

MICROBIAL SOURCE IDENTIFICATION AND APPORTIONMENT FOR POLLUTION REDUCTION

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ABSTRACT

State of the Environment reports highlight microbial contamination as a significant water management issue in Aotearoa New Zealand. Identifying sources of microbial contamination is difficult because most catchments contain multiple land uses and complex hydrology. In this paper, we report a 'satellite-to-genes' method for identification of sources of *E. coli* and apportionment of bacterial loadings to these sources to inform pollution reduction planning. The study was conducted in the Nelson catchment, where long-term hydrological, land use and microbial data are available for freshwater management units representing a range of catchment land uses. Overall, mean concentrations of *E. coli* in rivers were higher during high-flow than during base-flow conditions. The highest mean *E. coli* concentrations were found in areas of high producing grassland while the lowest concentrations were found in areas of native/exotic vegetation. Peak bacterial concentrations were found in urban areas affected by inflow and infiltration. Irrespective of the flow condition, the dominant discharge volume was from rivers. During base-flow, the dominant *E. coli* loading was from the Nelson WWTP discharge. Positive correlations were found between *E. coli* concentrations and high producing grassland/urban/wetlands. Faecal source tracking results indicated that human contamination was present in urban waterways.

KEYWORDS

Faecal source tracking, catchment modelling, faecal indicator bacteria, microbial risk assessment, NPS-FM 2020, water quality.

PRESENTER PROFILE

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INTRODUCTION

Population growth and urbanisation, intensifying agriculture and climate change are placing increasing pressures on water resources in Aotearoa New Zealand (NZ). Councils are required to commit significant expenditures to upgrade the Three Waters infrastructure while planning to 'give effect' to Te Mana o te Wai under the National Policy Statement - Freshwater Management 2020 (NPS-FM 2020) and maintaining/improving water quality in rivers and coastal areas. Essential to supporting this work is the identification of sources of water contamination and the apportionment of contaminant loadings to individual sources in catchments draining to recreational waters and other sensitive environments.

Microbial contamination is one of the most significant water quality management issues in NZ, particularly in urban areas (Ministry for the Environment & Stats NZ, 2019). *Escherichia coli* is used in recreational water monitoring programmes to signal an environmental pathway contaminated with faecal contamination which may contain one or more pathogens (Ministry for the Environment, 2003). Catchments draining to recreational waters commonly have multiple human (sewage) and animal (farm animals and wildlife) sources of contamination. However, testing of *E. coli* in water does not differentiate contamination from human and animal sources. In NZ, the recommended approach to ensure safe use of recreational waters is to combine *E. coli* monitoring with a sanitary survey of the catchment and, if required, faecal source tracking (FST) to confirm the sources of contamination suggested by the sanitary survey.

In this paper, we report results of a study undertaken to identify sources of microbial contamination and apportionment of microbial loadings to these sources to inform pollution reduction planning in the Nelson catchment. In the study, we used a 'satellite-to-genes' approach combining analysis of high-resolution remote-sensed and digital mapping data, long-term water quality and FST monitoring results and regression modelling to quantify contamination from point discharges and catchment diffuse sources to rivers and coastal waters.

MATERIALS AND METHODS

STUDY AREA

The Nelson catchment (13,014 ha) comprises multiple river systems and coastal streams and land uses. Freshwater inputs to the coastal area are dominated by the Maitai / Mahitai River which flows in a northwesterly direction from the Bryant Range in the upper catchment to the middle of the catchment then through the heart of the city where it meets Tasman Bay at Port Nelson/Nelson Haven (Figure 1). The Nelson Haven is a bar-built, fluvial erosion estuary of significant ecological value. The seaward boundary of the Nelson Haven is delineated by the Boulder Bank, a long and narrow strip of granodiorite pebbles, cobbles, and boulders. The Nelson Haven opens to Tasman Bay at its southwestern end with tidal flats and drainage channels extending northeast from Port Nelson.

The catchment is sub-divided into 27 Freshwater Management Units (FMUs). The land use categories within each FMU are presented in Figure 1. The total area and percentage of land use categories are listed in Table 1. In the upper catchment, the predominant land use category is native vegetation. Large areas of exotic forest occur in the Maitai and Brook Stream FMUs. Urban areas occur mostly in low lying FMUs. Akersten Street, Russel Street, Sealords, the Port, Vickerman Street, Victoria Road, Wakefield Quay, the Cliffs, and the Wood are 100% urban/residential. These drain directly into the Haven and Boulder Bank through stormwater drains and small, intermittent stream flows.

