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**Freshwater fish predictive modelling for
bioassessment;**

**A scoping study into fish bioassessment models as national indicators
in New Zealand**

**Mike Joy
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EXECUTIVE SUMMARY

The match between the biota expected at a site in the absence of impacts and what is found there when testing is a robust and popular bioassessment method in many countries worldwide.

The difference between the assemblage found and that expected is measured as the observed/expected ratio and is the basis of the RIVPACS¹ approach initially developed in the United Kingdom using invertebrates.

When the observed and expected assemblages match the O/E score is 1. An O/E score less than 1 means some impact and more than 1 suggests better than expected biota.

This scoping trial of the feasibility of a fish predictive RIVPACS type bioassessment using the New Zealand Freshwater Fish Database (NZFFDB) and predictive models of fish distribution from the Freshwater Ecosystems of New Zealand² (FENZ) was not successful.

This study revealed that the predictive bioassessment approach in this case failed mainly due to the lack of suitable predictive models for this not because of problems with the predictive bioassessment approach.

The problem with the available FENZ fish predictions used in this study is that they were developed to predict how the fish assemblages are today allowing for many land-use impacts rather than the predictions of the assemblages that would be expected in the absence of impacts crucial to RIVPACS type models.

Regional O/E fish models have been successfully applied with fish in New Zealand by taking all the steps in the RIVPACS process but have generally not been taken up by resource managers.

To validate the data used in this study an Index of Biotic Integrity (IBI) was successfully applied to the observed (NZFFDB) and predicted fish assemblages (FENZ) and revealed their suitability for bioassessment.

However, an assessment of the observed/expected IBI results was, like the fish community O/E unsuccessful, again because the predictions are for actual rather than expected fish communities.

¹ This is the River Invertebrate Prediction and Classification System, first developed in the United Kingdom in 1984/

² <http://www.doc.govt.nz/conservation/land-and-freshwater/freshwater/freshwater-ecosystems-of-new-zealand/>

The conclusions from this study are that predictive bioassessment models have great potential for use in New Zealand but there are no shortcuts. Consequently, new predictive models must be produced based on reference sites and using habitat descriptors that are least influenced by human impacts.

In the meantime the IBI is a useful measure of the biotic integrity of freshwater in New Zealand, and improvements in sampling and metrics to take into account abundance and size/age classes show that the IBI can be updated and the outputs precision improved.

INTRODUCTION

FISH IN BIOASSESSMENT

Freshwater biological communities are sensitive indicators of the relative health of their ecosystems and the surrounding catchment (Fausch et al. 1990, McCormick et al. 2000). The relationship between the biological, physical and chemical components of ecosystems is the basis of biological monitoring. Fish are potentially effective indicators of the condition of aquatic ecosystems, because different species exhibit diverse ecological, morphological and behavioural adaptations to their natural habitat (Karr et al. 1986, Fausch et al. 1990). Fish communities integrate the ecological processes of streams across both temporal and spatial scales (Karr et al. 1986, Fausch et al. 1990), therefore they can be useful indicators of aquatic degradation (Karr 1981, Karr 1991b, a). Furthermore, because fish are a visible part of stream biological integrity, they represent a measure of stream quality easily and intuitively understood by the public (McCormick et al. 2000).

Despite this potential however, until recently fish were seldom used in biological assessment in New Zealand because of the overwhelming influence of altitude and distance from the sea on fish distribution (Joy et al. 2000, McDowall and Taylor 2000, Joy and Death 2001). The development in 2004 of a fish index of biotic integrity (IBI) (Joy and Death 2004a) resulted in national and regional freshwater fish integrity analyses in relation to land use and temporal trends (Joy 2009), and many regional councils (Southland, Tasman, Waikato, Auckland, Hawkes Bay and Wellington) now have regional IBI models for use in state of the environment and other monitoring e.g. (Joy 2005b, 2008).

BACKGROUND TO SCOPING STUDY

This assessment was undertaken to investigate the feasibility of using freshwater fish predictive models in national bioassessment in New Zealand. Although regional predictive bioassessment models have been developed (Joy and Death 2000, 2002b, a) they have rarely been used in bioassessment and being regional are not suitable for national assessment. The main objective of this scoping study was to see if the existing extensive database of fish distribution (the New Zealand freshwater fish database) could be combined with an existing national predictive model of fish distribution (Leathwick et al. 2008a) to give a baseline measure of fish communities at a national scale.

This study was undertaken with the recognition that many of the requirements of the predictive bioassessment models developed and used overseas would not be met, but given the lack of resources and time to address these issues an assessment of its potential use could be made with the existing data. The limitations included the lack of 'reference site' (Kennard et al. 2006, Robertson et al. 2006, Wang et al. 2008) data and the fact that the predictions used are predictions for how the communities are now including impacts not how they would be in the absence of those impacts.

