

Responses to the review of the original version of this report by Joanne Clapcott and Roger Young (Cawthron) are provided below. Our responses are indexed by the number of each of the review comments.

Ton Snelder and Susie Wood, 15 September 2016.

1. Report title has been altered to “Strategic assessment of New Zealand’s freshwaters for recreational use: a human health perspective”.
2. Relationships between *E.coli* and flow and the proportion of samples exceedances of threshold by month were explored to show that the annual statistics (i.e. the median and 95th percentile *E.coli* concentrations and PercGT260 and PercGT540) do not obscure strategically important temporal patterns. The reviewers pointed out that there were trends in the data associated with exceedances and that no statistical tests had been performed. We responded to this by better explaining the purpose of these analyses. Text has been altered accordingly in Sections 3.1.1. We have added to the discussion of these results in Section 6.1 and discussed our findings in light of findings by Davies-Colley (2013), McBride (2011) and Wilkinson et al. (2011). These studies have shown that the relationships between *E.coli* and flow are complex (e.g. characterised by hysteresis). This strengthens our conclusion that concentrations of *E.coli* in rivers, are not strongly related to flow or time of year. Therefore, accounting for flow or time of the year would not strongly influence conclusions about broad scale patterns drawn from our study. We have quantified the samples that had measured compared to predicted flow measurements in Section 2.1.
3. We added Kruskal-Wallis tests to test for differences in site exceedances by month. We slightly altered the definition of the exceedances in the dataset to the number of samples exceeding the threshold as a percentage of the total samples for each month. Text has been altered accordingly in Sections 3.1.1 and 4.1.3.
4. We do not think it is appropriate to discuss the at-site errors at this level of detail in the report because the assessment is strategic. We have been clear that the at-site predictions are uncertain and actual data should be used in preference to the modelled predictions at this scale. We have endorsed the use of the predicted regional to national scale patterns in *E.coli* in rivers and cyanobacterial biovolume in lakes for strategic purposes such as quantifying the proportion of New Zealand’s rivers and lakes that have high and low human health risks and identifying areas of most concern. However, we acknowledge the point the reviewers made about the magnitude of the at site errors and their distributions. The uncertainties of predictions made for individual river segments or lakes are expressed by the RMSD values (tables 6 and 8 of report). Because the *E.coli* variables PercGT260 and PercGT540 were not transformed prior to model fitting, the mean statistical error (i.e. uncertainty) associated with these estimates is plus or minus the reported RMSD values. Where the modelled variables were log₁₀-transformed prior to model fitting (the median and Q95 *E.coli* models and all lake water quality models), the reported RMSD have been reported in in the log₁₀-transformed space. The equation below is required to express the reported RSMD values in the original units.

$$\text{Mean Error} = 10^{[\log_{10}(x) \pm \text{RMSD}]}$$

where x is the estimated value in the original units, and RMSD is the reported model error. The mean error for the log₁₀-transformed variables, when expressed in the original units of the variables, is asymmetric and the values vary in proportion to the predicted water quality value (Figure 1).

Figure1 demonstrates the practical limitations associated with the predicted values for median *E.coli*. The three red horizontal lines indicate the NPS-FM thresholds for the secondary contact bands at 260, 540 and 1000 *E.coli* 100 mL⁻¹. The plot indicates that the mean uncertainties are large compared to the band thresholds. For example, the error associated with a predicted value of 540 *E.coli* 100 mL⁻¹ extends above the 1000 and below 260 *E.coli* 100 mL⁻¹ indicating that the true value could lie in any of three NPS-FM bands.