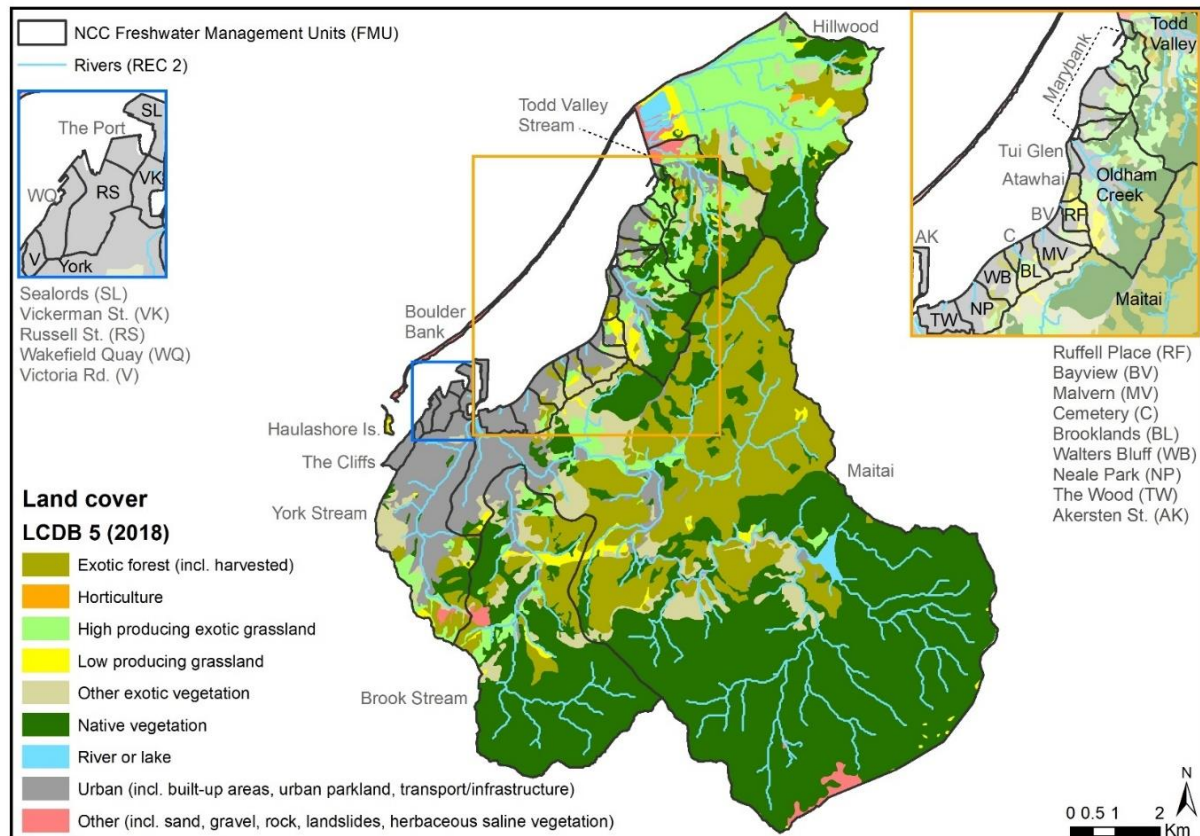


Figure 1: Land uses in the Nelson catchment. Data from Land Information New Zealand 1:50,000 topographic database LCDB5 (2018).

The public wastewater system owned and managed by Nelson City Council includes reticulation pipes, trunk mains, rising mains, pump stations, manholes, detention tanks, and the Nelson Wastewater Treatment Plant (WWTP). Wastewater from the eastern part of Nelson city (broadly represented by the two insets in Figure 1) flows to a pumping station at Neale Park and then to Nelson WWTP via an underground rising main. This rising main also collects wastewater from Atawhai, Tui Glen, and Marybank. Nelson WWTP discharges tertiary-treated effluent to Tasman Bay.

Table 1: Percentage land use categories in the 27 freshwater management units in the Nelson catchment.

