resulting concentration for both sources are very similar.

Norovirus

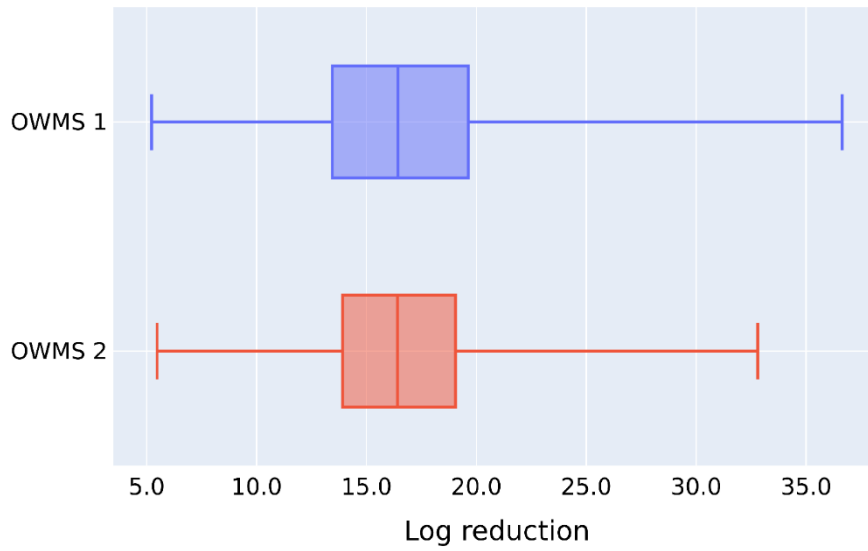
Norovirus: Initial concentration at the source



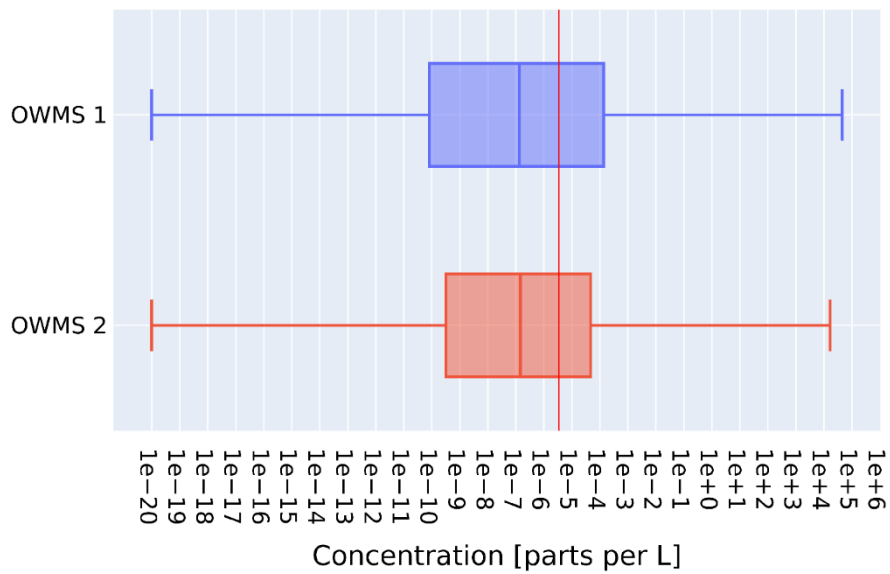
Norovirus: Log reduction components



Norovirus: Log reduction from source to well



Norovirus: Concentration at the well Max acceptable conc = 3e-06



The fifth figure displays the total resulting concentration from all sources at the pumping well, with a table of percentiles below the figure.

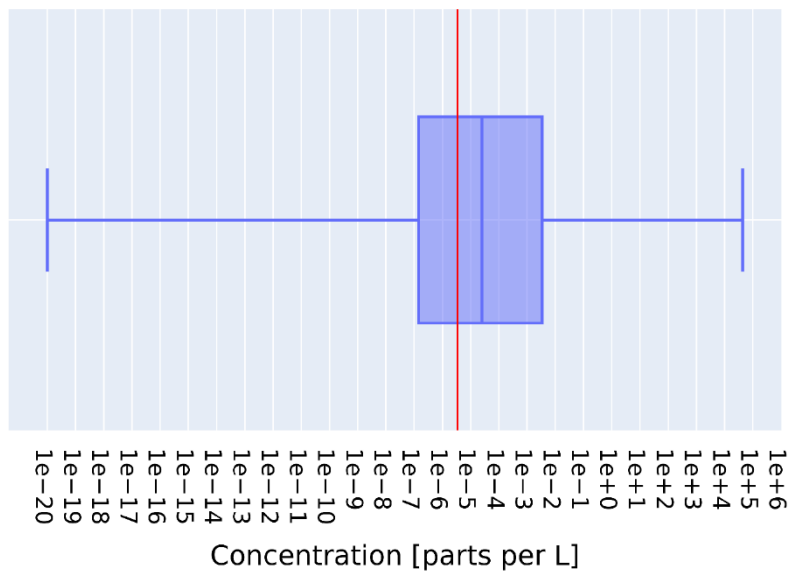
The resulting concentration of norovirus at the pumping well ranges from 1.0×10^{-20} to 4.4×10^4 per L. In this case the probability of the concentration exceeding the maximum acceptable concentration is 60%, where the maximum acceptable concentration is 3×10^{-6} per L (the concentration expected to result in the tolerable annual infection probability of 1 in 10,000 per year).

A similar analysis is presented for *E. coli* and *Campylobacter* in the PDF report, though only the total resulting concentration at the well is displayed here.

For *E. coli*, all three sources contribute to the total concentration which ranges from 7.2×10^{15} to 4.1×10^1 per L. In this case the probability of the concentration exceeding the maximum acceptable concentration is 0.02%, where the maximum acceptable concentration is 5 per L (based on the drinking water standard of < 1 per 100 mL set by the Ministry of Health).

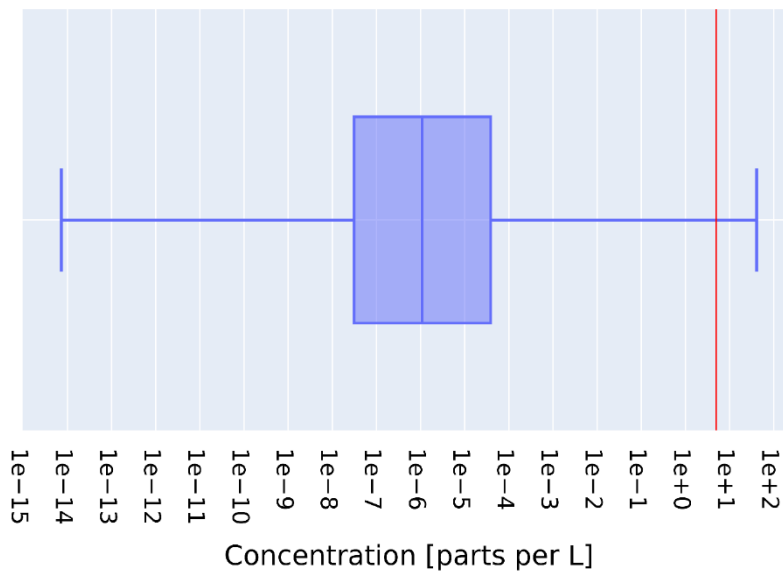
For *Campylobacter*, only the Dairy source contributes to the concentration at the well which ranges from 1.0×10^{-20} to 1.1×10^{-7} per L. In this case the probability of the concentration exceeding the maximum acceptable concentration is 0%, where the maximum acceptable concentration is 5×10^{-4} per L (the concentration expected to result in the tolerable annual infection probability of 1 in 10,000 per year).

Norovirus: Total concentration at the well
 P(above max acceptable conc of 3e-06) = 60%



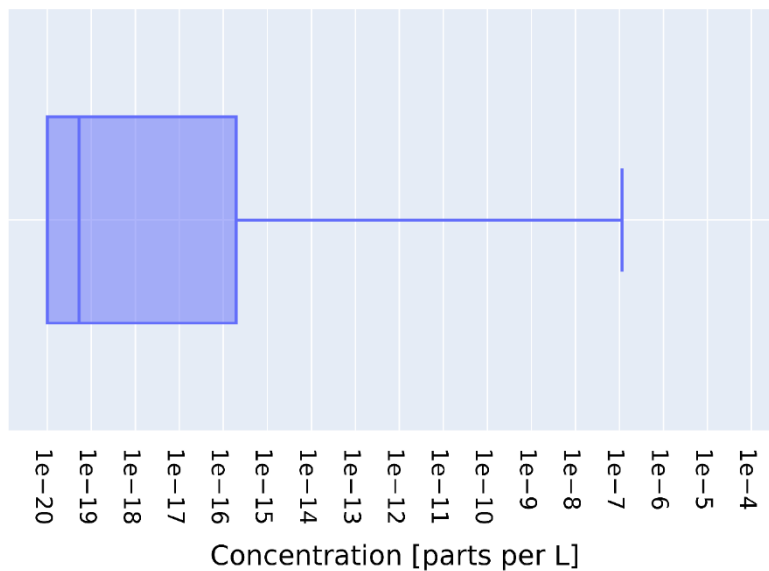
Percentile	Concentration [parts per L]
0%	< 1.0e-20
1%	5.6e-13
2%	4.1e-12
5%	8.5e-11
10%	1.3e-09
20%	3.9e-08
25%	1.4e-07
50%	2.5e-05
75%	3.5e-03
80%	1.1e-02
90%	2.2e-01
95%	2.1e+00
98%	2.4e+01
99%	9.9e+01
100%	4.4e+04

E. coli: Total concentration at the well
 P(above max acceptable conc of 5e+00) = 0.02%



Percentile	Concentration [parts per L]
0%	7.2e-15
1%	1.1e-11
2%	3.6e-11
5%	2.4e-10
10%	1.4e-09
20%	1.3e-08
25%	3.1e-08
50%	1.1e-06
75%	3.9e-05
80%	9.4e-05
90%	8.7e-04
95%	4.9e-03
98%	2.9e-02
99%	8.9e-02
100%	4.1e+01

Campylobacter: Total concentration at the well
P(above max acceptable conc of 5e-04) = 0%



Percentile	Concentration [parts per L]
0%	< 1.0e-20
1%	< 1.0e-20
2%	< 1.0e-20
5%	< 1.0e-20
10%	< 1.0e-20
20%	< 1.0e-20
25%	< 1.0e-20
50%	5.3e-20
75%	2.0e-16
80%	1.1e-15
90%	7.2e-14
95%	1.4e-12
98%	2.5e-11
99%	1.3e-10
100%	1.1e-07

3. Part 3 – Technical Appendix for Microbial Risk Assessment Tool

3.1 OVERVIEW OF TECHNICAL APPENDIX

This technical appendix explains the modelling approach and provides details regarding the loading rates and parameter values used in the various simulations. Some of the information and sections are an updated version of the information in the model scenarios report (Close et al., 2021). The revisions have been based on feedback from stakeholders on that report and from workshops held during the course of this project.

The technical appendix is set out in the following sections:

- Description of land-use scenarios
- Simulations of water flow and microbial transport
- Microbial loading and removal rates
- Tolerable concentrations of pathogens in drinking water
- Modelling approach

No new experimental work to determine microbial loading or removal rates was undertaken during this project, and these parameters were based on reviews of the scientific literature.

3.2 DESCRIPTION OF LAND-USE SCENARIOS

Figure 1 illustrates the land-use scenarios included in the MRA tool. Figure 2 shows the processes for microbial removal by an OWMS and LAS (land application system) with a potential risk to groundwater down gradient through a drinking water well.