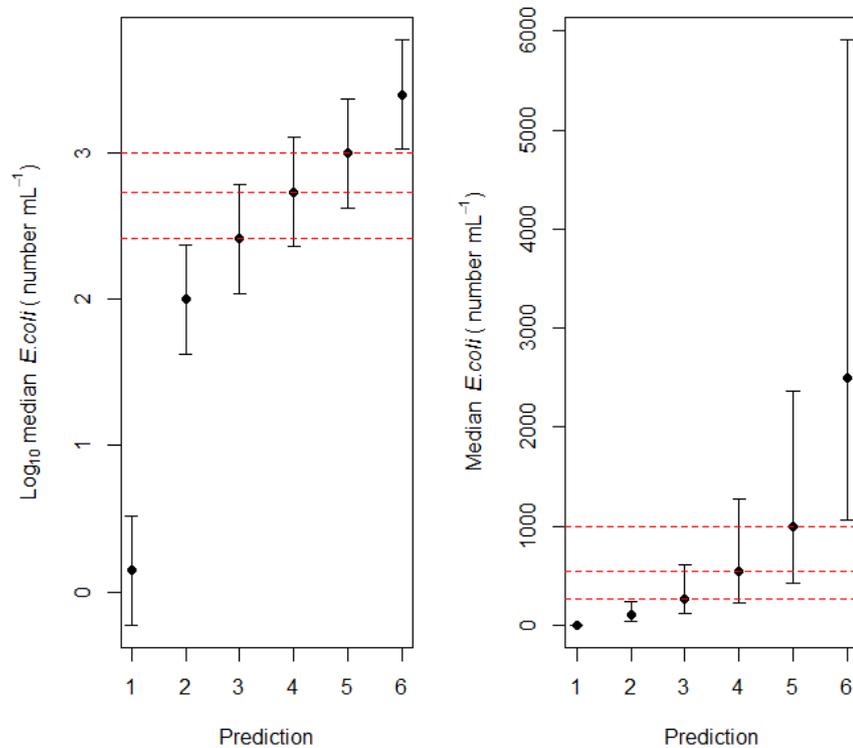


Figure 1. Transformed and back-transformed model predictions and associated error.

Predictions are made for six sites that span a range of predicted values of median percentile of Escherichia coli from the lowest predicted value to 2500 *E.coli* 100 mL⁻¹. The first graph shows the transformed predictions and the uniform mean error, which is the reported RMSD. The second graph shows the back transformed predictions and associated error, which are asymmetric and depend on the absolute value of the prediction. The three red horizontal lines indicate the NPS-FM thresholds for the secondary contact bands at 260, 540 and 1000 *E.coli* 100 mL⁻¹.

5. We have added commentary to Section 4.2.3 to acknowledge under-representation of low values of usAvTWarm and usAnRainVar. We have pointed out this reflects the lack of sites on the southern parts of the West Coast of the South Island in particular, but also in high altitude locations generally. We have also added further commentary to Section 6.2 that cautions that prediction error in poorly represented environments may be larger than the quantified model uncertainties. The reviewers suggested that “high levels of *E. coli* predicted on the West Coast are likely due to environmental gradient present rather than actual high values”. We agree that there was under-representation of sites with low values of catchment average summer air temperature (usAvTWarm) and catchment average variation of annual rainfall (usAnRainVar) and that these environmental gradients that were important in the *E.coli* models. However, we undertook some additional analysis and do not think the predictions are inconsistent with the observations. The reviewers concerns are

associated with predicted 95th percentile values for *E.coli* for the West Coast region. Predicted median *E.coli* values on the West Coast of the South Island (Figure 2) are low compared to NPS-FM secondary contact thresholds of 260 and 540 *E.coli* 100 mL⁻¹. The predicted median values for the West Coast region are also low compared to other regions where values above 500 *E.coli* 100 mL⁻¹ are common (see Figure 10 of report). However, predicted 95th percentile values for *E.coli* for the West Coast region (Figure 3) were generally higher than the NPS-FM primary contact thresholds of 260 and 540 *E.coli* 100 mL⁻¹ (applied to the 95th percentile). The reviewer comments reflect an apparent inconsistency of the 95th percentile values with the median values and with the dominance of largely undisturbed indigenous vegetation cover and expectation of high water quality on the West Coast of the South Island.