FMU	Area (ha)	Percentage cover								
		EF	H	HPEG	LPG	OEV	NV	R/L	U	O
Akersten Street	14.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0
Atawhai	13.8	65.8	0.0	4.4	12.1	0.0	0.0	0.0	17.7	0.0
Bayview	23.3	0.0	0.0	10.8	2.3	47.8	0.0	0.0	39.2	0.0
Boulder Bank	46.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
Brook Stream*	1,755.1	15.3	0.0	4.1	2.5	7.2	64.5	0.0	5.5	0.9
Brooklands	40.8	4.4	0.0	14.9	18.9	33.0	0.0	0.0	28.9	0.0
Cemetery	12.2	33.2	0.0	4.7	0.0	0.0	0.0	0.0	62.1	0.0
Haulashore Is.	5.7	59.4	0.0	0.0	40.6	0.0	0.0	0.0	0.0	0.0
Hillwood Stream*	1,466.0	11.5	0.3	45.0	3.8	9.7	23.2	2.8	0.9	2.8
Maitai River*	7,454.9	28.5	0.0	1.7	0.9	5.7	57.1	0.5	4.6	0.9
Malvern	57.8	9.5	0.0	0.6	5.5	28.4	0.0	0.0	56.0	0.0
Marybank	165.3	4.1	1.4	45.9	0.0	2.5	10.8	0.4	34.8	0.1
Neale Park	63.7	14.3	0.0	11.6	0.0	8.2	0.0	0.0	66.0	0.0
Oldham Creek	360.6	9.0	0.0	17.2	4.7	9.7	43.8	0.0	15.7	0.0
Ruffell Place	27.6	2.5	0.0	14.0	43.1	9.9	0.0	0.0	30.5	0.0
Russell Street	36.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0
Sealords	8.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0
The Cliffs	28.1	0.0	0.0	0.0	0.0	0.0	0.3	0.0	99.7	0.0
The Port	8.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0
The Wood	44.7	0.0	0.0	0.0	0.0	0.0	0.0	0.1	99.9	0.0
Todd Valley*	571.5	8.6	0.6	22.1	1.2	15.6	41.3	0.1	6.5	4.2
Tui Glen	11.5	0.0	0.0	0.0	0.0	0.0	14.8	0.0	85.2	0.0
Vickerman Street	13.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0
Victoria Road	6.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0
Wakefield Quay	16.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0
Walters Bluff	52.4	15.2	0.0	2.8	1.1	20.1	0.0	0.0	60.9	0.0
York Stream*	712.1	11.9	0.0	7.7	1.2	13.0	9.0	0.0	56.0	1.2

FMU: freshwater management unit; EF: exotic forest; H: horticulture; HPEG: high producing exotic grassland; LPG: low producing grassland; OEV: other exotic vegetation; NV: native vegetation; R/L: river or lake; U: urban; O: other. Other includes sand, gravel, rock, landslides, and herbaceous saline vegetation. * Sites selected for correlation between *E. coli* concentrations and land use categories.

STUDY APPROACH

The pollution source identification and apportionment study comprised:

1. Analysis of *E. coli* monitoring data for selected river sites in the Nelson catchment during high-flow and low-flow conditions.
2. Regression modelling to estimate *E. coli* concentrations in individual FMUs based on catchment characteristics.
3. Quantification of discharge volume and *E. coli* loadings for Nelson WWTP discharge and catchment sources.
4. FST testing to identify sources of microbial contamination at sites with high *E. coli* contamination.

(1) *E. COLI* MONITORING DATA

We downloaded a database of *E. coli* concentrations monitored at 11 river sites in the Nelson catchment during the period January 2017–December 2019 from the Land, Air, Water Aotearoa website (LAWA, 2021). The dataset contains a total of 254 valid results. In the database, results reported below the limit of quantification of the method ($n=11$; 4.3%) were replaced by values determined by regression on order statistics (Helsel, 2012). The selected sites represent a range of land uses in the Nelson catchment. We computed summary statistics for these 11 sites and compared mean *E. coli* concentrations under base-flow and high-flow conditions using t-tests.

(2) DATA INPUTS TO THE REGRESSION MODEL

We used existing monitoring data to develop regression models of the relationships between base-flow/high-flow *E. coli* concentrations in rivers (dependent variables) and key catchment characteristics (independent 'predictor' variables). These models were then used to predict *E. coli* concentrations in other FMUs from their catchment characteristics. A full description of the method is given by Crowther et al. (2016). The input model parameters were:

CATCHMENT LAND USE

Land use data for the Nelson catchment were obtained from the LCDB v.5.0 developed by Landcare Research New Zealand Ltd. LCDB5 complements in theme, scale, and accuracy New Zealand's 1:50,000 topographic database and identifies 33 land use classes. In the database, land use features are described by a polygon boundary, a land use code, and a land use name at each nominal time step. The database was downloaded from LRIS Portal as ESRI Shapefile format and incorporated into a geographical information system (GIS) using ArcGIS software (LRIS 2020) for spatial analyses and mapping.

LIVESTOCK NUMBERS

Numbers of farmed livestock (beef and dairy cattle, deer, sheep) in the Nelson region collected from surveys conducted by Stats NZ and the Ministry for Primary Industries were downloaded from the Ministry for the Environment's Data Service (Ministry for the Environment, 2018).

NUMBER OF RESIDENTIAL PROPERTIES

The total number of residential properties in each FMU was derived from the 'Top of the South Maps' database (Nelson City Council & Tasman District Council, 2021). This database contains information on individual properties and the corresponding planning zone category. These data were integrated with the FMU boundaries for the Maitai catchment.

BASE FLOW INDEX

A fixed Base Flow Index of 0.4 was used (Singh et al., 2019).