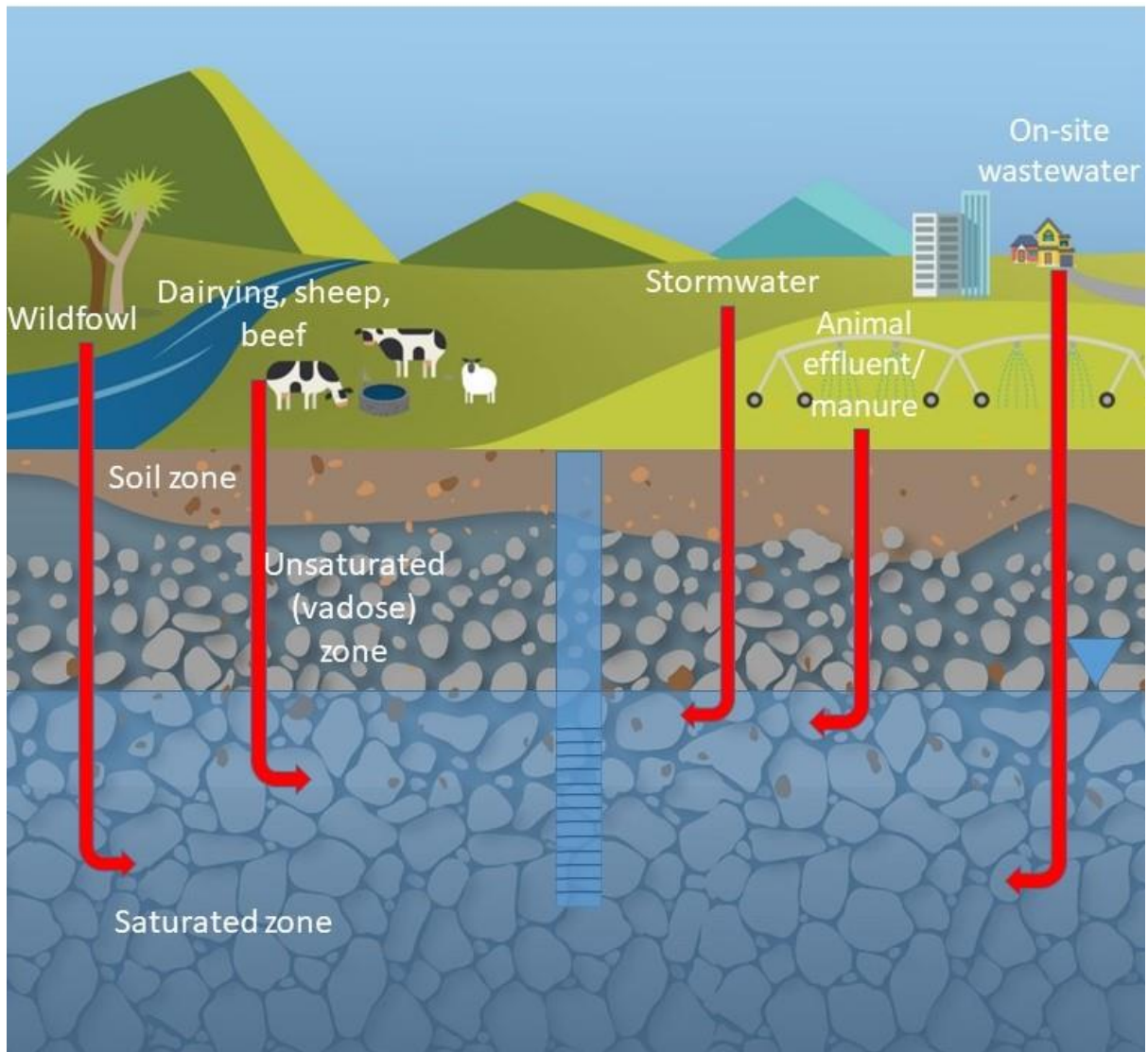


Figure 1: Schematic for land-use scenarios

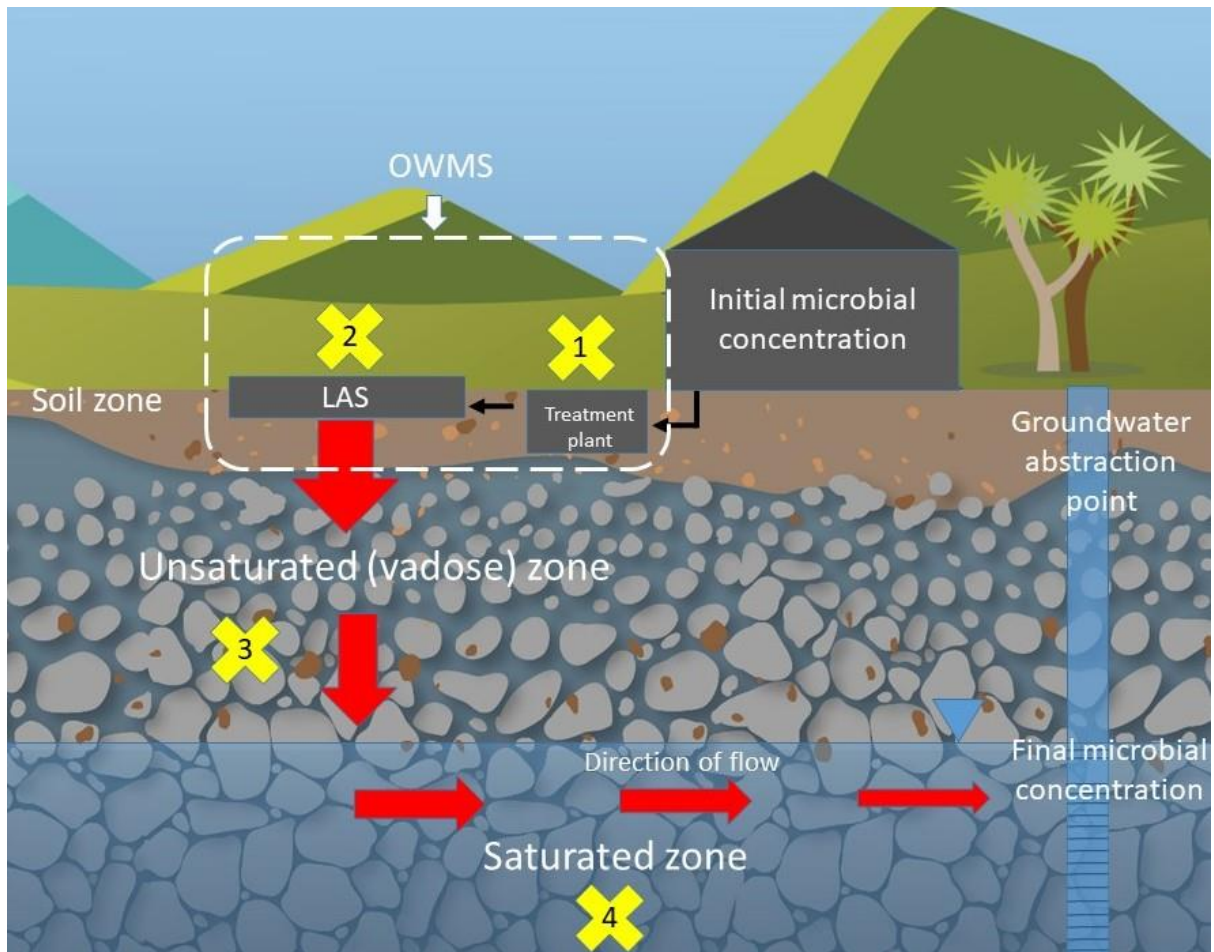


Figure 2: Components of microbial removal between the On-site Wastewater Management System (OWMS) and groundwater abstraction point. 1) microbial reduction within the treatment plant, 2) microbial reduction within the Land Application System (LAS), 3) microbial reduction within the unsaturated (vadose) zone, 4) microbial reduction within the saturated zone. Note: The abstraction well is directly down gradient of the LAS. The red arrows give the direction of flow and predicted reduction in microbial concentration from the OWMS to the abstraction well.

A summary of the assumptions and limitations used for each land-use scenario with the MRA tool is given below.

3.2.1 Multiple domestic on-site wastewater management systems

The term septic tank has been used historically in New Zealand to describe a system which processes human excreta and domestic wastewater and discharges it to the receiving environment. This term, however, does little to describe the variety of systems which are now commonly used in New Zealand. These systems may include primary treatment systems

(solids settling tank) to secondary and advanced treatment systems which may involve biological processes to assist microbes to digest and break down the wastewater, sand filters or ultraviolet light units for reduction of faecally-associated microbes (MfE, 2008). The wastewater is then discharged to the receiving environment using a LAS such as a soakage trench or subsurface drip irrigation. A common term which has now been adopted by the industry in New Zealand to cover multiple types of systems is an OWMS.

As in 2010, there remains a dearth of information concerning quantitative measured enteric virus concentrations within domestic OWMSs (Blaschke et al., 2016, Humphries et al., 2020). The enteric virus concentration data that is available for domestic OWMSs is highly variable compared to the data that is available for homogenised effluent from centralised treatment systems. This is because the concentrations within individual domestic OWMSs depend on whether there are infected people in the individual dwelling. When occupants of a household are unwell, the peak concentrations of those enteric viruses being shed into the OWMS will be much higher than at a centralised wastewater facility, which offers dilution with non-contaminated wastewater (Blaschke et al., 2016). The literature review also found that available microbial loading concentrations were typically sourced from a single domestic OWMS and not community sized OWMSs (Humphries et al., 2020).

The performance of OWMSs is variable based on the level of maintenance undertaken, with some studies finding that around 30% of systems reported some failure (Canterbury Public Health, 2014). We have allowed for a lower level of treatment in a proportion of OWMSs in the simulations.

Assumptions

- For a typical 3-bedroom (5 person) home, it is assumed that the daily volume of wastewater entering an OWMS is approximately 750 – 1000 L/day.
- Wastewater entering an OWMS consists of toilet, shower/bath, kitchen, and laundry wastewater.
- That 70% of the domestic OWMS are correctly operated and maintained by the homeowner to ensure optimal performance (see below) and 30% of domestic OWMS are not correctly operated and operate at 0.5 log removal lower than the expected performance given below.

- Three types of OWMS that currently exist in New Zealand are simulated with the following levels of microbial treatment (as summarised in Moore et al., 2010):
 - o Primary treatment OWMS: solids settling tank followed by an effluent disposal field such as a soakage trench or subsurface low pressure effluent distribution drip irrigation. Treatment = 0.6 log removal
 - o Secondary OWMS: additional treatment such as aerobic biological processing and settling or filtering of effluent received from a primary treatment unit. Additional treatment of 1.0 log removal
 - o Advanced secondary treatment: an advanced treatment system may pass the effluent through a sand filter, a packed bed filter or a textile bed reactor, where effluent trickles through the bed material containing micro-organisms that treat any remaining fine solids before being pumped to the disposal field. Additional treatment of 1.0 log removal.
- Users are able to specify the number and locations of OWMSs in a cluster that is assessed.

Limitations

- Since 2008, 44 OWMS designs have been tested by the On-Site Effluent Testing (OSET) testing facility in Rotorua. The MRA Tool does not factor in the level of treatment provided by any one particular OWMS design.
- This work does not incorporate any details on various OWMS designs and how systems are installed or operated and maintained.
- The MRA tool assumes full occupancy which will provide the highest risk and does not consider intermittent occupancy of a dwelling.
- The MRA tool does not consider other forms of on-site wastewater management systems such as composting toilets and vermiculture systems.

3.2.2 Community size on-site wastewater management systems

The first land-use scenario (3.2.1) considers the impact of clusters of OWMS such as non-reticulated towns and subdivisions while this scenario (3.2.2) considers the impact of a community sized OWMS located, for example, at marae, schools, camping grounds, hotels, motels and restaurants. There are more data available for large, centralised wastewater systems with regard to enteric virus concentrations than an individual OWMS (reviewed in Humphries et al., 2020). The same can be said for community size on-site wastewater

management systems. The review of the literature revealed no additional microbial loading data other than what is available for a single domestic OWMS.

Assumptions

- For the community sized OWMS land-use scenario it assumes an occupancy of between 40 – 250 people using a single OWMS.
- A community scale OWMS could include up to 250 households but for the MRA tool we have simulated scenarios for 40 people and 250 people. Estimates for community OWMS serving different populations can be approximated using interpolation.

