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Does artificial intelligence modelling have anything to offer traditional management of freshwater food resources?

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EXECUTIVE SUMMARY

Management of freshwater systems and the ecosystem services they provide has become a multi-stakeholder activity. This requires information on resources and how to manage them to be disseminated to a wide range of users. While artificial intelligence modelling can provide a powerful tool in managing and understanding resources and their drivers, they can be confusing to many users. In this study, we explored the potential use of two alternative modelling approaches (Boosted Regression Trees (BRT) and Bayesian Belief Networks (BBN)) for managing three species of freshwater mahinga kai species–kākahi or kaeo (freshwater mussel), kōura (freshwater crayfish) and tuna (freshwater eel). While the BBN model is better for stakeholder communication, the BRT produced more accurate models for all species. However, variables identified as being important for predicting abundance and biomass of these species were often environmental parameters that cannot be managed to improve yield. The artificial intelligence modelling does provide some accurate linkages between the target species and their environmental drivers. Nevertheless, translating these relationships into management plans remains challenging. The models are clearly not a panacea for better resource management, but provide one more tool in the tool box that might assist multi-stakeholder understanding of how best to manage freshwater resources.

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Introduction

The management of freshwater resources is becoming an increasingly challenging task as water abstraction and degradation continue to increase globally (Gleick 1998; Postel and Richter 2003; Gleick 2014; Richter 2014). This is equally, if not more, challenging for indigenous peoples faced with the task of managing resources that are often influenced by factors outside their immediate sphere of control, including climate change. To achieve more enduring and inclusive outcomes, there is a need to develop ways of using scientific knowledge alongside traditional knowledge for application in resource management (Berkes and Berkes 2009; Hudson *et al.* 2016).

Within science there is a wide range of modelling approaches that are increasingly being applied to understand ecological systems and to allow for better management of those systems (Schindler and Hilborn 2015; Houlahan 2017; Stillman Wood and Goss-Custard 2016; Brudvig 2017). Artificial intelligence (AI) modelling is a subset of those approaches whose application offers many advantages for dealing with the complexity, level of uncertainty and large size of data sets that often arise in resource management (Pourret, Naim and Marcot 2008; Crisci, Ghattas and Perera 2012; James *et al.* 2013; Death 2015; Death *et al.* 2015; Kuhn and Johnson 2016). However, even within AI modelling there is an extensive range of approaches that all have their advantages and disadvantages.

We have previously evaluated the usefulness of a range of modelling approaches in the New Zealand context, including several AI methods (Collier *et al.* 2014; Hudson *et al.* 2016), for informing holistic management of freshwater resources, such as mahinga kai (here we use mahinga kai to refer to indigenous freshwater species that have traditionally been used as food, tools, or other resources). In this report, we compare two AI approaches, Bayesian Belief Networks (BBNs) and Boosted Regression Trees (BRTs), for modelling and communicating a science perspective for consideration in the management of three freshwater mahinga kai species–kākahi or kaeo (freshwater mussel), kōura (freshwater crayfish) and tuna (freshwater eel). Bayesian Belief Networks have been used extensively for modelling in resource management (Pourret *et al*. 2008; Death *et al.* 2015) and are very good for communicating the interconnectedness of important environmental variables behind the model working, but are often more challenging for generating accurate models (Uusitalo 2007). In contrast, Boosted Regression Trees (BRTs) seem to be one of the currently preferred modelling tools in ecology (Elith, Leathwick and Hastie 2008) because they can be used to build models quickly and accurately. However, they are considerably more ‘black box’ in approach, to the point that the ensemble of multiple regression trees created are not even visible. The two techniques thus represent a rough contrast from being good for knowledge transfer but weaker for modelling (BBN), to weaker for communication but more accurate in predictive capacity (BRT).

Bayesian Belief Networks have been used a number of times to represent traditional knowledge for resource management (Newton *et al.* 2006; McGregor *et al.* 2010). McGregor *et al.* (2010) used them for portraying the knowledge on wetland health of traditional owners in Kakadu National Park, Australia, and Newton *et al.* (2006) used them to show the impacts of commercialising non-timber forest products on central-American communities. The modelling framework of a BBN is initially represented as a conceptual linkage diagram and this adds to engagement and understanding of the community who can be involved in the development of the linkage diagram (Liu *et al.* 2008; Kragt *et al.* 2011). The BBN is also able to capture qualitative data more easily than numerically based models; thus outcomes of ‘always’, ‘never’ and ‘sometimes’ are easily translated into a BBN model. Traditional understanding from experience, informed opinion and non-quantifiable concepts, can also be incorporated relatively easily into a BBN model. This approach, therefore, offers many advantages for a range of knowledge forms, including traditional knowledge, although BBNs are considerably more cumbersome for constructing models, especially as discretisation of nodes requires creating divisions in usually continuous environmental variables (Death *et al.* 2015). Boosted Regression Trees have not been used for modelling to support traditional knowledge as far as we are aware; however, BRTs are now used extensively for ecological and environmental modelling (Elith *et al*. 2008).