(3) DISCHARGE AND E. COLI BUDGETS

RAINFALL AND RIVER FLOWS

Daily flow data (average in m³/s) for the River Maitai at Forks and Avon Terrace for the period January 2017–April 2020 were supplied by Nelson City Council for this study. Total daily rainfall data (mm) for two gauging stations in the catchment (Forks and Founders) for the same time period were also supplied by Council. Raw data were supplied as csv. files along with data quality reports as pdf files.

BUDGET CALCULATIONS

The flow records were split into base-flow and high-flow conditions in response to rainfall by analysis of hydrographs. Discharge and *E. coli* budgets were calculated using methods described by Stapleton et al. (2011).

(4) FAECAL SOURCE TRACKING TESTING

During the period October 2014–December 2017, 34 water samples were collected on seven occasions and tested for FST markers. Details of the FST methods can be found in Kirs et al. (2011) and Cornelisen et al. (2012).

RESULTS

***E. COLI* CONCENTRATIONS**

Summary statistics of *E. coli* concentrations at the 11 sites under base-flow and high-flow conditions are presented in Table 2. Overall, the highest concentrations under base- and high-flow conditions were found at Hillwood Stream which drains the largest area of high producing grassland in the catchment. The lowest concentrations were found at Brook Stream (Motor Camp) which drains a large area of native and exotic vegetation (Figure 1; Tables 1, 2). The highest maxima were found at York Stream.

Except for Hillwood Stream and Todd Valley Stream, geometric mean concentrations were higher under high- than base-flow conditions. However, results of t-tests indicated that only in the Maitai at Riverside and Brook Stream at Burn Place the elevations in mean bacterial concentrations are significant (Table 2). The monitoring results also suggest a gradient of contamination in the Maitai River with the lowest concentrations at the upland sites (Groom Road; South Branch) and the highest at the lowland site (Riverside).

Analysis of *E. coli* results as a function of broad land uses indicated higher *E. coli* concentrations in rural FMUs than in urban and forested FMUs (Figure 2). Differences in median concentrations between the three land use categories are

statistically significant (MANOVA; $p < 0.001$). Median *E. coli* concentrations are also higher during high-flows than during base-flows in the three land use categories, but the differences are not statistically significant. The similar sizes of the top and bottom halves and similar lengths of the whiskers in the boxplots in Figure 2 also show similar *E. coli* distributions around median values.

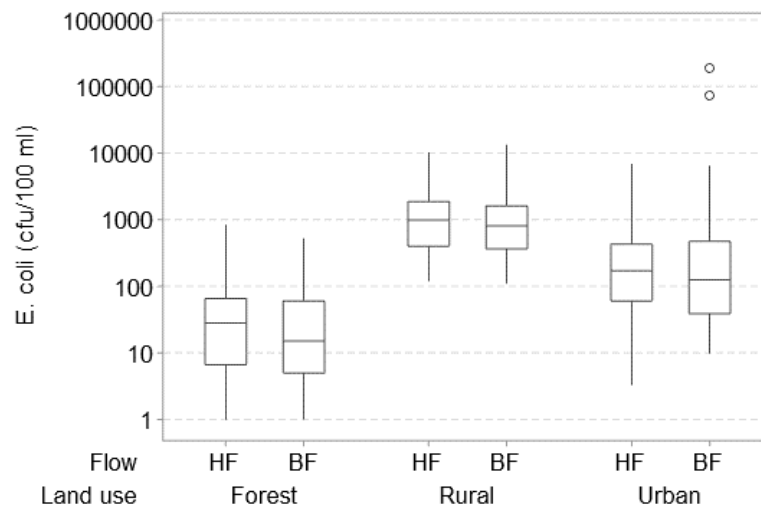


Figure 2: Boxplots of E. coli at 11 riverine sites grouped into land use categories in the Nelson catchment during base-flow and high-flow conditions, 2017–2019.

Table 2: Summary statistics of *E. coli* concentrations in freshwater at 11 sites in the Nelson catchment.

Site name	Base-flow							High-flow						
	n	Min.	Max.	GM	SD	Lower 95% CI	Upper 95% CI	n	Min.	Max.	GM	SD	Lower 95% CI	Upper 95% CI
Hillwood at Glen Road	10	120	10,000	1,232	0.606	458	2,581	24	110	13,100	1,200	0.532	662	1,764
Todd Valley at SH6	13	260	9,000	950	0.531	445	1,681	22	150	6,400	697	0.371	463	944
York at Waimea Road	16	18	73,000	728	0.899	189	1,436	18	120	190,000	1,116	0.771	409	2,108
Groom at Maitai Confluence	6	56	320	95	0.303	52	160	9	30	820	149	0.497	63	281
Brook at Manuka Street	16	10	460	68	0.468	35	100	19	31	360	129	0.286	91	165
Maitai at Riverside	16	15	220	54	0.402	31	77	19	3	600	78*	0.656	29	111
Sharland at Maitai Confluence	15	5	480	27	0.564	11	42	20	2	270	34	0.583	13	42
Brook at Burn Place	16	3	140	25	0.477	12	34	19	8	220	55*	0.382	34	74
Maitai at Groom Road	15	2	150	10	0.470	4	13	20	2	260	22	0.606	9	30
Maitai South Branch at Intake	14	<1.6	70	8	0.524	3	11	19	<1.6	1.6	14	0.732	3	15
Brook at Motor Camp	14	<1	60	5	0.505	2	6	17	<1	120	7	0.596	2	9