Limitations

- The risks of a town or city wastewater treatment plant and the associated disposal of wastewater to land is out of scope for the MRA tool.
- The MRA tool assumes full occupancy which will provide the highest risk, and does not consider intermittent occupancy of a facility.

3.2.3 Dairy farming

Dairy farming accounts for just over 14% of New Zealand's agricultural and horticulture land use with nearly 5 million cows nationally (DairyNZ, 2019). This land-use scenario includes the faecal inputs of dairy cows directly onto open pasture as they are rotated around the farm. Results for dairy farming microbial loading rates are generally presented as outputs per animal per day.

We have simulated microbial transport from typical grazing patterns, as detailed below, for varied intensity dairy farming where the herd size is taken as a user input. We have simulated transport under near saturated conditions for varied dairying intensity in different regions of New Zealand, as described more fully in Section 3.3.4. The effluent application to land is covered in Section 3.2.7. In depth simulation of a working dairy farm is out of scope for this MRA tool.

Assumptions

- The dairy land-use scenario assumes 25-day stock rotation (Ministry for Primary Industries, 2012a).

Limitations

- The MRA does not model the microbial loading implications of off-paddock facilities such as dairy cow housing/barns, stand-off pads or permanent feed pads.
- The MRA tool does not account for practices such as wintering off and feeding of supplements.

3.2.4 Sheep and beef farming

This land-use scenario includes the faecal inputs from sheep and beef directly onto open pasture. Sheep and beef grazing rotations are typically much longer than the grazing rotations for dairy cows.

Assumptions

- For the purposes of the MRA tool, it has been assumed that the most relevant sheep and beef farming land type for groundwater contamination risks is flat land farming. It has therefore been assumed that:
 - Flat dry sheep and beef farming typically has between 10 – 12 stock units per hectare and a typical farm size of 400 hectares (L Fietje, pers. Comm, 2020).
 - Flat irrigated sheep and beef farming typically has between 20 – 22 stock units per hectare and a typical farm size of 400 hectares (Ministry for Primary Industries, 2012b).
- It is assumed that sheep and beef farming grazing patterns consist of set stocking during lambing and calving (varies nationally from Aug – Oct), approximately 30-day rotations from Nov – May and winter crop grazing during June – July (L Fietje, pers. Comm, 2020).

Limitations

- The impact of high country and hill country sheep and beef farming has not been included in the MRA tool due to the limited groundwater resources used for community drinking water supplies commonly found in these areas. If hill country sheep and beef is likely to impact a particular drinking water supply, then a scaled estimate could be made using a stocking rate of around 4 stock unit per ha for hill country and around 1 stock units per ha for high country sheep and beef farm

compared to the stocking rate for flat country of around 10 stock units per ha (Ministry for Primary Industries, 2012b).

3.2.5 Wildfowl

Microbial contamination from wildfowl faeces is a nationwide issue particularly around wetlands and lakes. Wildfowl may also camp around effluent and irrigation ponds. This can pose a risk to the quality of water found in both effluent and irrigation ponds which may be hydraulically connected to groundwater if not properly contained, and microbes can also be transported directly from the camping areas into groundwater. For example, flock size can be up to 500 birds for geese with a camping area of 1 – 2 hectares (L Fietje, 2020, pers. comm.) Most impacts from wildfowl are expected to be direct inputs to surface waters. However, for the MRA tool we are focussing on microbial transport and impacts to groundwater.

Studies of microbes in wildfowl faeces in New Zealand have been carried out by Moriarty et al. (2011). Where there was little information on concentrations of microbes in New Zealand faecal samples for particular wildfowl species, international studies were used alongside New Zealand prevalence data to generate loading rates. Prevalence data helps to inform priority research on pathogen concentrations in New Zealand wildfowl with high prevalence.

Assumptions

- Due to the difficulties in determining wild bird flock numbers the MRA tool assumes a flock size of between 100 – 500 birds (L Fietje, 2020, pers. comm.)
- The transport to groundwater is assumed to occur from the camping areas near wetlands, ponds or lakes.
- Microbial loading rates were sourced for four wildfowl species: geese, ducks, swans and gulls.

Limitations

- Any microbial transport from wildfowl to surface waters has been excluded from these scenarios as transport to groundwater is the focus.

3.2.6 Stormwater systems

Pathogens can be found in stormwater runoff and subsequently transported to environmental water bodies through sewer overflows, and urban and agricultural runoff. Faecal contamination in stormwater is largely dependent on the land use in the catchment and mostly includes sewage, septage and animal faeces. Storm events have the potential to re-suspend sediment-bound faecal indicator bacteria (FIB) and pathogens back into the water column, resulting in elevated levels of contamination. Depending on the catchment, runoff can be expected to occur year-round with stormwater runoff occurring primarily in winter and spring, and dry-weather runoff from irrigation of residential landscapes and car washing occurring when precipitation is low (Huang et al., 2018).

Routine monitoring of stormwater quality focuses on quantification of *E. coli* and *Enterococcus*. Rainfall-induced microbial contamination of surface waters due to stormwater runoff, combined sewer overflows (CSO) and sanitary sewer overflows (SSO) has been well documented. High concentrations (>4 log₁₀ cfu/100 ml) of FIB are generally found in stormwater runoff and receiving waters, and a number of studies report the presence of enteric pathogens or faeces-associated genetic markers in stormwater (for example, Jiang et al., 2015, Steele et al., 2018). Nonetheless, data on pathogen abundance in stormwater runoff and outfalls remain scarce, and the overall quality of stormwater in terms of microbial contaminants, particularly pathogens, is poorly understood (Ahmed et al., 2019). Rural or high-density residential areas are reported to contribute 30-50 times greater *E. coli* levels in stormwater compared with sparsely populated residential areas (as reviewed by Humphries et al., 2020).

Assumptions

- The MRA tool has assumed that stormwater includes combined sources of sewage, septage, runoff and animal faeces (including avian sources).
- We have assumed that major urban centres will have stormwater treatment systems and that the greater risks will be associated with smaller centres that have stormwater disposal into a simple soak pit
- Flow from stormwater is assumed to be discharged to groundwater via a soak pit (essentially a point source).
- The first flush of stormwater recharge is assumed to contain most of the microbial load and a saturated discharge for 6 hours has been used to simulate this concentrated discharge of stormwater to groundwater

Limitations

- The MRA tool does not differentiate between various types of stormwater but treats all stormwater as combined from various sources.

3.2.7 Animal effluent/manure application to land

In New Zealand sheep, beef and pig farming commonly only contribute animal manure to land in association with their normal grazing rotations. With regard to dairying, large volumes of Farming Dairy Effluent (FDE) are concentrated at the dairy shed and winter herd housing facility. The effluent is subsequently collected and stored within a holding structure (i.e. effluent storage pond or bladder system). These holding facilities may offer no or several forms of effluent treatment before its application to land via an irrigation system (i.e. travelling irrigator). The irrigation of dairy shed effluent onto land is therefore a common and integral part of New Zealand's farming practice.

Specific notes on animal effluent/manure application to land include:

- Travelling irrigators typically have high instantaneous rates of application, >100 mm/hr. Assuming the average depth of FDE is divided by the time for a complete pass, average application rate is approximately 20-30 mm/h.
- Low rate applicators apply at rates of <10 mm/h, and therefore, reduce the chance of exceeding the soils infiltration capacity, preventing ponding and surface runoff.

Assumptions

- It is assumed that a FDE storage pond and its application to land is tailored to farm-specific requirements that considers catchment rainfall, shed water use, number of cows, irrigation hardware, management and soil information.
- It is assumed that the land application of FDE is avoided when soils are saturated and applied at an average rate less than the infiltration rate to prevent ponding in soils with impeded drainage or low infiltration rate.
- It is assumed that FDE is avoided on land with a slope greater than 7 degrees.

Limitations

- The MRA tool does not consider the case where storage ponds are not correctly designed, installed or maintained, which might result in overtopping of effluent ponds and/or land application to already saturated soils. These situations need to be separately assessed.

3.3 SIMULATIONS OF WATER FLOW AND MICROBIAL TRANSPORT

For the MRA Tool, the most important flow parameters are:

- Rainfall recharge
- Pumping rate
- Soil type and properties
- Aquifer type and properties
- Soil, vadose zone and saturated thicknesses.

The following sections provide an overview of these parameters and the values, and/or value ranges, that are used as input parameters for the MRA Tool.

3.3.1 Climate and Recharge estimates

New Zealand-wide annual, monthly and daily rainfall recharge for the MRA Tool was derived from the IrriCalc soil water balance model (Bright, 2009; Wheeler and Bright, 2015). IrriCalc is a single-layer soil water balance model that calculates daily soil water content based on daily measurements or estimates of irrigation, rainfall, drainage, and actual evapotranspiration (AET). The key assumptions used in the IrriCalc modelling include:

- a) The soil is free draining.
- b) Crop canopy development is sufficiently consistent across years to enable use of a crop factor time series to transform evapotranspiration of a reference crop into evapotranspiration from the crop or pasture of interest. In east-coast New Zealand environments, crop factors developed for irrigated conditions should not be used for un-irrigated conditions, and vice versa.
- c) All rainfall and irrigation intercepted and retained on leaf and stem surfaces is effective for meeting the evapotranspiration load.

IrriCalc has been tested against Overseer (Wheeler and Bright, 2015) and both models gave similar estimates of recharge (drainage) in the absence of irrigation. IrriCalc is used to provide frequencies of soil saturation across New Zealand for 10 different climatic regions taken from the New Zealand Meteorological Service delineation (New Zealand Meteorological Service, 1983) over 44 years from 1972 to 2016, where the climatic regions are shown in Figure 3. We obtained an annual average recharge rate and a 1-in-10 year 1-day event recharge rate for each climatic region for both irrigated and unirrigated conditions. To reduce computational burden, these regions were grouped into 4 categories with recharge rates taken as the average of each climatic region in the group (Tables 1 and 2).

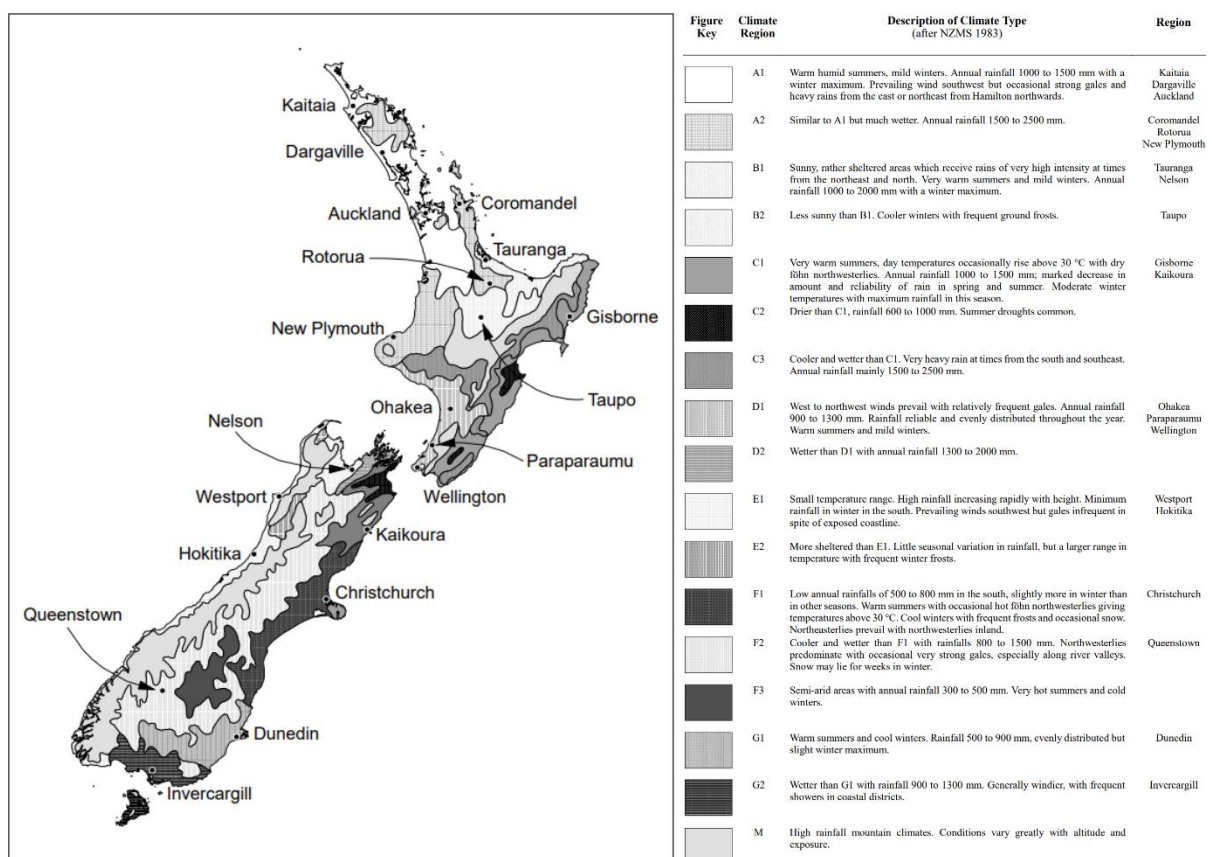


Figure 3: Map of New Zealand climate regions from the New Zealand Meteorological Service delineation (New Zealand Meteorological Service, 1983).