Most broad-scale modelling of the mahinga kai species examined in New Zealand has been for predicting presence/absence (Joy 2000; Broad *et al.* 2001; Joy and Death 2002, 2004; Leathwick *et al.* 2008a, 2008b, 2010; Crow *et al.* 2014). Abundance models have been built, but for a very small number of New Zealand sites: Booker and Graynoth (2013) used linear regression to model New Zealand eel abundance in 10 rivers, and Jowett, Parkyn and Richardson (2008) modelled kōura (*Paranephrops planifrons*) abundance in 30 rivers using Generalised Additive Models (GAMs). Presence/absence models are likely to be less helpful for indigenous peoples who might want to use those species as a sustainable food resource.

Rather, it will be more important to know whether there is a good size population suitable for harvesting, rather than knowing that the probability of detecting at least one individual of a species is high. Although both of these outcomes can be achieved with models, the types of model that will be useful for either goal may be quite different.

In this report, we compare the efficiency of the two modelling approaches on five culturally important freshwater species to Māori: two species of freshwater mussel (*Echyridella aucklandica* and *E. menziesii*), one species of freshwater crayfish (*P. planifrons*) and two species of freshwater eel (*Anguilla dieffenbachii* and *A. australis*). We used data collected from 100 – 250 rivers in the Waikato region (2.5 million hectares) of the North Island, New Zealand, to model abundance. Additionally, for eels we also estimated total and per fish biomass (based on length), as both population parameters are likely to be more important for management of these species as traditional food resources.

Study area

The Waikato region covers 2.5 million hectares across latitudes 36^{o} and 39^{o}S in New Zealand's central North Island, including New Zealand's largest lake (Taupō) and longest river (Waikato). Landforms range from active volcanoes (up to 2,797 m a.s.l.) and upland plateau (c. 600 m a.s.l.) in the south of the region, to steep erodible hill-country (300 – 600 m a.s.l.) along the west coast, through the central parts of the region and towards the east, and extensive lowland peatlands and plains in the north. The region is very diverse geologically with extensive areas of volcanic rock (rhyolites, andesites, basalts and dacites) around the southern and western volcanoes and eastern peninsula (McCraw 1971), with limestone common along western parts of the region. Pre-European vegetation cover was predominantly podocarp-hardwood forest in hill-country and western areas, with extensive areas of beech in the south. Fernland/scrubland also occurred over wide areas prior to European colonisation, and sub-alpine grassland and scrubland still occurs at higher altitudes on the southern mountains.

Average annual rainfall is variable, but lower in the north (1,000 – 1,500 mm p.a.) than in the eastern and western ranges (up to 2,500 mm p.a.), and high (5,000 mm p.a.) on southern mountaintops. Mean annual air temperatures in most of this region are in the range 12.5 to 15.0^{o}C, but decline to <8.0^{o}C on southern mountains (Kilpatrick 1999). Most of the

Waikato region has been developed for pastoral agriculture or pine forestry, with extensive remnants of original forest persisting only in upland parts of region (28% of pre-European extent).

Methods

Data sources

Biological data

Biological data were supplied from Waikato Regional Council environmental monitoring records. Two mussel species, *E. aucklandica* and *E. menziesii* were surveyed by visual/tactile inspection at 104 sites between 2010 and 2015 in the western Waikato region (Fig. 1). *P. planifrons* (kōura) and longfin and shortfin eel were sampled 256 times at 127 locations throughout the Waikato region between 2010 and 2016 using electro-fishing (Joy, David and Lake 2013) (Fig. 1). More detail on sampling methodology and fish collected can be found in (David *et al.* 2016). Eel length measurements recorded in the field were converted to biomass using the specific weight length relationships for each species of eel provided in (Jellyman *et al.* 2013).

Environmental field data

Concomitant with biological sampling, standard Regional Ecological Monitoring of Streams (REMS) field methods were used for qualitative assessment or measurement of sampling reach canopy cover/shade, fencing, dissolved oxygen, temperature, conductivity, wetted width, thalweg depth (maximum depth at transects), percent macrophyte cover, percent substrate size (clay, silt, sand, small gravel, etc), and percent wood (Collier and Kelly 2005). Water samples were collected at some sites for ammonia/ metal/ hardness analysis.