n - number of samples; Min. - minimum; Max. - maximum; GM - geometric mean; SD - standard deviation of log₁₀-transformed results; lower 95% CI - lower 95% confidence level; upper 95% CI - upper 95% confidence level. * Statistically significant elevation in the geometric mean concentration at high flow compared with that at base flow (t-test; $p < 0.05$).

PREDICTED *E. COLI* CONCENTRATIONS IN FRESHWATER MANAGEMENT UNITS

Mean *E. coli* concentrations predicted by the regression model are presented in Figure 3. In all FMUs, the differences between mean base-flow and high-flow concentrations are $< 1\log_{10}$ which agrees with the rivers water monitoring data presented in Table 2. The largest difference ($0.6\log_{10}$) was predicted for Victoria Road, an urban FMU in the lower catchment. Victoria Road also had the highest predicted mean *E. coli* concentration during base-flow and high-flow conditions. The model also predicted relatively high concentrations at York Stream which is also consistent with the water quality monitoring data. However, the results also suggest that the model under-predicted *E. coli* contamination at Todd Valley and Hillwood, possibly because of the effect of sources not considered in our model (e.g., septic tank discharges).

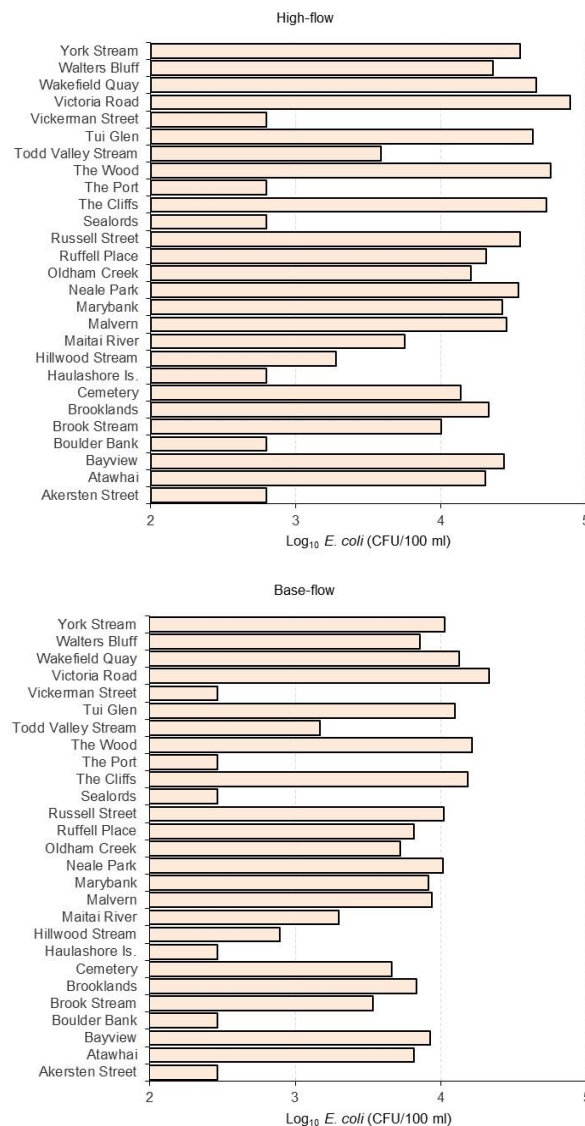


Figure 3: Predicted *E. coli* concentrations in freshwater management units in the Nelson catchment.

DISCHARGE AND *E. COLI* BUDGETS

The river discharge and *E. coli* budgets in Figure 4 below compare the relative proportions of the Maitai River and the Nelson WWTP discharge to the total discharge from the catchment. The budget for the Maitai River describes the *E. coli* loading from the single largest FMU in the catchment. These calculations are based on *E. coli* concentrations measured at Riverside and include the combined inputs from all point-source discharges and diffuse sources upstream of the tidal limit.

The Maitai River was estimated to contribute $4.2 \times 10^4 \text{ m}^3/\text{day}$ and $2.6 \times 10^5 \text{ m}^3/\text{day}$ (on average) to Tasman Bay during base-flow and high-flow conditions, respectively. The base-flow and high-flow river discharge values used in these calculations were $0.49 \text{ m}^3/\text{s}$ and $3 \text{ m}^3/\text{s}$, respectively. The discharge budgets show that the Maitai contributes much larger flow volumes to the bay than the Nelson WWTP discharge. This discharge was estimated to represent only 4% of the volume during high-flow conditions. During base-flows, *E. coli* loadings from the Maitai River contribute 21% of the total catchment loading. However, during high-flow, the contribution of the river increases to 61%.