The recharge rates are used to simulate a 1-in-10 year rainfall event for all land use cases except for OWMS. In the unsaturated and saturated models, the 1-in-10 year rate is active for 1 day, then the annual average recharge rate is used for the remainder of the simulation.

For the OWMS land use case the discharge rate is set at 35 mm/d at the source (based on the infiltration rates used in Moore et al., 2010) and the annual average recharge rate is used across the model area.

3.3.2 Shedding Period

The shedding period is the time that the faeces of an infected person, animal, or bird contains the microbe under consideration. The norovirus shedding period for OWMS and Community OWMS is assumed to be 29 days (Tu et al., 2008). The *E. coli* shedding period for OWMS/Community OWMS is 100 days (i.e. the full length of the model simulation) as it is assumed to be always present. The same is assumed for *E. coli* and *Campylobacter* in the animal effluent land use case. For dairy, sheep and beef, and wildfowl, the shedding period is 1 day (due to the 1-in-10 year 1-day recharge rate). For stormwater land use we assume a shedding period of 0.25 days based on a saturated discharge of 6 hours discussed in Section 3.2.6. The shedding periods are shown in Table 3.

Table 1. Recharge rates for 10 climatic regions in NZ, obtained with the IrriCalc model based on 44 years of data.

Group	Climatic region	Irrigation	Annual average recharge rate [mm/d]	1-in-10 year 1-day recharge rate [mm/d]
G1	C1/C2 (Martinborough)	Y	1.2	43.63
		N	0.92	38.32
	D1/D2 (Palmerston North)	Y	1.3	42.83
		N	0.97	34.12
	F1 (Canterbury)	Y	1.08	38.68
		N	0.77	41.83
	G1/G2 (Southland)	Y	1.36	36.7
		N	1.08	36.7
G2	F2 (South Canterbury)	Y	1.15	55.06
		N	0.84	55.06
G3	A1 (Hamilton)	Y	2	62.66
		N	1.64	68.99
	A2 (Mt Taranaki)	Y	3.87	63.53
		N	3.53	60.97
	C3 (Taranaki Lowlands)	Y	3.2	62.8
		N	2.83	29.69
G4		Y	3.82	103.46

	B1/B2 (Bay of Plenty)	N	3.41	96.01
	E1/E2 (West Coast)	Y	5.47	89.64
		N	5.08	87.63

Table 2. Annual average and 1-in-10 year 1-day recharge rates for 4 climate groups based on the 10 climatic regions in NZ.

Climate Group	Annual average recharge rate [mm/d]	1-in-10 year 1-day recharge rate [mm/d]
G1	1.09	39.10
G2	1.00	55.06
G3	2.85	63.11
G4	4.45	94.19

Table 3. Shedding periods (days) for each microbe in relation to faecal source/land use.

Land use	Norovirus	<i>E. coli</i>	<i>Campylobacter</i>
OWMS	29	100	
Community OWMS	29	100	
Dairy		1	1
Sheep & beef		1	1
Wildfowl		1	1
Stormwater	0.25	0.25	0.25
Animal effluent		100	100

3.3.3 Water Supply Well Pumping Rate

The rate of pumping affects the hydraulic gradient and pathogen transport velocities in the vicinity of the pumped well. The higher the pumping rate is, the larger will be the cone of depression or zone of influence around the well or wells. Whereas the 2010 guidelines only addressed single domestic groundwater supplies (pumping rate approx. 20 m³/day), the Microbial Risk Assessment Tool considers three possible pumping depths and associated long term pumping rates that can be selected by the user (Table 4).

Assumptions

- Only single bores, pumping from unconfined aquifer are considered.

- Pumping rates are assumed constant so that steady-state flow conditions have been achieved in the aquifer.

Limitations

- Interference from other existing pumping wells within the same or other aquifers are not considered.

Table 4. Pumping rate ranges and screen depths per aquifer type. Numbers in the parentheses are the assumed screen depths in metres below the water table (mbwt).

Aquifer type	Pumping rate (m ³ /d) and screen depths (mbwt)		
	Single dwelling	Small community supply	Larger community supply
Alluvial gravel (AlGr)	10 (0)	200 (30)	500 (50)
Alluvial sand (AlSa)	10 (0)	200 (30)	-
Pumice sand (PuSa)	10 (0)	200 (30)	-
Coastal sand (CoSa)	10 (0)	200 (30)	-
Sandstone and non-karstic limestone (SaSt)	10 (0)	200 (30)	-
Karst and fractured rock (KaFr)	-	200 (30)	500 (50)

3.3.4 Soil type and properties

The extent to which soil horizons can reduce the microbial loading of wastewater percolating through them depends on such factors as their composition, structure, and depth. The vast majority of microbial transport through the soil occurs at saturated or near-saturated conditions (Close et al., 2008; 2010) so the transport of microbes has been simulated for near-saturated conditions and the frequency of those conditions for each land use is used to estimate the total microbial transport. The 2010 guidelines assumed that saturated or near-saturated conditions existed under OWMS, so the approach and microbial removal rates used for the guidelines are assumed to be similar to those used in the 2010 guidelines.

The virus and bacterial removal rates in a range of specific and generic soils are given in Table 5. Removal rates for specific soil types are obtained from Pang et al. (2008) and a recent review by Schijven et al. (2017), while removal rates for generic soil types are obtained from McLeod et al. (2008). Multiplication of these removal rates (log₁₀/m) by the soil thickness gives the extent of microbial reduction in the soil (a log₁₀ value). All removal rates are given

in terms of their minimum and maximum values with possible values assumed to be uniformly distributed between these limits.

Table 5. Virus and bacteria removal rates in specific and generic soil types (Pang et al., 2008; Schijven et al., 2017; McLeod et al., 2008).

Soil type		Virus removal rate [log10/m]	Bacteria removal rate [log10/m]
Specific	Clayey soil	0.1 - 2.1	0 – 0.86
	Silt loam	1 – 2.7	1.6 - 6.5
	Silty sands and gravel	1.3 - 2.9	2.3 - 8.3
	Deep silt loam	1.6 - 2.6	0.1 - 6.3
	Clay	1.6 - 2.2	3.7 - 6
	Clay loam	1.8 - 2.2	0.5 - 3.2
	Silty clay loam	1.9 - 4.2	2.8 - 5.2
	Recent sandy soil	2.1 - 2.9	2 – 2.8
	Fine sandy loam	2.4 - 5.5	8.9 - 9.6
	Loamy sand	2.7 - 4.9	1.4 - 6.7
	Pumice	15.8 - 17.5	16
	Allophanic soil	20	5.2 - 5.8
Generic	Organic/ultic/granular/melanic/podzol/gley soil	1 – 1.8	1 – 1.8
	Brown/pallic/oxidic soil	2 – 2.3	2 – 2.3
	Raw/recent/semiarid soil	2.5 - 20	2.5 - 20

3.3.5 Unsaturated (vadose) zone types and properties

The vadose zone may provide substantial microbial removal depending on the type and thickness of the vadose zone and the infiltration rate, among other factors.

The types of vadose zone materials considered by the tool are:

- Alluvial gravel
- Alluvial sand
- Pumice sand
- Coastal sand
- Sandstone and non-karstic limestone
- Karst and fractured rock

- Silt
- Clay
- Ash
- Peat

The methodology of how the parameters for the vadose zone contaminant transport and virus removal modelling were derived is described in detail in Moore et al. (2010) Section 5.6.2. The bacterial removal rates for alluvial gravel and alluvial sand are obtained from Schijven et al. (2017). The remaining bacterial removal rates are assumed to be the same as the virus removal rates, as Moore et al. (2010) derived these parameters from a range of sources including both viral and bacterial data. The removal rate ranges for the vadose zone media considered in the tool are given in Table 6. For the uncertainty analyses these rates are assumed to be uniformly distributed, except for the alluvial sand virus removal rate which is assumed to follow a triangular distribution.

Table 6. Virus and bacteria removal rates in different vadose zone media (Moore et al., 2010; Schijven et al., 2017).

Vadose zone media	Virus removal rate [log10/m]	Bacteria removal rate [log10/m]
Alluvial gravel	0.05 - 0.61	0.27 - 0.5
Alluvial sand	0.15 - 1.5 (mean 0.74)	0.42 - 1.26
Pumice sand	1.3 – 4.0	1.3 – 4.0
Coastal sand	0.43 - 2.1	0.43 - 2.1
Sandstone and non-karstic limestone	0.01 - 0.04	0.01 - 0.04
Karst and fractured rock	0.0004 – 0.00122	0.0004 – 0.00122
Silt	0.78 - 2.4	0.78 - 2.4
Clay	0.43 - 1.3	0.43 - 1.3
Ash	0.52 - 1.5	0.52 - 1.5
Peat	0.43 - 1.3	0.43 - 1.3

3.3.6 Aquifer types and properties

Groundwater flow and pathogen transport through aquifers are influenced by aquifer hydraulic properties (i.e., hydraulic conductivity and porosity) as well as the thickness of the aquifer (see Section 3.6) and the pathogen removal rates, which are a result of the physical and chemical properties of the aquifer media.

The removal rates used in the groundwater modelling are defined as the spatial removal rate of microbes as they are transported through an aquifer. The viral removal rates in Table 7 are taken from the 2010 guidelines (Moore et al., 2010). The ranges are given in terms of distributions using @RISK® notation, which enables uncertainty quantification using a Monte Carlo framework. These removal rates are split into dispersion and other distance-based processes because dispersion is handled separately in the physically based modelling (MODFLOW and MT3D) via movement through the heterogeneous aquifers. The removal rates (adjusted so that they do not include dispersion) are applied to the model outputs on a distance specific basis.

Table 7. Summary of virus removal rates in groundwater and assumptions of the likely dispersion contributions to these rates that were adopted in the modelling work (Moore et al., 2010).

Aquifer media	Removal rate average [log10/m]	Removal rate distribution	Contribution from dispersion
Alluvial gravel	0.0139	RiskInvgauss(0.013139,0.0029229, RiskShift(0.00089314))	36%
Alluvial sand	0.07	RiskNormalAlt(0.1,0.0103,0.5,0.07, RiskTruncate(0))	10%
Pumice sand	1.655	RiskNormalAlt(0.05,1.46,0.95,1.85)	2%
Coastal sand	0.085	RiskNormalAlt(0.01,0.0142,0.5,0.085)	5%
Sandstone & non-karstic limestone	0.49	RiskNormal(0.5,0.46,RiskTruncate(0))	2%
Karstic & fractured rock	0.0153	RiskNormal(0.0153, 0.0245)	NA

The majority of the bacterial removal rates are taken from Schijven et al. (2017) and described in detail in Table 8. When only a mean value is given for a particular aquifer medium, the range is assumed to be +/- 50% of the mean. The alluvial sand removal rate is taken from Pang (2009). The bacterial removal rates that were used in the simulations are summarised in Table 9.