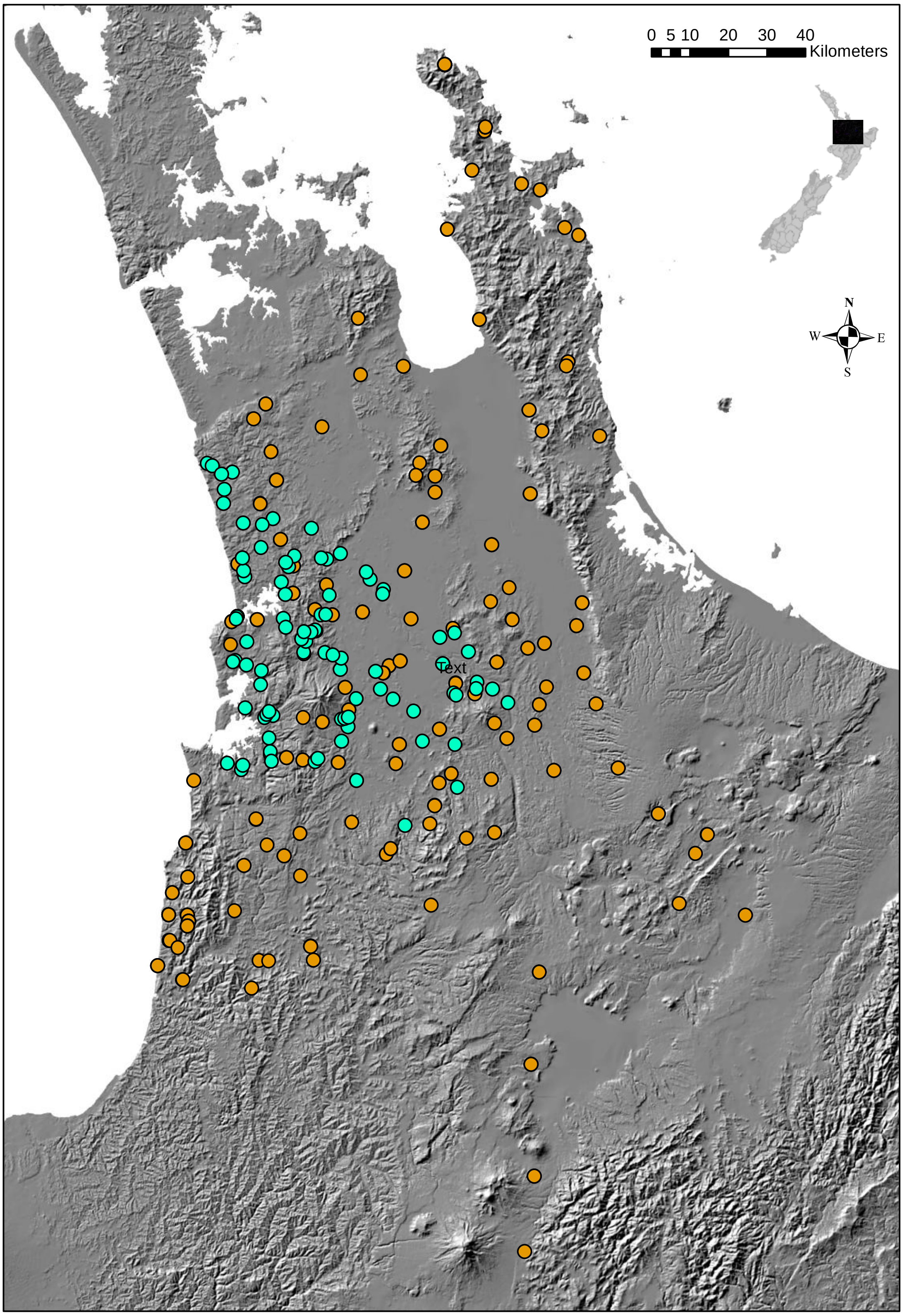

Figure 1: Map of 104 sites sampled for mussels (blue circles) and 256 sites sampled for kōura and eel (orange circles) between 2010 and 2015 in the Waikato region of New Zealand

GIS data

GIS environmental data on nutrients, flow regime, catchment geology and topography, temperature and shading, MCI (Macroinvertebrate Community Index) and deposited sediment for each sampled reach were included in the model construction as potential predictor variables in BRT models. Modelled nutrient, MCI and *E. coli* were sourced from Unwin and Larned (2013), flow data from Booker and Woods (2014), catchment geology, topography and temperature from the Freshwater Ecosystems of New Zealand (FENZ) database (Leathwick *et al.* 2010), and modelled sediment data from Clapcott, Goodwin and Snelder (2103). Subsets of these data considered relevant to specific species were used for constructing BBNs (see below). Consideration of both commercial (in the case of eels), traditional and recreational harvest from sampling locations was not possible as, to the best of our knowledge, there are no site-specific records of commercial, recreational or cultural collections of the focal species.