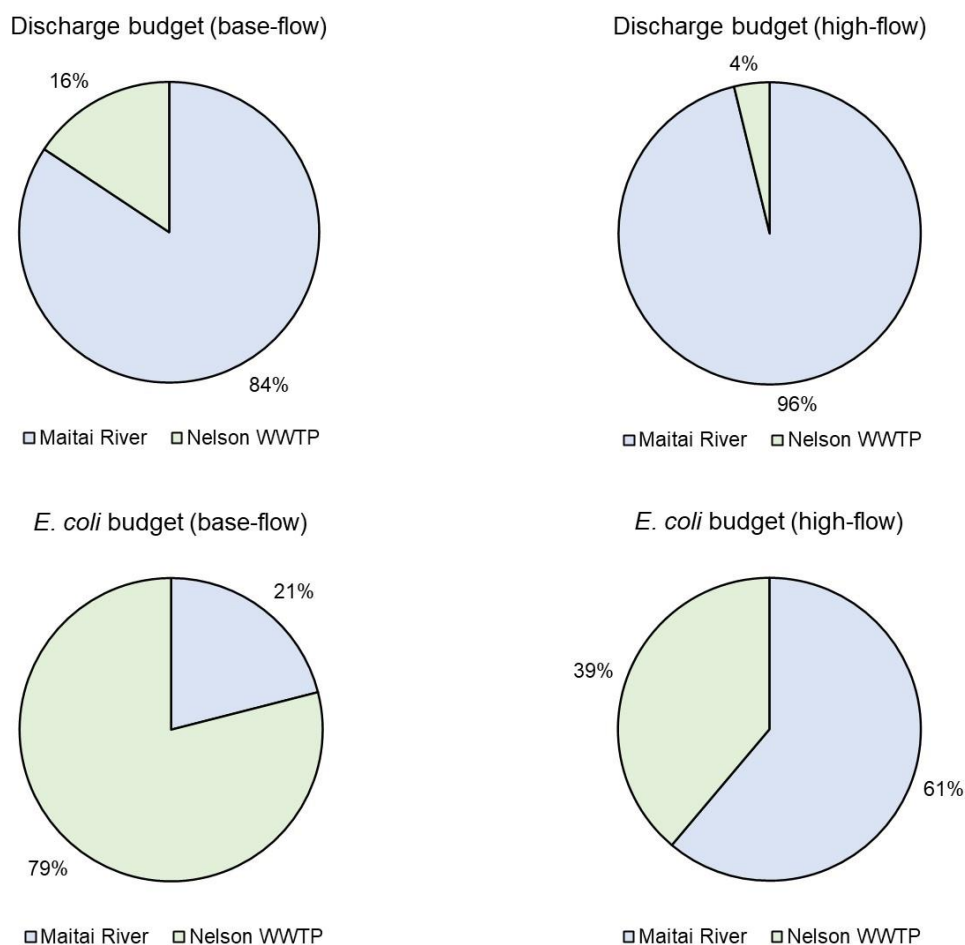


Figure 4: Estimated discharge and *E. coli* budgets from the Maitai River and Nelson WWTP to Tasman Bay during base-flow and high-flow conditions.

CORRELATIONS BETWEEN *E. COLI* AND LAND USE

The results of correlation tests indicate a moderate negative correlation between both base-flow/high-flow *E. coli* concentrations, and forest/exotic and native vegetation (Table 3). Low positive correlations were found between bacterial concentrations and high producing exotic grassland, horticulture, urban and 'Other' land use categories during both base-flow and high-flow.

Although the total human resident population (c. 28,190) is higher than the total number of farm animals (c. 12,773), human sewage is treated at tertiary level and discharged to the coastal marine environment. Therefore, the *E. coli* flux in the rivers can be assumed to originate primarily from livestock production areas. *E. coli* contamination in lowland urban areas (the greater number of FMUs with high *E. coli* predicted by the regression model) could be associated with inflow and infiltration or misconnected pipes.

Table 3: Results of Pearson correlation tests performed to describe the relationships between log₁₀E. coli concentrations and percentage of land use categories.

Independent variables	Dependent variable (log ₁₀ <i>E. coli</i>)	
	Base flow (n=71)	High flow (n=102)
	<i>r</i>	<i>r</i>
Forest, exotic, and native vegetation (FENV) ¹	-0.618*	-0.640*
Horticulture (H)	0.450*	0.349*
High producing exotic grassland (HPEG)	0.523*	0.486*
Low producing grassland (LPG)	0.137	0.241*
River or lake (R/L)	0.246*	0.291*
Urban (U)	0.264*	0.243*
Other (O)	0.504*	0.404*

¹ Exotic forest, other exotic vegetation and native vegetation categories combined.
Statistical significance of *r* values: **p*<0.05. Other includes sand, gravel, rock, landslides, and herbaceous saline vegetation.