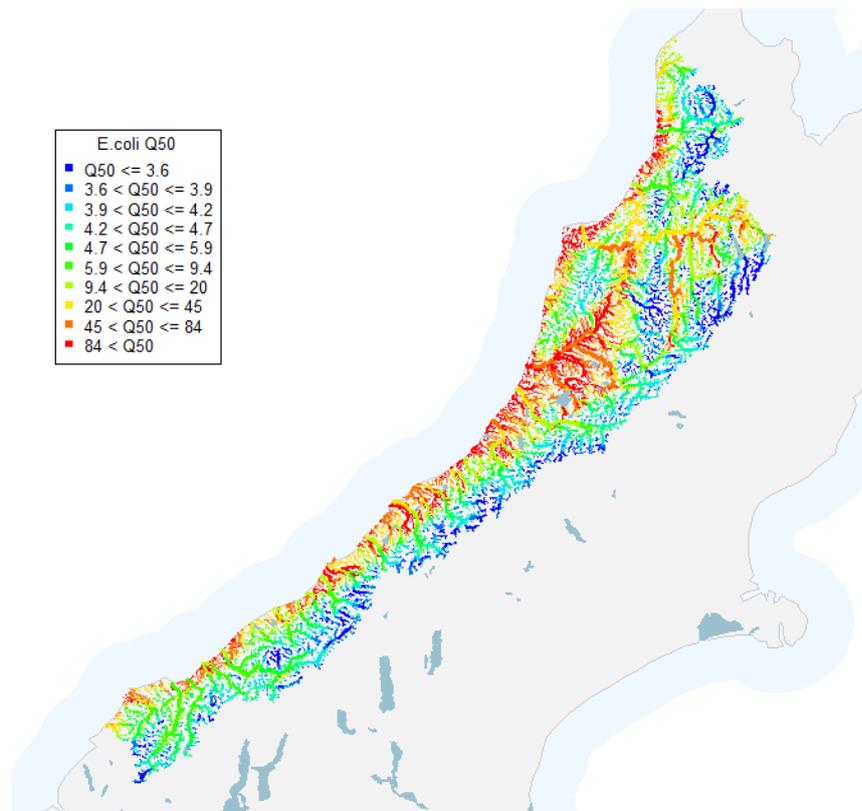


Figure 2. Predicted median *Escherichia coli* values for the West Coast region (South Island). The map shows all stream orders.

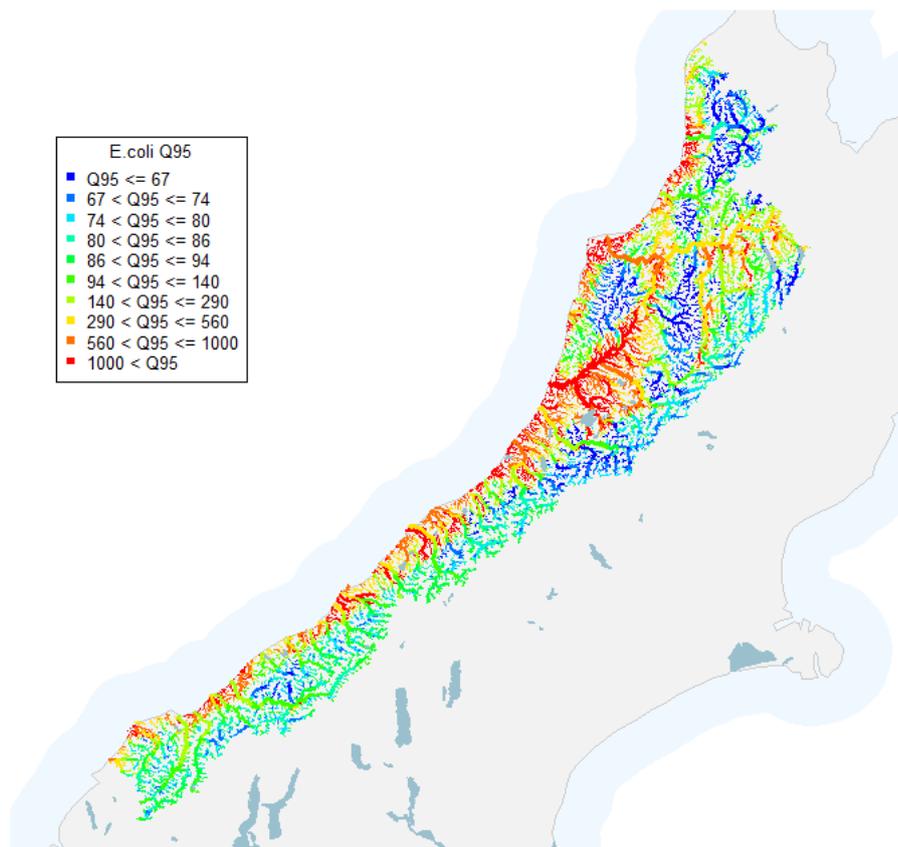


Figure 3. Predicted 95th percentile Escherichia coli values for the West Coast region (South Island). The map shows all stream orders.