EXPECTATIONS OF SCOPING STUDY

The advantage of using predictions that include all sites (not just reference sites) and human-influenced variables is that the predictions are more accurate, as there is always a trade-off between accuracy of predictive models and limiting predictions by removing sites and variables. The hypothesis in this case was that using the large number of sites in the database the O/E scores would represent baseline conditions and that the upper and lower ends of the distribution of scores would represent extremely good and extremely bad sites respectively. It was anticipated that the upper end of the range of O/E score would include many of the sites in native vegetation and not many sites in developed catchments as a validation of the method.

PREDICTIVE MODELS IN BIOASSESSMENT

The basis of the analysis assessed in this report is the River Invertebrate Prediction and Classification System (RIVPACS) approach, originally developed in the U.K. by Wright and colleagues (Wright 1995) later advanced by Simpson & Norris in Australia with the Australian River Assessment Scheme

(AUSRIVAS) (Simpson and Norris 2000) and more recently in the USA (Hargett et al. 2007, Carlisle and Hawkins 2008, Yuan et al. 2008, Aguiar et al. 2011, Tsang et al. 2011). These predictive bioassessment models are similar and will be referred to in this report as RIVPACS models. RIVPACS models assess biological status by comparing the biotic condition at sites being evaluated with the biota expected to occur in the absence of stress (Wright 1995). A detailed account of the background to this type of predictive modelling has been covered in numerous publications e.g. (Wright 1995, Hawkins et al. 2000, Simpson and Norris 2000, Joy and Death 2001), and hence will not be explained in detail here. But a basic summary of the steps are:

1. A predictive model is built using biological, physical and chemical data collected at a number of unimpacted or minimally impacted sites, generally referred to as reference sites.
2. The reference sites are classified into groups based on the homogeneity of their fauna, and the physical and chemical characteristics that best describe variation among the groups are determined.
3. Some form of discriminant analysis is used to predict the biotic communities expected to occur in the absence of environmental stress.
4. Finally the expected community is defined as the sum of probabilities for all predicted species and this is divided by the observed list of species (only if predicted to be there) to give the observed over expected ratio.

In this assessment some of the steps described above were omitted or altered. The main differences were: 1) the predictions did not come from reference sites and 2) the predictions included land use and other human influenced variables so were effectively “how it is” rather than “how it would be in the absence of impact”.

METHODS

FISH DATA

All fish records were taken from the New Zealand Freshwater Fish Database (NZFFDB) (McDowall and Richardson 1983, Richardson 1989, Richardson 1993) for the years 1970 – 2010 for all sampling methods which gave a total of 27300 sites. However, not all sites had matching predictive fish or environmental data so approximately 27000 sites were analysed for this project. Since this is a scoping study to trial different methods no attempt was made to

select database entries with different levels of sampling intensity or gear type, the assumption was that a large number of sites would lessen the effects of sampling variability.

LAND COVER DATA - RIVER ENVIRONMENT CLASSIFICATION (REC)

The REC classifications were used to validate the O/E. The O/E and IBI scores for each database record were associated with its REC classification (Snelder and Guest 2000, Snelder and Biggs 2002, Snelder et al. 2002, Snelder et al. 2004).

PREDICTIVE SPATIAL MODELS

The predictive models used came from freshwater ecosystems of New Zealand (FENZ) project (Leathwick et al. 2008b). As part of the FENZ, the spatial distribution of most fish species were extended out over the entire river network was predicted using boosted regression trees by John Leathwick. This technique known as fish mapping was first developed in New Zealand by Joy and Death (Joy and Death 2004b). In this study, the predictive models for all fish species were used, only native fish and trout were used for the O/E models, all non-native as well as native for the IBI assessment.

CALCULATING OBSERVED OVER EXPECTED O/E RATIOS

The predicted fish assemblages from the Leathwick models were compared with the observed fish assemblages using an O/E ratio following the procedure originally described by Wright et al. (1984). To do this the following procedure was used: The probabilities of the predicted taxa were summed to give the 'expected number of taxa' (E). The number of species actually captured at a site, providing they were predicted to occur (and met the threshold used) was the 'observed number of taxa' (O). The ratio of the observed to the expected number of taxa (O / E) is the output from the model.

BEST PROBABILITY THRESHOLDS

Using the probabilities of occurrence from predictive models in bioassessment raises the issue of deciding on the probability threshold to use. Many models use the 0.5 (or 50% probability

threshold) - so that a probability greater than 0.5 means the species is present and less than 0.5 means absence (Fielding and Bell 1997). This approach is acceptable if the data that were used to create the model are balanced i.e. that the species modelled has a prevalence of around 50%, but in the data set used in these models prevalence varied from 0.003 to 0.37 so the 0.5 or any single threshold over all species would not give the best representation of the likelihood of finding it. To circumvent this problem the threshold that gave the best prediction was found for each species. This was done by trying all thresholds between 0 and 1 in 0.01 steps and then selecting the threshold that gave the best overall prediction measured as the maximum Cohen's Kappa (Cohen 1960, Olden et al. 2006b).