Table 8. The efficiencies of bacterial removal in different aquifer media (after Schijven et al., 2017, Table 7).

Aquifer Media	Contamination Source	Microbe	Removal Rate (Log10/m)		
			Mean	Minimum	Maximum
Coarse gravel	Sewage effluent	<i>Bacillus stearothermophilus</i>	0.003	NR	NR
Coarse gravel	Sewage effluent	<i>E. coli</i>	0.005	0.004	0.01
Coarse gravel	Sewage effluent	Faecal coliforms	0.003	NR	NR
Coarse gravel	Tracer	<i>Bacillus subtilis</i> spores	0.031	NR	0.045
Coarse gravel	Tracer	<i>E. coli</i> J6-2	0.021	NR	NR
Coarse gravel	Tracer	Faecal coliforms	0.003	NR	NR
Coastal sand	Septic tank effluent	Faecal coliforms	0.159	NR	NR
Dune sand	Sewage effluent	Faecal coliforms	0.014	NR	NR
Dune sand	Sewage effluent	Streptococci	0.005	NR	NR
Fine sand	Septic tank effluent	<i>Clostridium perfringens</i>	0.024	NR	NR
Fine sand	Septic tank effluent	<i>Clostridium</i>	0.044	NR	NR
Fine sand	Septic tank effluent	Coliforms	0.05	NR	NR
Fine sand	Septic tank effluent	<i>E. coli</i>	0.048	NR	NR
Fine sand	Septic tank effluent	Enterococci	0.025	NR	NR
Fissured chalk	Sewage effluent	Faecal coliforms	0.023	0.004	0.067
Fractured gneiss	Tracer	<i>E. coli</i>	0.115	0.087	0.143
Fractured limestone	Sinkhole	<i>Clostridium</i>	0	NR	NR
Fractured limestone	Sinkhole	<i>E. coli</i>	0.001	NR	NR
Fractured limestone	Sinkhole	Faecal coliforms	0.001	NR	NR
Fractured limestone	Sinkhole	Streptococci	0.001	NR	NR
Gravel and sand	Tracer	<i>E. coli</i>	0.004	0.003	0.004
Karst limestone	Creek	Enterococci	0.017	0.001	0.215
Karst limestone	Creek	Faecal coliforms	NR	0.052	0.067
Limestone	Pig manure pit	Faecal streptococcus	0.016	0.015	0.017
Pumice sand	Sewage effluent	Faecal coliforms	3.847	NR	NR
Pumice sand	Tracer	<i>E. coli</i>	1.54	1.46	1.61
Sandstone	Pig manure pit	Faecal streptococcus	0.041	NR	NR
Sandy gravel	River bank filtration	Aerobic spores	0.145	0.08	0.27
Sandy gravel	River bank filtration	<i>Bacillus</i>	0.052	0.015	0.081
Sandy gravel	River bank filtration	<i>Clostridium</i>	0.053	0.015	0.126
Sandy gravel	River bank filtration	Faecal coliforms	0.102	0.031	0.148

Table 9. Summary of bacterial removal rates in groundwater and assumptions of the likely dispersion contributions to these rates that were adopted in the modelling work (Schijven et al., 2017; Moore et al., 2010).

Aquifer media	Removal rate average [log10/m]	Removal rate distribution	Contribution from dispersion
Alluvial gravel	0.005	RiskTriang(0.004, 0.005, 0.01)	36%
Alluvial sand	0.07	RiskUniform(0.035,0.105)	10%
Pumice sand	1.54	RiskUniform(1.46, 1.61)	2%
Coastal sand	0.159	RiskUniform(0.095, 0.2385)	5%
Sandstone & non-karstic limestone	0.016	RiskUniform(0.015, 0.016)	2%
Karstic & fractured rock	0.001	RiskUniform(0.0005, 0.0015)	NA

The MRA Tool has been developed for a range of hydrogeological settings found in New Zealand. In summary, the types of unconfined aquifers considered in the tool are:

- Alluvial gravel
- Alluvial sand
- Pumice sand
- Coastal sand
- Sandstone and non-karstic limestone
- Karst and fractured rock

Hydraulic properties and their variances that were used as input data for the MRA Tool (Table 10 and 11) were taken from the 2010 guidelines (Moore et al., 2010). The hydraulic properties (transmissivity, hydraulic conductivity, porosity), sourced from regional authorities and small-scale tracer tests conducted by ESR at the time, were generally in the same range as values from the literature, and no major change is expected for the mean and variances with the addition of more data.

In general, aquifers can be very heterogeneous, and hydraulic properties can vary over several orders of magnitude even if measured at wells in close proximity to each other. Too few field data are available to allow aquifer heterogeneity to be precisely described. The accepted approach to overcoming this difficulty is to determine the variability in the aquifer's

hydraulic properties and use this as the basis of a statistical model of the aquifer. This allows aquifer properties to be simulated at every unsampled point.

Geostatistical models are used to describe the spatial continuity of a property. Variograms are one version of a geostatistical model. These geostatistical models allow hydraulic property values to be interpolated to locations without any observed values. A semi-variogram shows the semi-variance as a function of the distance between two locations, and the semi-variogram properties for the aforementioned aquifer types are listed in Table 11.

The sill is the maximum value the semi-variogram reaches as the distance between observations increases. The separation distance at which the semi-variogram levels off to the sill is the practical range. Within the range there is spatial correlation of the aquifer property, and beyond the range there is no correlation, i.e., the semi-variance is independent of separation distance. The “a” value ($\sim 1/3$ the range) is defined as the distance at which the tangent line to the curve at zero separation intersects the sill. Further information on the development of the semi-variograms is provided in the 2010 guidelines (Moore et al., 2010). Variograms have been used to describe the heterogeneity of the aquifer materials for these simulations.

Karst and fractured rock aquifers were treated differently as it was not possible with existing knowledge to define the heterogeneity of the discrete fracture networks within the karst or fractured rock in a probabilistic sense (e.g., generation of stochastic realisations of the fracture networks). This work is beyond the budget and scope of this current project. In the interim, a conservative approach has been used where the spatial removal rate distributions are simply applied to a range of distances. This simple approach tends to inflate the calculated separation distances required, but this conservatism is appropriate in the face of scarce data.

It is noted that while there are few data in the literature, what is reported indicates very high values of hydraulic conductivity can occur in this setting (up to 1000 m/day) that is associated with flow within the fractures of these aquifer media.

Table 10. Summary of mean aquifer properties adopted in the MRA Tool (from Moore et al., 2010).

Aquifer type	Transport porosity	Hydraulic conductivity (m/day)
Alluvial gravel (for permeable channels)	0.0032	1300
Alluvial (coarse) sand	0.2	80
Pumice sand	0.3	80
Coastal Sand	0.2	10
Sandstone and non-karstic limestone	0.1	0.01

3.3.7 Soil, vadose zone, and saturated zone thickness

- Soil thickness/depth

Soil depth is entered by the user, or if unknown, should be assumed to be 1 m in accordance with the 2010 guidelines and Pang (2009). Soil thickness is not considered in the domestic and community on-site wastewater management system land uses that, by design, discharge below the soil layer.

Table 11. Summary of the exponential semi-variogram properties for hydraulic conductivity used to represent the selected aquifer types – sill values in log₁₀ (from Moore et al., 2010).

Aquifer type	Sill for log ₁₀ hydraulic conductivity	Sill for porosity	a value (1/3 Range)	Anisotropy
Alluvial gravel	0.6	0.0025	500	10:1
Alluvial (coarse) sand	0.5	0.0025	400	2:1
Pumice sand	0.01	0.002	100	1:1
Coastal sand	0.33	0.014	100	1:1
Sandstone and non-karstic limestone	0.44	0.014	100	1:1

- Vadose zone thickness

Vadose zone thickness can be entered by the user directly into the tool. A value of zero can be entered for situations where there is a very high groundwater table, and no significant reduction is expected in the vadose zone.

- Saturated zone thickness

Saturated thickness is assumed to be 60 m for all aquifer types; therefore, thickness is always at least 10 m greater than the well screen depths shown in Table 4.

3.3.8 Other assumptions and limitations of the flow scenarios

Other assumptions that apply to the flow scenarios are:

- Water is abstracted at the screens for each type of well – domestic, small town and municipal.
- As described above, only single wells pumping from an unconfined aquifer will be considered as within scope for this tool's project, as the inclusion of pumping interferences and of variable confinement status, would introduce significant complexity, requiring individualised site information. For such cases, a more detailed site-specific assessment should be undertaken. An assessment based on an unconfined aquifer would be expected to be conservative.
- The effect of boundary conditions (other than the pumping well and the surface loading) will not be considered in the tool. When such boundaries are in proximity to the source or are expected to affect the flow patterns or microbial transport and removal characteristics, a site-specific assessment should be undertaken.
- The soil and vadose zone directly below the OWMS disposal field are assumed to be constantly saturated. The modelling has been undertaken assuming the maximum typical effluent disposal design flux of 35 mm/day.
- The vast majority of microbial transport through the soil occurs at saturated or near-saturated conditions (Close et al., 2008; 2010) so the transport of microbes has been simulated for near-saturated conditions. We assume a worst-case scenario of a 1-in-10 year 1-day rainfall event, where the resulting recharge rate for each land use is used to estimate the total microbial transport.

3.4 MICROBIAL LOADING AND REMOVAL RATES

The collation and quantification of the source microbial loading inputs was reported by Humphries et al. (2020) based on a review of the international literature and experimental data from New Zealand and is used to estimate the microbial loading rates for each land-use in this section. The international literature for microbial removal rates has been recently reviewed by Schijven et al. (2017). With respect to microbial removal rates in soils, the vadose zone, and groundwater types, they summarise the data from Pang (2009) as the most comprehensive source of removal rates. As there are no new data and the rates from Pang (2009) were used in the 2010 guidelines, it follows that we can also use the same summarised viral removal rates. The bacterial removal rates are taken from Pang (2009) and Schijven et al. (2017). The virus and bacterial removal rates have been given in Sections 3.3.4 to 3.3.6.

In general, reductions in microbe concentrations take place in each of the following four components of the transport process (Figure 1 and Figure):

1. the wastewater treatment plant or input source for other land-use scenarios
2. the land application system (LAS) and the soil, if any, beneath the disposal field for OWMS scenarios or soil layer for other land-use scenarios
3. the unsaturated (vadose) zone above the water table and
4. the groundwater as it flows through the aquifer.

The initial concentration of microbes entering the sewage tank, or that are introduced from a specific land use, determine the overall reduction that must be attained by the total of the four components to achieve the maximum acceptable concentration in the well water.

For the land-use scenarios modelled in the MRA tool, microorganisms were chosen that best represented the risk to groundwater resources and public health. The type of microorganism and why it was chosen is explained in the following sections.

3.4.1 Microbe selection for human related land-uses

Out of the seven land uses in the MRA tool, two land uses involve human faecal sources:

- Multiple domestic on-site wastewater management systems
- Community size on-site wastewater management systems

Since rotavirus was included in the 2010 setback distance guidelines as a modelled viral pathogen it was again considered for the MRA tool. However, on 1 July 2014 Rotarix®¹, an oral vaccine given at 6 weeks, 3 months and 5 months of age, was added to the New Zealand national childhood immunisation schedule (ESR, 2016). The introduction of a rotavirus vaccination in Australia resulted in a 70% decrease in rotavirus hospitalisations in under 5-year olds in the two and a half years following the vaccines introduction (ESR, 2016). A similar decline (85%) was reported following the first year of the vaccine's introduction to New Zealand (ESR, 2016). Due to the rotavirus vaccine being included on the national immunisation schedule, contracting rotavirus is now not as common as it once was. For the MRA tool, therefore, rotavirus was not considered to be a suitable microorganism to be modelled.