Data analysis

Bayesian Belief Networks

BBNs were constructed for mussels and eels using Netica^{TM} 5.02 software (Pourret, Naim and Marcot 2008). The network linkage diagram was developed slightly differently for each of the target species, reflecting the individualised approach to target variables and model architecture that is possible with BBNs. For the two species of freshwater tuna (Fig. 2), nodes and the discretisation of those nodes were developed from a review of all the relevant literature on New Zealand freshwater eels (Niessen *et al.* in prep). The BBN was then populated with data from the 127 electro-fished sites. Conditional Probability Tables (CPTs) were developed with the expectation-maximisation algorithm (EM Learning) in Netica^{TM} from the compiled data. The expectation–maximisation (EM) algorithm is an iterative method for finding maximum likelihood estimates of parameters in statistical models, where the model depends on unobserved latent variables (Do and Batzoglou 2008). CPTs calculate the probability of each state in a node occurring, given each combination of conditions in the parent (input) nodes.

The kākahi BBN was developed for the combined abundance of both species as they were not expected to be differentiated during traditional food collections. Biota and/or environment matching analyses using the BVSTEP method on a Euclidean distance resemblance matrix were conducted in Primer 7 (Primer-E Ltd, Plymouth, U.K.; version 7.0.7) using density per m^2 of stream bed and density per m of stream channel as many mussels were collected associated with banks. The BVSTEP algorithm successively adds and removes a variable to get the optimum correlation between the environmental and biological data. Recurrent and dominant variables identified by these analyses were grouped into intermediate nodes representing access for fish which are an important host for larval kākahi, physicochemical conditions, riparian conditions and instream habitat conditions. These intermediate nodes were subsequently linked to kākahi abundance. Variables were discretised into thirds for all nodes based on their data distributions or professional judgement. Conditional Probability Tables (CPTs) for the data from 104 sites were again developed using the expectation-maximisation algorithm (EM Learning) in Netica™.

Models were evaluated by hold-out validation with a randomly selected 10% subset of the training data. There are a wide range of metrics that can be used to evaluate model fit and performance (for a detailed review see Witten, Frank and Hall (2011); Marcot (2012)). We used several commonly used metrics that assess both raw predictive ability and ability relative to occurrence. The percentage of incorrect predictions (percent error) is a simple, easily understood metric but is sensitive to the number and size of the nodes. For example, if you have a very common state in the node and predict it will always occur (P=1.0) then you have a high probability of being correct simply because it usually occurs. For BBNs, Spherical payoff is similar to the area under receiver operating curves (Hand 1997; Marcot 2012). Cohen's kappa also ranges from 0 to 1, with 1 being perfect classification that also assesses correct predictions relative to how common a state actually is (Boyce *et al.* 2002; Olden, Lawler and Poff 2008). The logarithmic loss score (Dlamini 2010) was used to compare BBNs of alternate architecture. The index ranges from 0 to infinity, with 0 the best possible score. Unlike the indices above that must be calculated outside Netica™, this index is provided within the program and gives a quick metric for evaluating alternate BBNs.

Boosted Regression Trees

Boosted regression trees (BRTs) are a powerful modification of classification and regression tree analyses that are now widely used in ecological research (De'ath and Fabricius 2000; Elith *et al.* 2008). BRTs combine the algorithms of regression trees, that relate predictors of a single response variable by recursive binary splits, and boosting, an ensemble method that combines multiple simple models to increase predictive performance (Elith *et al*. 2008). One disadvantage of the approach is that models are complex and cannot be represented by a single decision tree that might allow a researcher to explain the model relationships to a potential end-user. However, the advantage of the technique is it can provide robust models of predictor and response variable relationships from a limited dataset and allow extrapolation from that model to new data scenarios.