INDEX OF BIOTIC INTEGRITY (IBI)

The Index of Biotic Integrity (IBI) was originally developed using fish in the USA by James Karr during the early 1980s (Karr et al. 1986). The original version had 12 metrics that reflected fish species richness and composition, number and abundance of indicator species, trophic organization and function, reproductive behaviour, fish abundance, and condition of individual fish. This process has been repeated and IBIs developed on many continents. The fish fauna of New Zealand is however, radically different from the continental faunas thus the IBI developed for New Zealand includes a number of changes see (Joy and Death 2004a) for full details.

The six metrics that are used in the New Zealand IBI measure taxonomic richness over a number of habitat guilds, and as well use indicator species by measuring the number of species showing intolerance to degraded conditions and the ratio of native to exotic species. Many studies have shown that New Zealand's fish fauna is largely structured by elevation and distance from the coast (McDowall 1988, McDowall 1990, Joy and Death 2001). Because elevation and distance from the coast are the overriding controllers of native fish species distribution they were used to structure expectations of fish assemblages. The six metrics were assessed for both elevation and distance from the coast to give 12 metrics overall and these were summed to give the final score. IBI scores were calculated for all the sites used in this study to compare with the O/E scores.

RESULTS

Thirty one native species and two introduced fish the trout were used for the O/E ratio calculations and forty two fish species were used for IBI calculations. The best thresholds for all the native species with their prevalence in the database are shown in Table 1.

Table 1. Common and scientific names for all species used in the analysis, the best threshold from ROC analysis and their prevalence in the freshwater fish database records used.

Common name	Scientific name	Best	
		Threshold	Prevalence
Shortfin eel	<i>Anguilla australis schmidtii</i>	0.535	0.187
Longfin eel	<i>Anguilla dieffenbachia</i>	0.710	0.376
Torrentfish	<i>Cheimarrichthys fosteri</i>	0.230	0.071
Roundhead galaxias	<i>Galaxias anomalus</i>	0.240	0.004
Giant kokopu	<i>Galaxias argenteus</i>	0.365	0.032
Koaro	<i>Galaxias brevipinnis</i>	0.435	0.088
Kakanui Lowland longjaw galaxias	<i>Galaxias cobitinis</i>	0.105	0.004
Flathead galaxias	<i>Galaxias depressiceps</i>	0.585	0.008
Dwarf galaxias	<i>Galaxias divergens</i>	0.972	0.020
Eldon's galaxias	<i>Galaxias eldoni</i>	0.668	0.004
Banded kokopu	<i>Galaxias fasciatus</i>	0.923	0.120
Gollum galaxias	<i>Galaxias gollumoides</i>	0.345	0.007
Bignose galaxias	<i>Galaxias macronasus</i>	0.085	0.005
Inanga	<i>Galaxias maculatus</i>	0.525	0.120
Alpine galaxias	<i>Galaxias paucispondylus</i>	0.225	0.018
Shortjaw kokopu	<i>Galaxias postvectis</i>	0.555	0.022
Upland longjaw galaxias (Canterbury)	<i>Galaxias prognathous</i>	0.380	0.004
Dusky galaxias	<i>Galaxias pullus</i>	0.393	0.003
Lower Shag galaxias	<i>Galaxias</i> sp. E.	0.173	0.005
Canterbury galaxias	<i>Galaxias vulgaris</i>	0.353	0.044
Lamprey	<i>Geotria australis</i>	0.250	0.021
Crans bully	<i>Gobiomorphus basalis</i>	0.170	0.042
Upland bully	<i>Gobiomorphus breviceps</i>	0.300	0.121
Common bully	<i>Gobiomorphus cotidianus</i>	0.430	0.168
Giant bully	<i>Gobiomorphus gobioides</i>	0.315	0.017
Bluegill bully	<i>Gobiomorphus hubbsi</i>	0.485	0.035
Redfin bully	<i>Gobiomorphus huttoni</i>	0.563	0.139
Grey mullet	<i>Mugil cephalus</i>	0.110	0.006
Common smelt	<i>Retropinna retropinna</i>	0.620	0.047
Black flounder	<i>Rhombosolea retiaria</i>	0.093	0.010
Brown Trout	<i>Salmo Trutta</i>	0.580	0.249
Rainbow trout	<i>Oncorhynchus mykiss</i>	0.455	0.066

OBSERVED OVER EXPECTED RATIOS

The O/E scores were calculated for all sites using the three different thresholds (0.01, best threshold and 0.00001; Table 2). The O/E ratios were mostly lower than 1 and the average was higher for the individual best threshold (0.63) than for the uniform across all species thresholds of 0.1 and 0.0001. All three thresholds had many O/E scores of zero (around 7000 sites) these are sites where none of the predicted fish species occurred or there were no native fish present (Figure 1).