The correlations obtained with 'Other' land uses suggests diffuse inputs of microbial contamination from avifauna in lowland coastal sites. There is no special significance in the correlation results with horticulture land because of its small area relative to the total area of the catchment and that they are represented by the same catchment outlet as grassland areas.

FAECAL SOURCE TRACKING RESULTS

Samples collected in the upper Maitai River at confluence with the Brook Stream and at Aratuna Bridge were positive for the duck marker (Table 3). In the lower Maitai River, samples collected at Collingwood Bridge were positive for duck, gull, and human markers. One sample taken at Collingwood Bridge was positive for the ruminant, duck, gull, human, dog, and possum markers. Samples taken in the York Stream were positive for the universal, duck, human and possum markers. The presence of both bird markers in the Maitai River is consistent with the frequent observation of seagulls and ducks in the area of the Maitai River that was sampled.

The human *Bacteroidales* marker was detected in 12 samples suggesting contamination of human origin in the lower reaches of the Maitai River. However, the results are not fully conclusive because of the potential for cross-reactivity between this marker and that of other animals such as possums (Kirs et al. 2011).

Table 3: Results of faecal source tracking markers in water samples taken from sites in the Nelson catchment.

Sampling site	Marker									
	A	B	C	D	E	F	G	H	I	J
Brook Stream		-	-	-	-		-			
Maitai River (M1)		-	+	-	-		-			
Maitai River (M2)		-	+	-	-		-			
Maitai River (M3)		-	+	+	-		-			
Maitai River (M4)		-	+	+	+		-			
Saltwater Creek		-	-	-	+		-			
Collingwood St Bridge		+	+	+	+		+	+	-	
Collingwood St Bridge (CB1)			+		+		-			
Collingwood St Bridge (CB2)			+		-		+			
Collingwood St Bridge (CB-3)			+		+		+			
Collingwood St Bridge (CB-4)			+		+		-			
Collingwood St Bridge (BW)			+		+		-			
Collingwood St Bridge (CB1a)			-		-		-			
Collingwood St bridge (CB5)			+		-		-			
Collingwood St bridge (CB6)			+		-		-			
York Stream (YS1)	+	+	+	-	+	-	+	+		-
York Stream (YS2)	+	+	+	-	+	-	+	+		-
York Stream (YS3)	+	+	+	-	+	-	-	+		-
York Stream (YS4)	+	+	+	-	+	-	+	+		-
York Stream (YS5)	+	+	+	-	+	-	-	+		-

-not detected; +(orange)-detected; +(gold)-detected, but faint signal; blank cells-not tested. A-Universal (faecal) *Bacteroidales* marker (Bac32); B - Ruminant *Bacteroidales* marker (Bac128); C - Duck marker (DE2); D - *Catellibacillus* marker; E - Human *Bacteroidales* marker (Bac183); F - Human *Methanobrevibacter smithii* marker (nifH); G - Dog *Bacteroidales*; H - Possum *Bacteroidales*; I - Sheep mitochondrial cytochrome b gene; J - Pig *Bacteroidales*.

DISCUSSION AND CONCLUSIONS

This paper reports results of a 'satellite-to-genes' study undertaken to identify and apportion microbial contamination from catchment diffuse sources and point discharges to rivers and coastal waters in Nelson. In the study area, the largest input of human contamination to coastal waters is associated with a single WWTP discharge while diffuse contamination to rivers/streams originates predominantly from dairy, beef and sheep farming and wildlife in the wider catchment.

Microbial water quality in rivers and streams is generally good in the middle/upper reaches of the catchment, where large areas are covered by exotic forest and native vegetation. Detrimental effects of contamination of human and animal origins on stream water quality are evident in parts of lower catchment.

The regression model predicted higher *E. coli* contamination in predominantly urban FMUs in the lower catchment than in larger FMUs with greater diversity of land uses. However, the differences between mean bacterial concentrations in base-flow and those in high-flow conditions were very small ($< 1\log_{10}$) presumably because of the very low number of rainfall-dependent discharges in the catchment.

Long-term water quality monitoring data provided information on sites mostly affected by *E. coli* contamination. The highest mean *E. coli* concentrations during both base-flow and high-flow conditions were found at Hillwood Stream and Todd Valley. These are large FMUs with low number of residential properties and drain large areas of high producing grassland. Consistent with these results is the significant correlation obtained between *E. coli* and areas of high producing exotic grassland although urban land was also significantly associated with bacterial contamination (see below discussion on York Stream).