To further investigate this, we compared the distributions of observed median and 95th percentile values on the West Coast with all other sites across New Zealand (Figure 4). In general, median values were low compared to NPS-FM *E. coli* (Figure 4-left panel) and our modelled predictions for this region were consistent with this (Figure 2). However, the observed 95th percentile values were generally higher than the NPS-FM *E. coli* primary contact thresholds of 260 and 540 *E.coli* 100 mL⁻¹ (Figure 4-right panel), and our modelled predictions for this region were consistent with this (Figure 3).

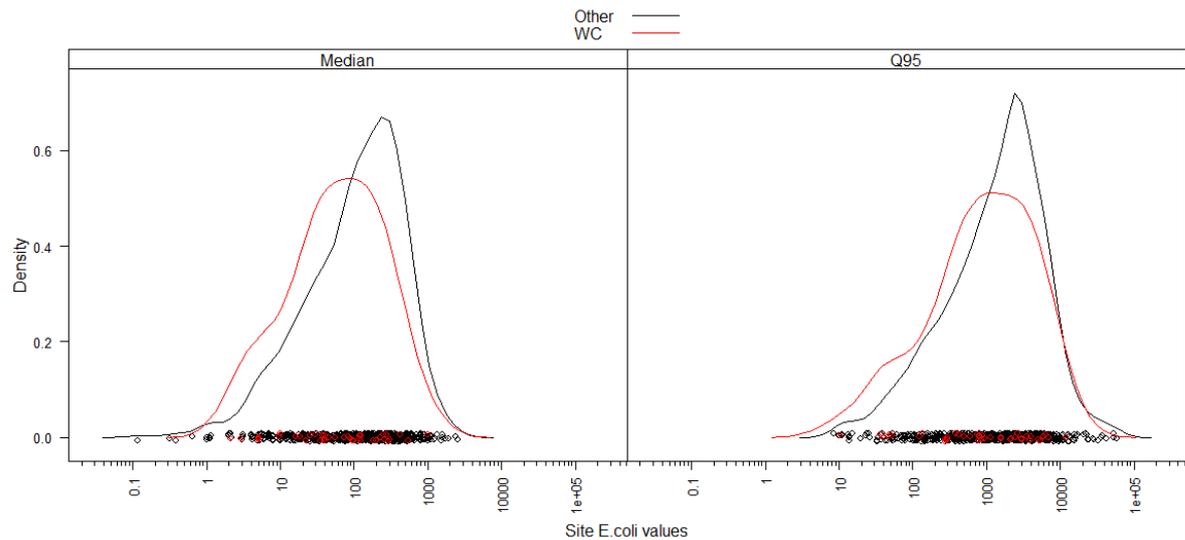


Figure 4. Median (left), 95th percentile (right) for observed *Escherichia coli* concentrations in West Coast (South Island) and all other sites in New Zealand. The horizontal line of points at the base of the plot represent the individual sites. Note sites on the West Coast cover much of the national range of both the median and 95th percentile values.

Finally, we inspected plots of the predicted versus observed values (Figure 5). This confirms the model predictions are as accurate for the West Coast region as elsewhere (i.e. the distribution of errors is similar and within the national distribution). We conclude that predictions of *E.coli* on the West Coast are reasonable and as reliable as elsewhere in the country.