Table 2. Descriptive statistics for the O/E scores for all NZFFDB sites where a score could be calculated for the three probability thresholds.

Statistic	O/E 0.1	O/E best	O/E 0.0001
Mean	0.56	0.63	0.57
Standard Error	0.0029	0.0036	0.0029
Median	0.54	0.63	0.54
Standard Deviation	0.49	0.56	0.49
Sample Variance	0.24	0.32	0.24
Kurtosis	15.20	14.13	9.30
Skewness	1.84	1.45	1.66
Range	8.13	11.24	7.02
Minimum	0	0	0
Maximum	8.13	11.24	7.02
Count	27062	24867	27211

Apart from the zero O/E scores all three threshold O/E scores had relatively normal distributions. The distribution of for the ‘best threshold’ scores was less skewed and the ‘best threshold’ scores had a greater range (Table 2).

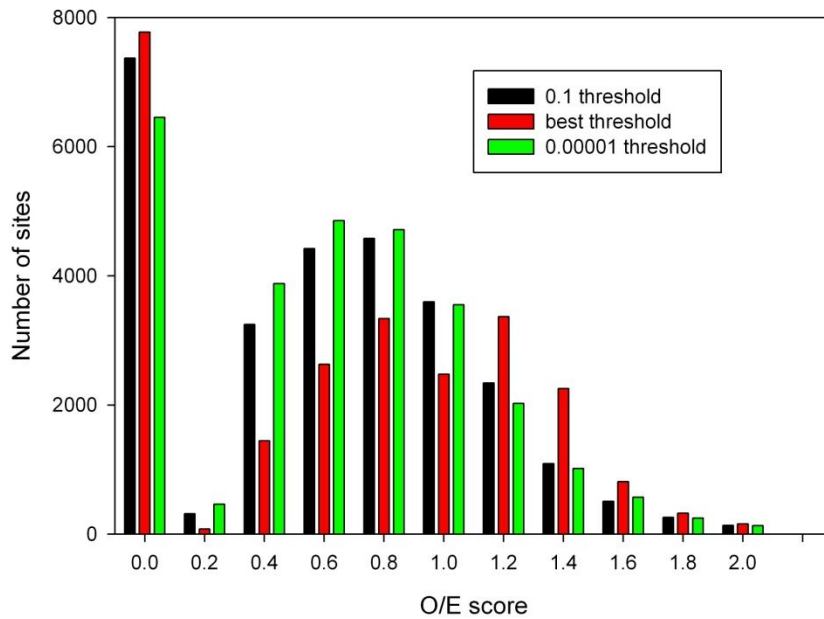


Figure 1. Histogram for the O/E scores using the three probability thresholds.

VALIDATION USING THE RIVER ENVIRONMENT CLASSIFICATION

The usefulness of the O/E scores was assessed by how well the scores they could discriminate between land-cover classes and if the average scores showed consistent logical differences between them and whether the highest scores contained more sites in unimpacted catchments. The three thresholds all produced O/E score distributions that discriminated between REC classes but the relative differences were not consistent over all thresholds or logical (figures 2 - 4). The relative ranking changed for each threshold and for example pasture and indigenous forest

Table 3. The number and proportion of sites in each REC class

REC class	Sites	Proportion of total
Bare ground	563	0.02
Exotic forest	1888	0.07
H pasture	11052	0.39
Indigenous forest	7126	0.25
L Pasture	1914	0.07
Scrub	1459	0.05
Tussock	2312	0.08
Urban	1718	0.06

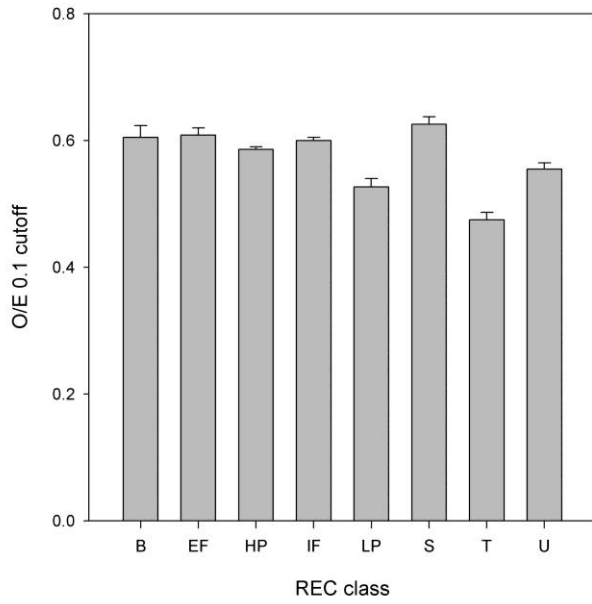


Figure 2. Average O/E score (\pm SE) for each REC class using the prediction threshold of 0.1. See table 3 for details on number of sites in each class