We suggest that measures to reduce microbial contamination in Hillwood Stream and Todd Valley should target identification of 'direct' contamination pathways (e.g., sites where faecal matter is deposited directly into waterways) and 'indirect' pathways such as the transport of faecal matter via surface runoff and sub-surface seepage or drainage. Work has been undertaken to prevent livestock access to streams, riparian planting, and community education activities.

Indirect transport pathways are very dependent upon rainfall events. However, we found no significant elevations in mean *E. coli* concentrations in high-flow conditions at most sites suggesting that direct contamination pathways could be more important in this catchment. It should be noted that there is no direct hydrological connectivity between Hillwood Stream/Todd Valley FMU outlets and the coastal marine environment because of tidal flood gates and the Boulder Bank. This is relevant because the main pathways of microbial contamination to tidal waters are the Maitai River, urban streams to The Haven and the Nelson WWTP discharge. Budget calculations indicated that while the Maitai River contributes the largest discharge volume to tidal waters during all flow conditions, the *E. coli* loading from the Maitai only dominates during high-flow conditions.

High *E. coli* concentrations were also found at York Stream. The FST results indicated the presence of duck, human and possum markers in the water samples indicating multiple sources of microbial contamination at this site. The York FMU has been subject to sewerage infrastructure improvements and investigations to

reduce inflow and infiltration and elimination of misconnections to improve water quality in the river and tributaries. Investigations comprising intensive *E. coli* monitoring and dye tracing studies (Photograph 1) have also been undertaken in the lower Matai at Collingwood Bridge where a substantial number of samples were positive for the human Bacteroidales marker.



Photograph 1: Dye tracing test to identify wastewater leakage into the stormwater system near Collingwood Bridge.

To conclude, the satellite-to-genes method helped identify appropriate measures to reduce microbial contamination in areas of the catchment where they are most needed. The availability of high resolution remote-sensed and digital mapping data, and long-term water quality and FST monitoring results enabled the development of models to predict *E. coli* contamination at different scales and for different river flow conditions. This study provides important evidence to assist Nelson City Council in achieving the target water quality objectives for urban waterways and other obligations under the NPS-FM 2020.

ACKNOWLEDGEMENTS

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REFERENCES

Cornelisen, C.D., Kirs, M., Gilpin, B., and Scholes, P. (2012) Microbial Source Tracking (MST) Tools for Water Quality Monitoring. Cawthron Report No. 2047 prepared for Regional Councils and the Coastal Special Interest Group. 28 p. plus appendices.

Crowther, J., Kay, D., Anthony, S., Gooday, R., Burgess, C., and Douglass, J. (2016) Developing a methodology for screening and identifying potential sources of bacteria to improve bathing, shellfish and drinking water quality. Phase 1: to design and scope suitable methodology, CRW2015_01.

Helsel, D.R. (2012). Statistics for Censored Environmental Data Using Minitab® and R, Second Edition. John Wiley & Sons, Inc.

Kirs, M., Harwood, V.J., Fidler, A.E., Gillespie, P.A., Fyfe, W.R., Blackwood, A.D., and Cornelisen, C.D. (2011). 'Source Tracking Faecal Contamination in an Urbanized and a Rural Waterway in the Nelson-Tasman region, New Zealand. New Zealand Journal of Marine and Freshwater Research, 45, 1, 43–58.

LAWA (2021). <https://www.lawa.org.nz/>.

LRIS (2020). LCDB v5.0 - Land Cover Database version 5.0, Mainland New Zealand. <https://lris.scinfo.org.nz/layer/104400-lcdb-v50-land-cover-database-version-50-mainland-new-zealand/>.

Ministry for the Environment (2003) Microbiological Water Quality Guidelines for Marine and Freshwater Recreational Areas.
<https://environment.govt.nz/assets/Publications/Files/microbiological-quality-jun03.pdf>.

Ministry for the Environment (2018) <https://data.mfe.govt.nz/table/95344-livestock-numbers-19942017/>.

Ministry for the Environment, and Stats NZ (2019) New Zealand's Environmental Reporting Series: Environment Aotearoa 2019.
<https://environment.govt.nz/assets/Publications/Files/environment-aotearoa-2019.pdf>.

Nelson City Council, and Tasman District Council (2021).
<https://www.topofthesouthmaps.co.nz/app/>.

Singh, S.K., Pahlow, M., Booker, D.J., Shankar, U., and Chamorro, A. (2019) Towards Baseflow Index Characterization at National Scale in New Zealand. *Journal of Hydrology*, 568, 646–657.

Stapleton, C.M., Kay, D., Magill, S.H., Wyer, M.D., Davies, C., Watkins, J., Kay, C., McDonald, A.T., and Crowther, J. (2011) Quantitative Microbial Source Apportionment as a Tool in Aiding the Identification of Microbial Risk Factors in Shellfish Harvesting Waters: the Loch Etive Case Study. *Aquaculture Research*, 42, 1–20.