A viral pathogen that is not included in the national immunisation schedule and poses a risk to the community is norovirus. In recreational waters it has been determined that exposure to norovirus contributes the majority of the risk from illness when human faecal contamination scenarios are encountered (Boehm et al., 2018). This is due to the persistence of norovirus in fresh and aged sewage inputs. Norovirus is currently the organism of choice for modelling risk assessments in recreational waters (Boehm and Soller, 2020, Crank et al., 2019), supporting its relevance for this MRA tool. Norovirus, therefore, was chosen as the most suitable viral pathogen for the MRA tool with regards to the human related land-use scenarios. Values for norovirus shedding during illness are taken from a study by Borchardt et al. (2011).

We have also included *E. coli* as a bacterial indicator for human related land-use scenarios as it is a good indicator of faecal contamination, it is often monitored, and it is the indicator of faecal contamination in the Drinking Water Standards (Ministry of Health, 2018).

The loading rates adopted for these two pathogens for OWMS are:

- Human norovirus loading rate range: $1 \times 10^4 - 1 \times 10^{10}$ viruses/L
- Human *E. coli* loading rate range: $4.3 \times 10^5 - 1.4 \times 10^7$ cfu/100 mL

For Community OWMS, we have assumed a norovirus range of $1 \times 10^2 - 1 \times 10^7$ viruses/L. This allows for greater dilution of the norovirus from infected individuals in the community compared to a single OWMS and is consistent with the levels of norovirus measured in one of the few studies (Borchardt et al., 2011) for a community OWMS with a norovirus outbreak of 8×10^4 gene copies/L.

¹ The immunisation Advisory Centre <https://www.immune.org.nz/vaccines/available-vaccines/rotarix>

As *E. coli* is an indicator of faecal contamination, we have assumed that *E. coli* loading rate range doesn't fluctuate with OWMS size (single, multiple, community etc) and so is assumed to be the same for single and multiple OWMS: $4.3 \times 10^5 - 1.4 \times 10^7$ cfu/100 mL.

3.4.2 Microbe selection for animal related land-uses

Out of the seven land uses in the MRA tool, four land uses involve animal faecal sources:

- Dairy farming
- Sheep and beef farming
- Animal effluent/manure application to land
- Wildfowl

According to Moriarty et al. (2008) and Devane et al. (2005), *Campylobacter* has been widely recorded in cattle faeces throughout New Zealand. In a Canterbury study 97.8% and 93.9% of samples from composites of five dairy and beef cattle respectively, were reported to contain *Campylobacter* (Devane et al., 2005). During the Havelock North outbreak groundwater was found to be contaminated with sheep faecal matter which was subsequently identified as *Campylobacter* (Gilpin et al., 2020). Due to its widespread prevalence in dairy cows, beef cattle and sheep, and the high rate of infections within the New Zealand population, *Campylobacter* was considered the most appropriate organism to be used for agriculture related land-use scenarios in the MRA tool. The prevalence of *Campylobacter* in wildfowl faeces has been estimated for 4 different wildfowl species in New Zealand (Black swans, Canada Geese, ducks and gulls) by Moriarty et al. (2011). These data have been collated, along with international studies, by Humphries et al. (2020).

As in the human-related land-use scenarios (Section 3.4.1), we have included *E. coli* as a bacterial indicator for animal related land-use scenarios as it is a good indicator of faecal contamination from animal and avian sources in the NZ environment (Moriarty et al., 2015; Moriarty et al., 2011; Moriarty et al., 2008; Pattis et al., 2017), it is often monitored in recreational and drinking waters, and it is the indicator for faecal contamination in the New Zealand Drinking Water standards (Ministry of Health, 2018).

The loading rate ranges adopted for the agricultural animal sources are:

Campylobacter: $10^4 - 10^{10}$ MPN/species/day

E. coli: $10^7 - 10^{10}$ MPN/species/day

Table 12 shows the raw (pre statistical processing) mean/ranges of *Campylobacter* and *E. coli* in various livestock and in wildfowl. Ranges or means of the loading rate of each target microorganism are provided as concentration per animal per day. Loading rates include the prevalence (frequency of detection within a specified herd size) of each target microorganism in an animal species, as not all animals in a herd carry a particular microorganism. Data are taken from New Zealand studies unless otherwise indicated.

The loading rate ranges adopted for the wildfowl sources are:

Campylobacter: $10^4 - 10^6$ MPN/bird/day

E. coli: $10^6 - 10^{10}$ MPN/bird/day

Table 13 shows the raw mean/ranges of *Campylobacter*, *E. coli*, *Giardia* and *Cryptosporidium* in dairy farm effluent. Ranges of the loading rate of each target microorganism are provided as concentration per animal/day or hectare/day.

Table 12: Raw (pre statistical processing) loading rates for *Campylobacter* and *E. coli* in various livestock and in wildfowl.

Microorganism	Animal type	Loading rate	Units
<i>Campylobacter</i>	Dairy cow	$10^4 - 10^{10*}$	**MPN/cow/day
	Beef cattle***	$10^5 - 10^8^*$	MPN/cow/day
	Sheep	$10^5 - 10^8$	MPN or €CFU/sheep/day
<i>Campylobacter jejuni</i>	Dairy cow	$10^4 - 10^7$	MPN/cow/day
	Beef cattle***	10^8	CFU/cow/day
<i>E. coli</i>	Dairy cows	$10^7 - 10^{10}$	MPN/cow/day
	Beef cattle***	-	-
	Sheep	$10^{10} - 10^{11}$	MPN/sheep/day
Wildfowl			
<i>Campylobacter</i>	Black swans	10^4	MPN/bird/day
	Canada Geese	10^6	MPN/bird/day
	Ducks	10^4	MPN/bird/day
	Geese [‡]	10^7	CFU/bird/day
	Gulls	10^4	MPN/bird/day
<i>E. coli</i>	Black swans	10^8	MPN/bird/day
	Canada Geese	10^6	MPN/bird/day

	Ducks	10 ¹⁰	MPN/bird/day
	Geese [‡]	10 ⁶	CFU/bird/day
	Gulls	10 ⁸	MPN/bird/day

*This highest range could be indicative of high shedding periods of the year such as spring during the calving season

**MPN = most probable number culturing method, for example, Colilert Quantitrays

***Data based on international studies as no New Zealand studies of concentration of *Campylobacter* or *E. coli* (only STEC) in beef cattle faeces

€CFU = colony forming units for plate counts of bacteria

‡International studies

Table 13: Raw (pre statistical processing) loading rates for *Campylobacter*, *E. coli*, *Giardia* and *Cryptosporidium* in dairy farm effluent

Microorganism	Environmental sample type	Concentration	Units
<i>Campylobacter</i>	Dairy farm effluent	10 ⁴ - 10 ⁶	MPN/cow/day
<i>E. coli</i>		10 ⁷ - 10 ⁸	MPN/cow/day
<i>E. coli</i>		10 ⁶ - 10 ⁸	<i>E. coli</i> /ha/day
<i>Giardia</i>		ND by qPCR*	
<i>Cryptosporidium</i>		ND by qPCR	

*qPCR, quantitative Polymerase Chain Reaction

3.4.3 Microbe selection for stormwater systems

The remaining land-use scenario is stormwater systems which can be a mixture of sewage and septage (from leaks or overflows) and animal faeces, with the first flush of stormwater often approximating the concentration of weak sewage. Most routine monitoring of stormwater measures *E. coli* and *Enterococcus* (Humphries et al., 2020), but there are some measurements of pathogens including *Campylobacter* and viruses. In view of the mixed human and animal sources for stormwater we have simulated *E. coli*, *Campylobacter*, and norovirus for stormwater systems.

Table 14 shows the raw mean/ranges of *Campylobacter*, *E. coli*, *Giardia* and *Cryptosporidium* in stormwater. There were no available data on norovirus concentrations in stormwater, however, norovirus concentrations in small and medium wastewater treatment systems ranged between 10² and 10⁵ genome copies (GC)/L (Hewitt et al., 2011) and these values were reduced by a factor of 10 to approximate the “weak sewage” effluent for the stormwater

simulations. Ranges of the loading rate of each target microorganism are provided as concentration per volume.

Table 14: Raw (pre statistical processing) loading rates for *Campylobacter*, *E. coli*, *Giardia* and *Cryptosporidium* in stormwater.

Microorganism	Environmental sample type	Concentration	Units
<i>Campylobacter</i>	Stormwater [€]	10 ⁰ - 10 ²	**MPN/100 mL
<i>Campylobacter jejuni</i>	Stormwater	≤ 5	***GC/100 mL
<i>E. coli</i> [¥]	Stormwater	10 ¹ – 10 ⁷	€CFU or MPN /100 mL
<i>Giardia</i>	Stormwater	10 ² - 10 ⁵	Cysts /100 L
<i>Cryptosporidium</i>	Stormwater	10 ¹ - 10 ⁴	Oocysts/ 100 L

[€]very little data on viruses but what is there has low prevalence e.g., 0.02%

*Data based on international studies as no New Zealand studies of concentration or loading rate in stormwater

**MPN = most probable number culturing method, for example, Colilert Quantitrays

***GC = gene copy

€CFU = colony forming units for plate counts of bacteria

¥ 10³ – 10⁴/100 mL could be useful mean concentrations to model

The loading rate ranges adopted for the stormwater sources are:

E. coli: 10³ – 10⁴ MPN/100 mL

Campylobacter: 10⁰ – 10² MPN/100 mL

Norovirus: 10⁰ – 10³ copies/100 mL

3.4.4 Summary of loading rates

The loading rates are converted into initial concentrations at the source [microbe/L]. All concentrations are given in terms of their minimum and maximum values with possible values assumed to be uniformly distributed between these limits (Table 15).

Table 15: Non-climate dependent initial concentrations at the source [microbe/L] for each microbe for the human-related land-uses.

Land use	Microbe		
	Norovirus	<i>E. coli</i>	<i>Campylobacter</i>
OWMS	10 ⁴ – 10 ¹⁰	4.3 x 10 ⁶ – 1.4 x 10 ⁸	
Community OWMS	10 ² – 10 ⁷	4.3 x 10 ⁶ – 1.4 x 10 ⁸	
Stormwater	10 ¹ – 10 ⁴	10 ⁴ – 10 ⁵	10 ¹ – 10 ³

For the agricultural land use cases this requires additional parameters for conversion from MPN/animal/day to MPN/L (Table 16). The assumptions given below are discussed in more detail in Sections 3.2.4 – 3.2.7.

For sheep and beef we assume usage for 2-3 days per month = 30 days per year, so the area per day is given by the farm size divided by 30 (400/30 ~ 13 ha per day). The number of animals per day per ha is then given by the herd size divided by area per day (4400/13 ~ 330 animals per day per ha).

For wildfowl we assume an area of 1.5 ha with 100 birds, where the entire area is used during a day (so area per day = 1.5 ha).

For animal effluent land application, we assume irrigation on approximately 25% of the area with centre pivot return period of every 3 days, so the area per day is given by the 25% of the farm size divided by 3 (200 x 0.25 / 3 ~ 17 ha per day). We assume dairy cows are in the shed for 2 hours per day (2 hours/24 hours ~ 0.083). Then the number of animals per day per ha is given by the herd size divided by the area per day multiplied by 0.083 (700 / 17 x 0.083 ~ 3.5).

For dairy farming, the herd size is an input parameter by the user. As a guideline, a high intensity irrigated farm would have an average of 700-800 cows, and a medium intensity non-irrigated farm would have an average of 200-250 cows.

Table 16: Parameters for converting loading rates in MPN/animal/day (or cfu/animal/day) to MPN/day (or cfu/day).

Land use	Farm size [ha]	Herd size	Area per day	Animals per day per ha
Sheep & beef	400	4400	13	330
Wildfowl	1.5	100	1.5	67
Animal effluent	200	700	17	3.5

The climate-dependent recharge rates (discussed in Section 3.3.1) are then used to convert from MPN/day to MPN/L (Table 17). The dairy loading rates (per animal) are given in Table 18 and are later scaled by herd size.

Table 17: Climate dependent initial concentrations at the source [microbe/L] for each land use and microbe.