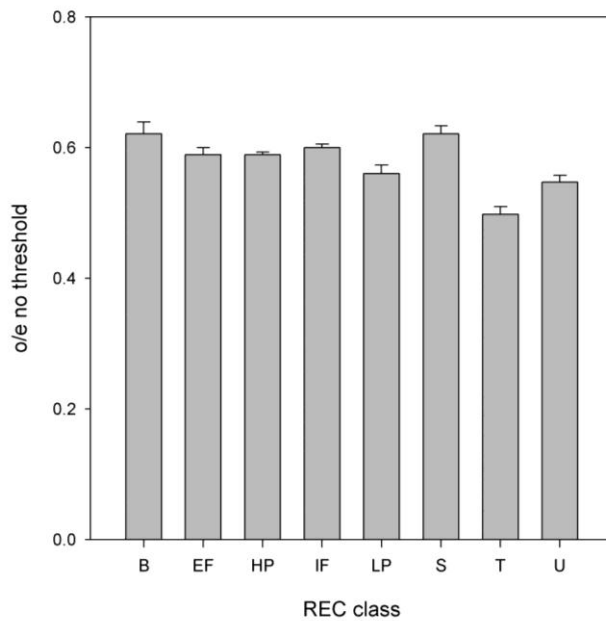


Figure 3. Average O/E score (\pm SE) for each REC class using the best prediction threshold. See table 3 for details on number of sites in each class

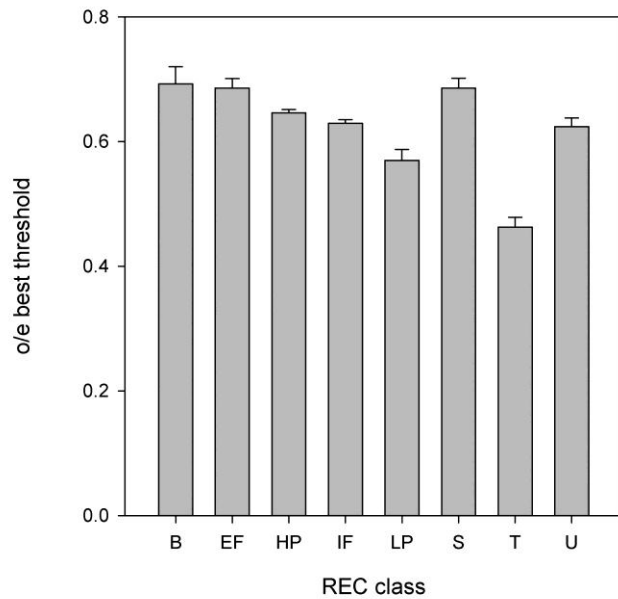


Figure 4. Average O/E score (\pm SE) for each REC class using the 0.00001 prediction threshold. See table 3 for details on number of sites in each class.

The next validation test was to take the higher scoring sites and see if the natural landcover classes were better represented. All sites with an O/E score greater than 0.9 were compared with the background distribution of O/E scores by land-cover class to see if there was a difference. The comparison revealed no difference in the land-cover site distribution for the greater than 0.9 scores (Figure 5). The O/E scores produced were not able to discriminate between land-cover and thus the assessment showed the O/E methods failed.

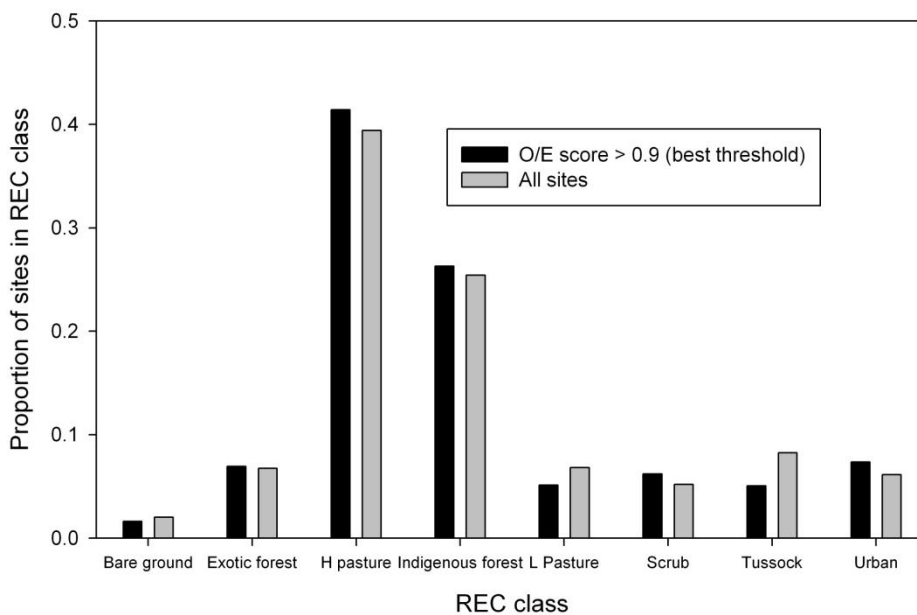


Figure 5. The number of sites in each REC class for all sites (black bars) and sites with an O/E score > 0.9 (grey bars).