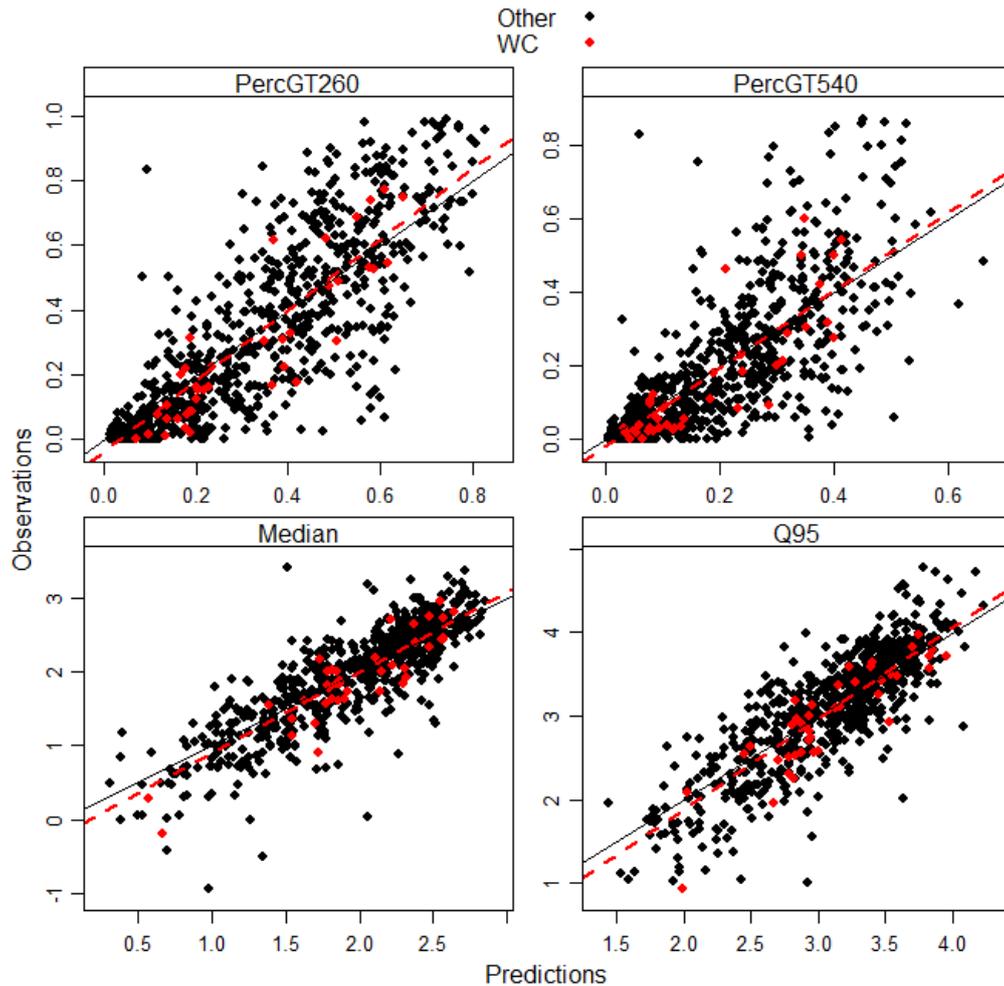


Figure 5. Comparison of observed *Escherichia coli* descriptor variable versus values predicted by the Random Forest models. The plots show the sites from the West Coast (WC) region as red points and from all other regions (Other) as black.

6. In consultation with MfE, we have avoided making any assessments of the state of rivers (*E. coli*) or lakes (cyanobacteria) with respect to NPS-FM attribute thresholds in the report. MfE will use the predictions as the base information for assessments that will be presented in other publications. This report is confined to how the analyses were performed and the output. We have removed the section on the proportion of lakes in NPS-FM attribute bands.
7. This point has been included in Section 6.2, which discusses the *E. coli* predictions.
8. We agree that *E. coli* also pose a health risk in lakes, however, current lake datasets are temporally and spatially limited preventing their inclusion in the analysis undertaken in this study. We have now acknowledged this in the executive summary, project approach and discussion sections. We recommend that future work should focus on assembling these datasets and assessing whether a more detailed analysis is feasible.
9. We have provided a more detailed rationale for the lake modelling including the reason for modelling five variables represented in the SOE data in Sections 2.2 and 3.1.2. We have removed the four irrelevant lake variables (DRP, NO₃-N, DO_{bottom} and NH₄-N).
 - An n_≥7 was chosen as a value that based on our expert judgement maintained as many datasets as possible while avoiding biases caused by low or only targeted (e.g. during a bloom event) sampling effort. We have now included this detail in Section 2.2.

-We agree that there were several places in the report that inferred that the cyanobacterial biovolume data was modelled, which is not correct. The modelled water quality data was used as 'new data' in the cyanobacterial biovolume multiple regression equation. The outputs of this provided estimated cyanobacterial biovolumes for all lakes. We have now clarified this in all relevant places in the report.

10. We have added further discussion of the potentially correlative, rather than causative, relationships between predictors and *E.coli* that are shown in the partial plots in Section 4.2.2.
11. We have clarified that censored values are those that were below the detection limit.
12. This has been reworded.
13. We agree that this paragraph was confusing. The main aim of this paragraph was to acknowledge that some of the cyanobacterial biovolume datasets are biased towards summer values which may have resulted in a slight over estimation of biovolumes. We have now rephrased and simplified this paragraph.

Minor editorial issues:

All minor editorial issues have been corrected as suggested.