Microbe	Land use	Climate group			
		G1	G2	G3	G4
<i>E. coli</i>	Sheep & beef	4.5×10^{10} – 4.5×10^{11}	3.2×10^{10} – 3.2×10^{11}	2.8×10^{10} – 2.8×10^{11}	1.9×10^{10} – 1.9×10^{11}
	Wildfowl	5.1×10^5 – 5.1×10^9	3.6×10^5 – 3.6×10^9	3.2×10^5 – 3.2×10^9	2.1×10^5 – 2.1×10^9
	Animal effluent	5.9×10^5 – 5.9×10^6	4.2×10^5 – 4.2×10^6	3.7×10^5 – 3.7×10^6	2.5×10^5 – 2.5×10^6
<i>Campylobacter</i>	Sheep & beef	4.5×10^5 – 4.5×10^8	3.2×10^5 – 3.2×10^8	2.8×10^5 – 2.8×10^8	1.9×10^5 – 1.9×10^8
	Wildfowl	5.1×10^3 – 5.1×10^5	3.6×10^3 – 3.6×10^5	3.2×10^3 – 3.2×10^5	2.1×10^3 – 2.1×10^5
	Animal effluent	5.9×10^2 – 5.9×10^4	4.2×10^2 – 4.2×10^4	3.7×10^2 – 3.7×10^4	2.5×10^2 – 2.5×10^4

Table 18: Climate dependent Dairy land-use initial concentrations [microbe/L] per animal. Concentrations are then scaled by herd size to obtain initial concentration at the source [microbe/L].

Microbe	Climate			
	G1	G2	G3	G4
<i>E. coli</i>	1.0×10^4 – 1.0×10^7	7.3×10^3 – 7.3×10^6	6.3×10^3 – 6.3×10^6	4.2×10^3 – 4.2×10^6
	1.0×10^1 – 1.0×10^7	7.3×10^0 – 7.3×10^6	6.3×10^0 – 6.3×10^6	4.2×10^0 – 4.2×10^6

3.5 TOLERABLE CONCENTRATIONS OF PATHOGENS IN DRINKING WATER

For the indicator microbe *E. coli*, a drinking water standard of < 1 per 100 mL has been set by the Ministry of Health (Ministry of Health, 2018). As the standard is specified as <1, a value of 50% of the limit (0.5 per 100 mL or 5 per L) has been used as the maximum acceptable concentration for *E. coli* for calculation purposes.

Figure 4 shows an overview of the approach used to determine the tolerable concentrations of norovirus and *Campylobacter* in drinking water and follows the approach outlined in the 2010 guideline (Moore et al., 2010). The maximum acceptable concentration is the concentration expected to result in the tolerable annual infection probability.

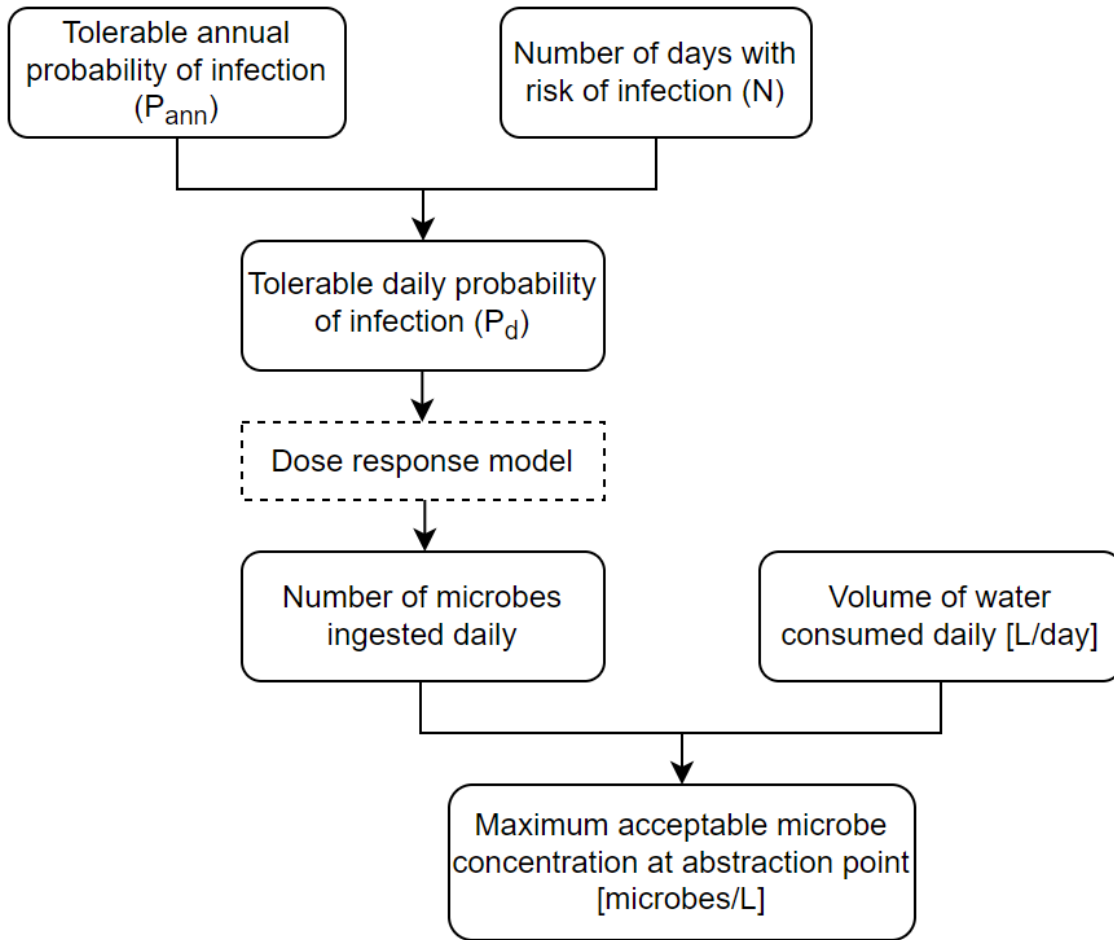


Figure 4: Algorithm for calculating the tolerable microbial concentration in water in a well.

Briefly, the tolerable annual probability of infection (P_{ann}) has been set at 1 in 10,000 following the level set out by USEPA (USEPA, 1989) and adopted widely internationally. A dose response curve is used to relate the number of infective organisms ingested by an individual to the likelihood of that individual becoming infected. The dose-response parameters (α and β) are given in Table 19 where norovirus parameters are obtained from Teunis et al. (2008) and *Campylobacter* parameters are taken from Black et al. (1988).

Table 19: Dose response curve parameters for norovirus and *Campylobacter* (Teunis et al., 2008; Black et al., 1988)

Dose response parameter	Norovirus	<i>Campylobacter</i>
α	0.04	0.145
β	0.055	8.007

The tolerable daily rate of infection (P_d) can be calculated from P_{ann} and the number of days with risk of infection (N) based on the equation:

$$P_{ann} = 1 - (1 - P_d)^N$$

This can be used with the dose response function to obtain the number of infective organisms ingested on a daily basis (D) according to the equation:

$$P_d = 1 - \left[1 + \left(\frac{D}{\beta} \right) \right]^{-\alpha}$$

Then the concentration [per L] of infective organisms in the water is the number of infective organisms ingested (D) divided by the amount of water consumed. Data from two New Zealand surveys have been used for the water consumption values in this modelling; the details of the distribution of values used are given in the Technical Appendix of the 2010 guidelines. The volume of water ingested [L] is assumed to be 0.8 L/day.

The number of days with risk of infection is dependent on microbe and land use (Table 20). For a single OWMS the value is taken from Moore et al. (2010), where 50 days of the year equates to a prevalence of approximately 14%. The prevalence of norovirus in a community OWMS should be between a large wastewater treatment system and an individual OWMS due to averaging and dilution. The mean prevalence for norovirus for 11 New Zealand wastewater treatment systems is ~ 70% (Hewitt et al., 2013), so for community OWMS we have assumed a prevalence of 40% = 146 days with risk of infection per year.

Table 20: Number of days with risk of infection per year (N), used for calculating the tolerable daily rate of infection P_d .

Land use	Norovirus	<i>Campylobacter</i>
OWMS	50	
Community OWMS	146	
Dairy		15
Sheep & beef		12
Wildfowl		183
Stormwater	0.1	0.1
Animal effluent		81

For the dairy land use case, animals are present approximately 1 in every 25 days of the year (therefore 365/25, i.e. ~ 15 days). For sheep and beef we assume 30-day stock rotations (365/30 ~ 12). For wildfowl there is little information, and we assume birds are around large irrigation ponds approximately 50% of the time (365/2, i.e. ~ 183). For stormwater we base this on a 1 in 10-year rainfall event, assuming that the peak flow for a storm event takes place over 2-3 hours (0.1 day). For animal effluent we consider that dairy shed effluent would be irrigated for approximately 8 months of the year (244 days), and assuming centre pivot with return period of 3 days this gives 244/3, i.e. ~ 81 days.

The maximum acceptable concentrations for norovirus and *Campylobacter* derived from this procedure are shown in Table 21.

Table 21: Maximum acceptable concentrations giving rise to an annual probability of infection of 1 in 10,000 per person [microbe/L].

Land use	Norovirus	<i>Campylobacter</i>
OWMS	3×10^{-6}	
Community OWMS	1×10^{-6}	
Dairy		5×10^{-4}
Sheep & beef		6×10^{-4}
Wildfowl		4×10^{-5}
Stormwater	2×10^{-3}	7×10^{-2}
Animal effluent		9×10^{-5}

3.6 MODELLING APPROACH

A modular approach is adopted, whereby the soil, vadose zone and saturated zone modelling components are decoupled. The outputs of each modelling component are the log reduction in the pathogen concentration achieved with increasing transport distances, which is combined to achieve a total log reduction that is achieved as the pathogen moves through the soil, vadose and saturated zone. This approach provides significant computational advantages, while it allows the assessment of microbial risk from multiple interacting sources.

3.6.1 Soil modelling

As microbial transport is order of magnitudes greater under saturated conditions, we only consider saturated conditions for the soil layer, considering the probabilities that such conditions may occur. The log₁₀ reduction in the microbe concentration in the effluent as it percolates through the soil is calculated by multiplying the log₁₀ reduction/m obtained from Table 5 by the depth of soil through which the effluent passes. As described in Section 3.3.7, if no soil depth information is available, a depth of 1 m is assumed. The removal rates for specific soil types are obtained from Pang et al. (2008) and a recent review by Schijven et al. (2017) while removal rates for generic soil types in Table 5 are obtained from McLeod et al. (2008).

3.6.2 Vadose zone modelling

The modelling of one-dimensional solute transport through the vadose zone will generally follow the methodology described in more detail in the 2010 guidelines. It is based on the 1D, mixing cell model described by Bidwell (2000), and was run with @RISK® which enables uncertainty quantification using a Monte Carlo framework by allowing some input parameters to be uncertain and sampled from predefined probability distribution functions (Table 6, Table 22). More complex models, such as Hydrus (Simunek et al., 1999), are available for vadose zone modelling and have been considered. However, the required input data are not available for a national assessment and there would need to be significant simplifying assumptions for the application of these complex models.

Exploring a range of values is required to represent both the natural variability in the parameter and the uncertainty of parameter values due to data scarcity. From the Monte Carlo calculations, a distribution of possible log₁₀ reductions predicted to be achieved within the vadose zone was obtained for range of depths (1 to 80 m). The recharge rates are discussed in Section 3.3.1, the shedding period in Section 3.3.2, and the microbial removal rates for each vadose zone material are found in Section 3.3.5.

Table 22: Input parameter values used for vadose zone modelling (from Moore et al., 2010).