INDEX OF BIOTIC INTEGRITY

Index of biotic integrity scores were calculated for all sites using; 1) the observed data and 2) the predicted IBI using 'best thresholds' predictions and 3) the IBI-O/E observed IBI scores obtained by divided the observed IBI scores by the predicted IBI scores.

The predicted IBI scores were on average higher than the observed and slightly less variable (Table 4). The IBI-O/E scores averaged 2.49 reflecting the higher expected than observed values and had a few extreme values where observed and expected IBI score were 60:0).

Table 4. Descriptive statistics for the IBI scores for all NZFFDB sites where a score could be calculated and for the Observed/expected IBI.

Statistic	Observed	Predicted	O/E - IBI
Mean	32.87	35.31	2.49
Standard Error	0.11	0.10	0.05
Median	36	36	1
Standard Deviation	16.82	15.34	7.37
Sample Variance	282.96	235.27	54.28
Kurtosis	-0.29	0.33	22.13
Skewness	-0.71	-0.84	4.74
Range	60	60	60
Minimum	0	0	0.02
Maximum	60	60	60
Count	22529	22529	22529

IBI LAND-COVER CLASSES

The validation of the IBI scores using the REC land-cover classes for both the observed and expected fish assemblages showed the expected relationships and rankings between classes with natural land cover scoring high and altered scoring low (Figures 6 & 7). Similar relationships and rankings between the REC land cover types have been found in other IBI studies using some of the same data nationally (Joy and Death 2004a, Joy 2009) and regionally (Joy 2005a, 2007, 2008). Inspection of the individual class average scores shows that the relative scores and rankings are virtually the same between observed and predicted IBIs for bare ground, high intensity pasture, indigenous forest, low intensity forest, miscellaneous, and scrub REC classes. Tussock, urban and exotic forest IBI scores and rankings were however less similar between observed and expected IBI average scores.

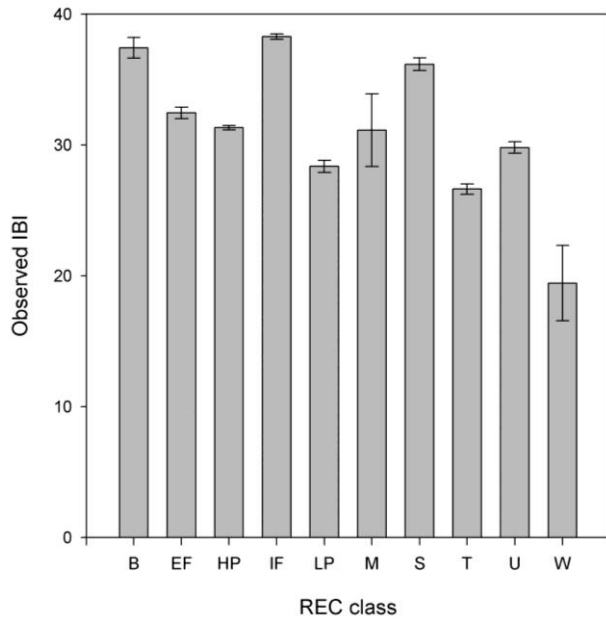


Figure 6. Average observed IBI score (\pm SE) for each REC class. See table 3 for details on number of sites in each class

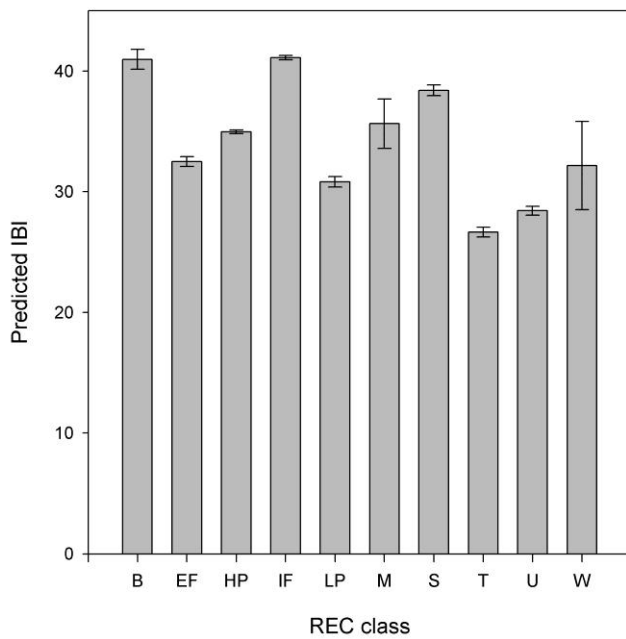


Figure 7. Average predicted IBI score (\pm SE) for each REC class using the best prediction threshold to maximise kappa from ROC analysis. See table 3 for details on number of sites in each class

OBSERVED OVER EXPECTED IBI

The O/E - IBI scores show contradictory and incongruous scores for the REC classes (Figure 8). The scores are a virtual the reverse of the rankings from the mainly congruent observed and predicted IBI

scores above. For example the pasture sites score higher than the indigenous forest sites.

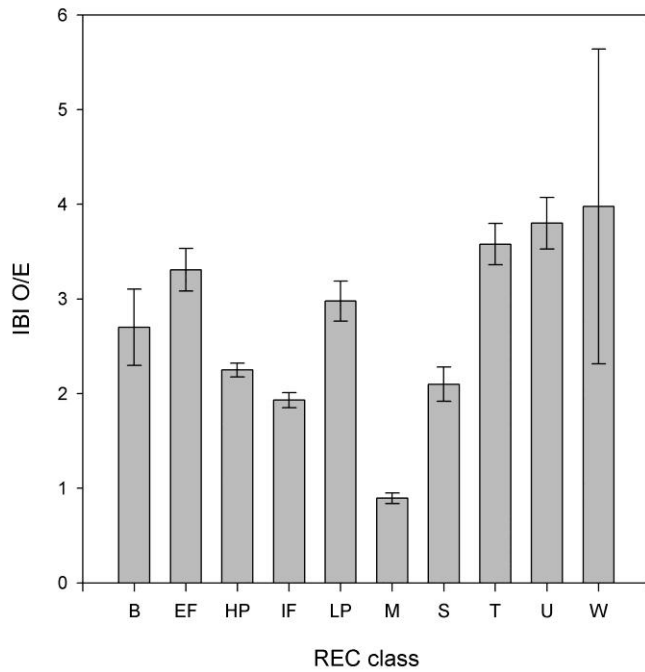


Figure 8. Average O/E - IBI score (\pm SE) for each REC class the predicted IBI using the best prediction threshold to maximise kappa from ROC analysis. See table 3 for details on number of sites in each class

DISCUSSION

Analysis of the O/E scores calculated for all the sites in the New Zealand freshwater fish database using predictions based on present conditions failed to give the hoped for results. Rather, it turned out to be a measure of the accuracy of the individual species predictive models at a community level (Olden et al. 2006a) rather than a useful bioassessment tool. The anticipated result that high scores would reflect good conditions did not transpire, rather it revealed that the Leathwick predictive species models are just as accurate (or inaccurate) at impacted sites as they are at unimpacted sites. The hypothesis that the observed fish communities divided by predictions of fish assemblages “as is” rather than ‘should be’ would give a baseline measure of condition was not supported as the scores could not discriminate logically between land-cover types. The IBI part of this report revealed that the fish data that failed for the O/E assessment can be effective in bioassessment if an index is used, thus the problem for both the O/E fish model and the IBI-O/E is with the land-cover influenced predictions.

O/E MODELS

The failure of the O/E scores developed in this report did however, emphasise the need to follow all the logical steps used in the RIVPACS (Wright et al. 1984)/AUSRIVAS (Smith et al. 1999) predictive bioassessment approach. Predictive models using invertebrates have been successfully developed in New Zealand (Joy and Death 2003) the United Kingdom (Wright et al. 1984, Wright 1995), Australia (Marchant and Hehir 2002), Indonesia (Hart et al. 2001, Sudaryanti et al. 2001) and in the USA (Hawkins et al. 2000, Hawkins and Hafele 2003).

Predictive RIVPACS models have been shown to work with fish regionally in New Zealand (Joy and Death 2002a, b) and internationally e.g. in Ireland (Joy 2004, Kelly et al. 2008), and the USA (Carlisle et al. 2008). Thus, there is no reason why they would not be successful in New Zealand but will require considerable up-front effort and investment in a database of reference sites and then model construction.

IBI MODELS

The IBI model calculated from the observed data worked well as expected and the predicted IBI scores from the predicted assemblages also performed well. The O/E - IBI output failed in a

similar way to the full O/E models, again it seemed to reflect the predictive ability of the individual predictive models rather than different impacts on assemblages. The IBI analysis was done to show that the same data that revealed a lack of usefulness of data when used as an O/E fish assemblage score can be useful when an index approach is taken. The predictive IBI added nothing to the analysis when using the O/E – IBI approach but would be useful for highlighting impacted areas of the country when mapped out nationally. The IBI assessment could be improved with the inclusion of abundance/density data and information on size classes so that population structure could be added. The information required to improve these models would require consistent sampling methods and protocols to achieve this and these are now available (David et al. 2010, Joy et al. 2013).

CONCLUSIONS & RECOMMENDATIONS

Predictive O/E bioassessment models using fish have great potential to improve freshwater ecological assessment in New Zealand. However, this study showed that taking short-cuts does not work with these models. The model building procedure outlined in many studies worldwide shows that initial investment in site selection and collection of reference data is crucial. This investment may seem expensive but is a one-off and can be used for many years. The IBI approach is useful in the absence of an O/E model, for regional and national reporting but to improve it there needs to be upgraded to include the consistent abundance data which is now being collected now protocols are available (David et al. 2010, Joy et al. 2013).