Hydrogeological setting	Macropore flow contribution to total flow	Transport porosity Θ		Péclet Number		Longitudinal dispersion ¹		Retardation factor
		Matrix flow	Macropore flow	Matrix flow	Macropore flow	Matrix flow	Macropore flow	
Alluvial gravel	25–50% ²	0.1–0.2	0.005–0.015	20	20	5%	5%	1
Alluvial sand (coarse)	1–10% ²	0.35–0.40	0.01–0.05	20	80	5%	1%	1
Pumice sand	0%	0.25–0.36		7–20		5–15%		1
Coastal sand (fine)	0%	0.35–0.40		7–20		5–15%		1
Sandstone and non-karstic limestone	0%	0.01–0.03		7–20		5–15%		1
Fractured rock and karstic geology	50–70%	0.01–0.03	1	7–20	80	5–15%	1%	1
Clay (cracking)	85–95%	0.45–0.65	0.015–0.035	7–20	80	5–15%	1%	1
Silt	0.5–2%	0.15–0.25	0.0025-0.0075	7–20	80	5–15%	1%	1
Peat	0%	0.35–0.55		7–20		5–15%		1
Ash	0.5–2%	0.05–0.15	0.0025-0.0075	7–20	80	5–15%	1%	1

Notes:

¹ Dispersion values are calculated from the Péclet Number and observation depth.

² Linearly decreased to 0% between 7 and 12 m

3.6.3 Saturated zone modelling

Contaminant transport and pathogen removal is addressed in a stochastic framework. For each aquifer type, 100 realisations of the heterogeneous hydraulic conductivity field were generated. Figure 5 shows a single realisation of a spatially correlated, heterogeneous, three-dimensional, hydraulic conductivity field. The generation of these stochastic realisations is based on field variograms from earlier studies, as appropriate for each aquifer type (Table 11). The flow solution for each heterogeneous realisation is generated using MODFLOW 2005 (Harbaugh, 2005). An initial steady state stress period (at background recharge rates;

Table 2) provided the conditions for transient stress periods, simulating the rainfall event (also

Table 2) and subsequent flow field recovery to a maximum simulation time of 500 days. Pumping rates (and depth) were time (stress-period) invariant, defined by the individual pumping scenarios (Table 4).

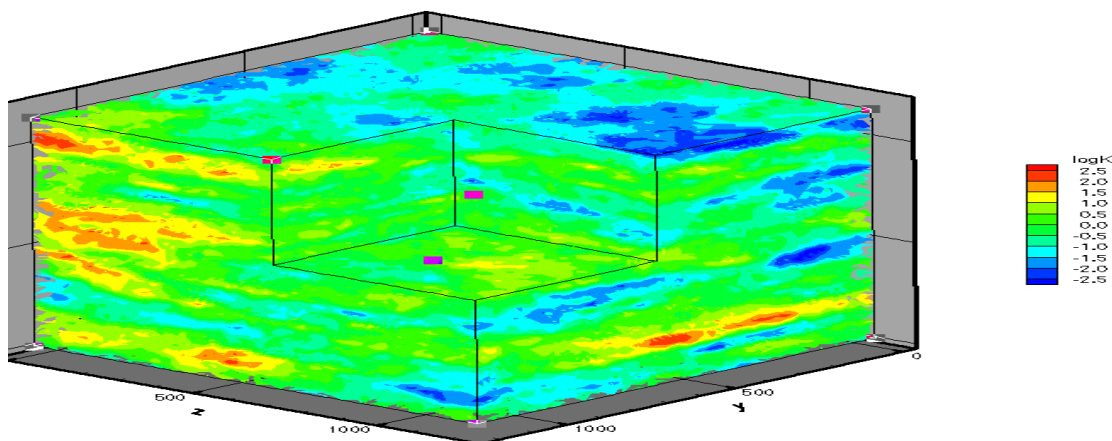


Figure 5: Single realisation of a 3D heterogeneous hydraulic conductivity field (distances in m).

The contaminant advective and dispersive log-removal is calculated using a novel inverse transport solution, using MT3D-USGS (Bedekar et al., 2016). In this solution the plume distance-dependent log reductions for each realisation are obtained by simulating a plume originating at the production well (Figure 6).

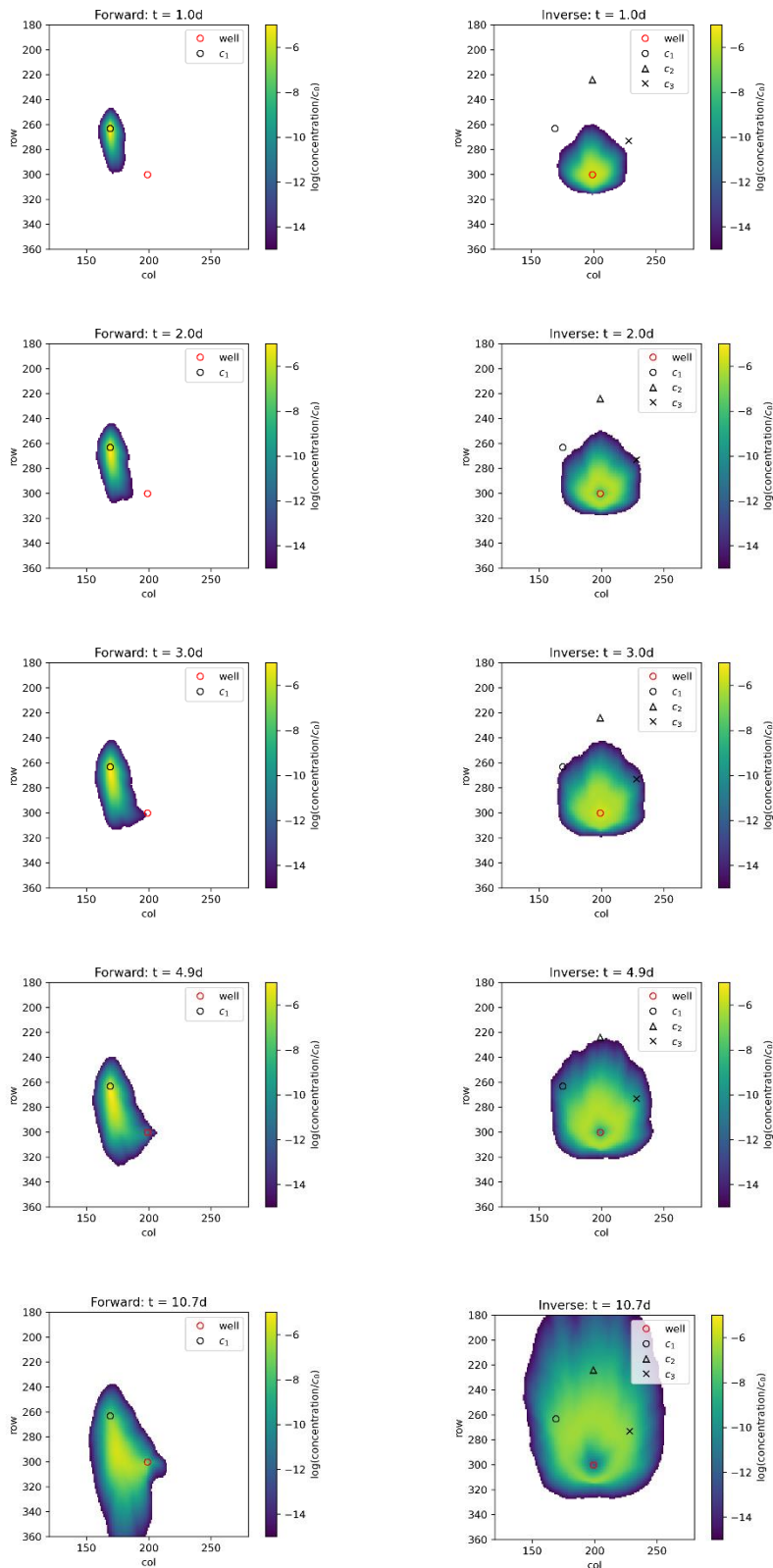


Figure 6: Forward and inverse transient transport solutions at various time steps (distance in m and time in days).

Contaminant removal is simulated as a first-order irreversible reaction quantified by a distance-dependent reaction constant. This approach allows multiple sources to be considered in the calculation of risks of microbial contamination, by superimposing solutions (Figure 7) which is done in the tool post processing step.

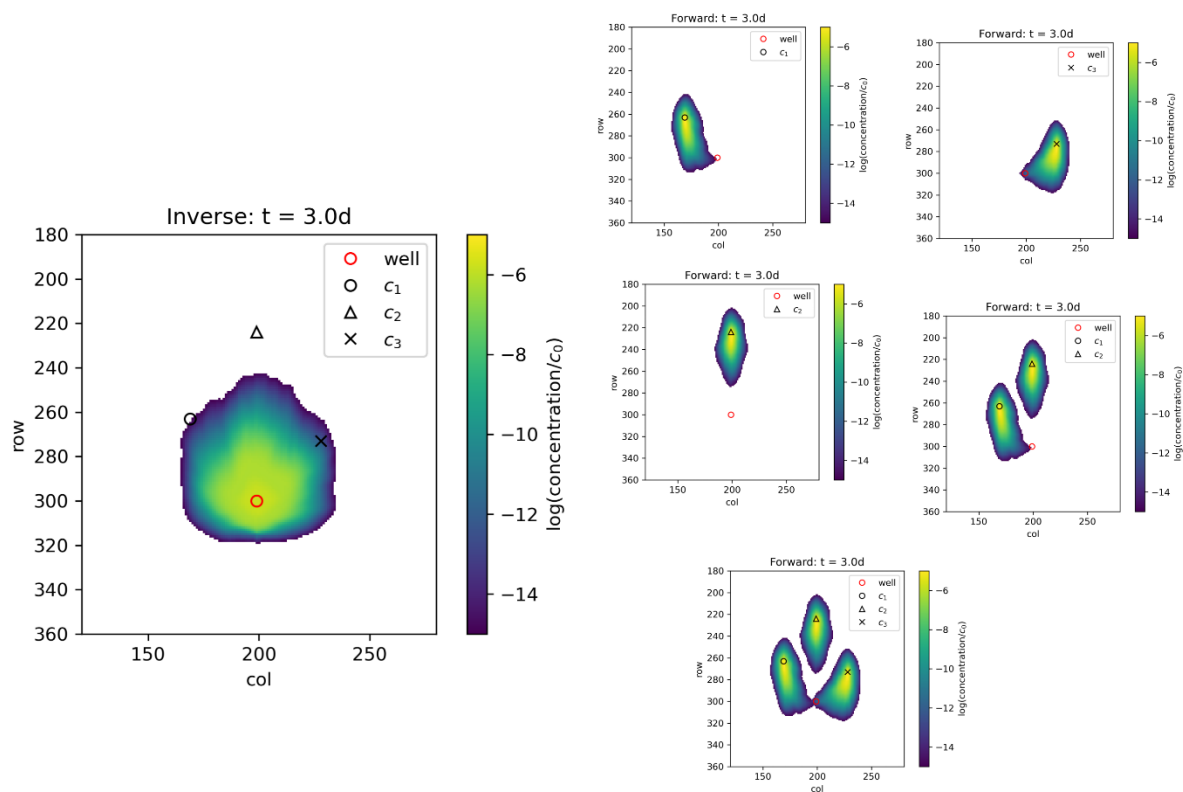


Figure 7: Cumulative effect of multiple sources (right side) from a single inverse transport simulation (left side) using the superposition principle.

The statistics across the ensemble of MT3D-USGS transport solution realisations are compiled and extracted. Ensemble percentile for maximum concentration in every surface model cell (5 x 5 m) form the basis of the probabilistic description of the microbial log-removal that is achieved in the aquifer.

3.7 SUMMARY OF FEATURES

The approach adopted in the MRA tool allows the following:

- Consideration for unlimited number of overlapping, proposed and/or existing microbial sources within a well capture zone.
- Consideration for multiple hydrogeological settings, both region specific (such as aquifer material and climate conditions) and source specific (such as soil type, vadose zone material and depth to water table).
- Consideration for three different well depths and pumping rates.
- Calculation of cumulative health risk for each relevant pathogen, from the existing and proposed pathogen sources. Separation distances for proposed activities can be back estimated iteratively, so that the health risk is lowered at acceptable levels.

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