RECOMMENDATIONS FOR FISH AS NATIONAL INDICATORS

Freshwater fish are ideal indicators of the overall health of freshwater ecosystems as they integrate all ecological components. At the top of food webs and influenced by both upstream and downstream conditions fish have the greatest potential as holistic river health indicators. The tools to enable the use of fish in national level assessment in New Zealand are available with the fish IBI and IBI models are already being used in state of the environment reporting by many councils. The existing fish IBI models do however, have potential for improvement with the quantitative data collection now becoming available with the new sampling protocols (David et al. 2010, Joy et al. 2013). This new data is collected using standardised procedures and includes information on abundance and population structure. While, the predictive modelling RIVPACs type fish models

have great potential as national indicators they require a considerable initial investment to gather reference site data, and model building although this investment is one-off.

INDEX OF BIOTIC INTEGRITY

In the short term, the presently available IBI (Joy and Death 2004a) would be appropriate as a national assessment indicator, however, in the long term investment in developing the IBI further to include the newly available standardised fish data would further enhance its precision. The next steps to develop the IBI would be to gather the fish data gathered already using the new protocols (David et al. 2010) and any in the database that includes abundance and size details and use this data to update the IBI. The inclusion of abundance and size class information will enhance the precision of the IBI by including metrics encompassing abundance and size/age structure. These new metrics have been added to an IBI developed for New Caledonia and shown to work well (Joy and Poellabauer In Prep).

In a trail run, a sample of new data collected using the New Zealand protocols was assessed using an upgraded IBI (with some abundance metrics added). The comparison of the presence absence and basic abundance data and new metrics in an IBI using around 90 sites sampled using the electrofishing protocols showed that the precision when comparing REC pasture sites with indigenous forest sites was higher. The P value for the test for the statistic for the difference between the average IBI scores at the two REC classes was: using presence/absence $P = 0.00001457$ and for the basic abundance model $P = 0.00000012$. This difference can be seen in figures 9 and 10 with tighter ranges in box plots with abundance versus presence/absence IBI scores. The comparison was limited because it was just a first attempt and didn't include size class data, but revealed the likelihood that there will advantages with upgrading the IBI and collecting more comprehensive data.

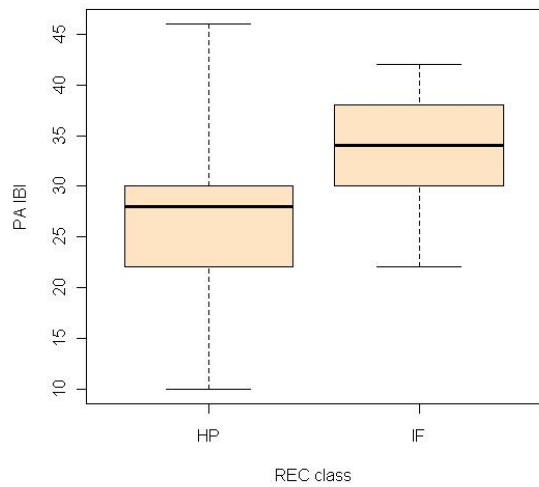


Figure 9. Presence/absence IBI scores at pasture and indigenous forest sites

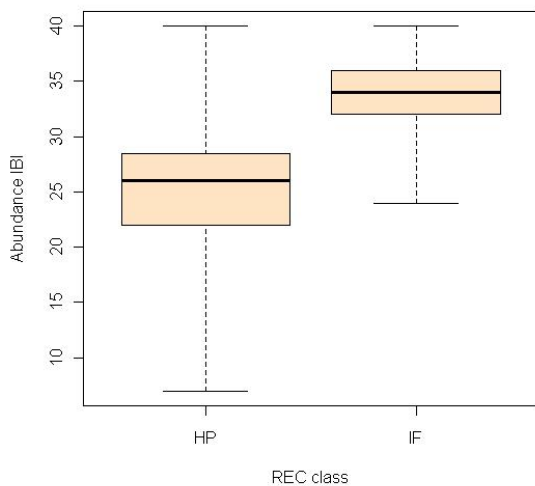


Figure 10. Abundance IBI scores at pasture and indigenous forest sites

RIVPACS PREDICTIVE O/E ASSESSMENT

Long-term the development of a predictive O/E model would be a useful addition to the available bioassessment toolkit in New Zealand. The minimum requirement for reference site data would be in the order of 200 sites nationally sampled using the protocols (Joy et al. 2013) although a reasonable proportion of these data may be able to be uncovered from existing databases. The accepted reality is that at lowland areas over most of New Zealand very few pristine sites can be found and thus the criteria of ‘best management practice’ rather than pristine must be applied for site selection.

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