We used the *gbm* package (Ridgeway 2013) in R (version 3.3.1; R Project for Statistical Computing, Vienna, Austria) to fit the BRTs. We used the Gaussian family of relationships as data were quantitative (number or biomass / m^2), a tree complexity of 8, learning rate of 0.01 (kōura) or 0.001 (mussels and eels), a bag fraction of 0.5 and cross-validation (CV) with 10 k-folds. These analysis settings were found to produce the highest correlations with left-out data by trial and error. The model was initially run with the full suite of 138 habitat and GIS variables, but potential predictor variables were then reduced to those that explained more than 1% of the variation in the BRTs for the final model analysis. This always improved model fit.

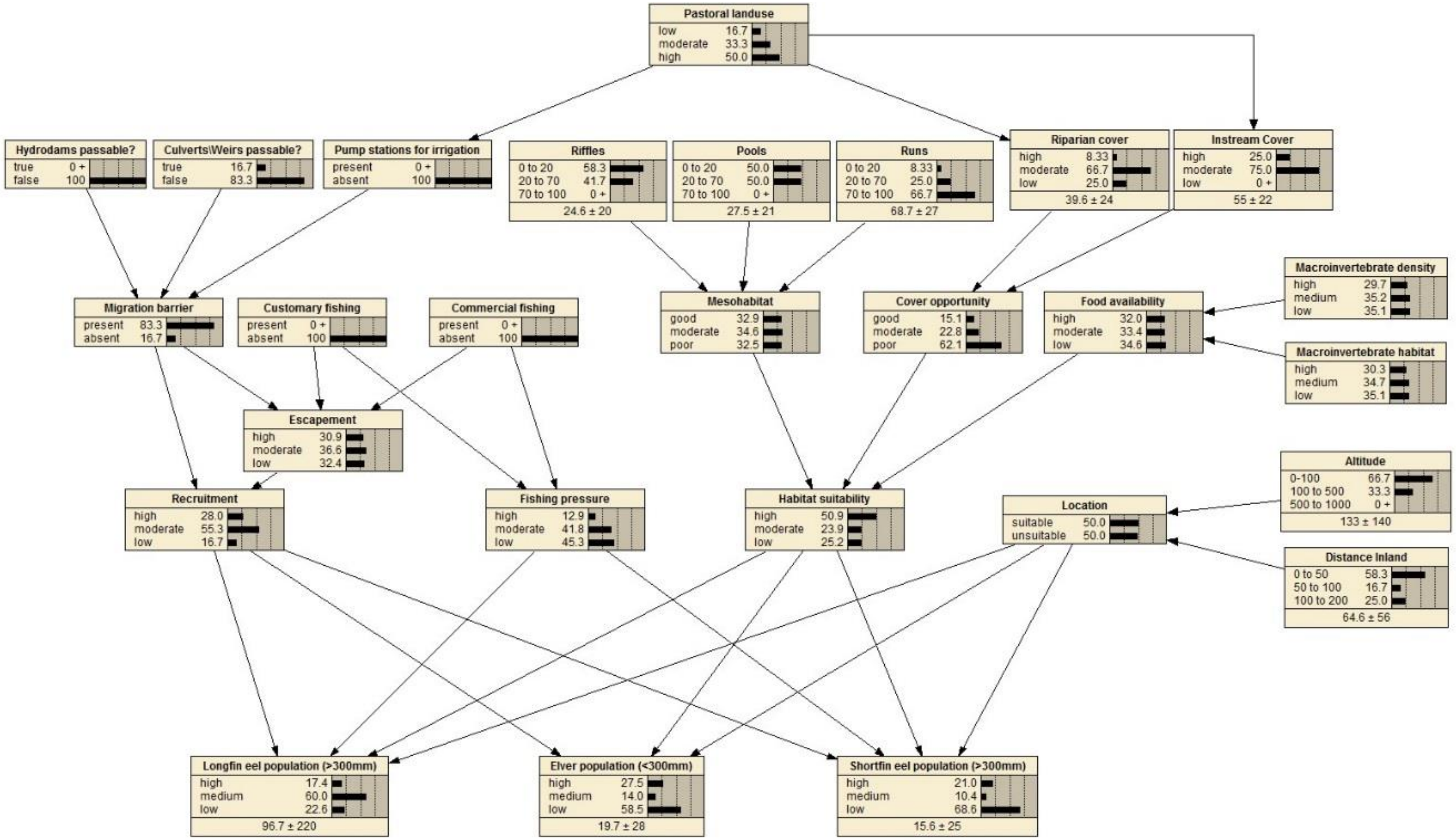

Figure 2: Bayesian Belief Network for two species of New Zealand freshwater eel

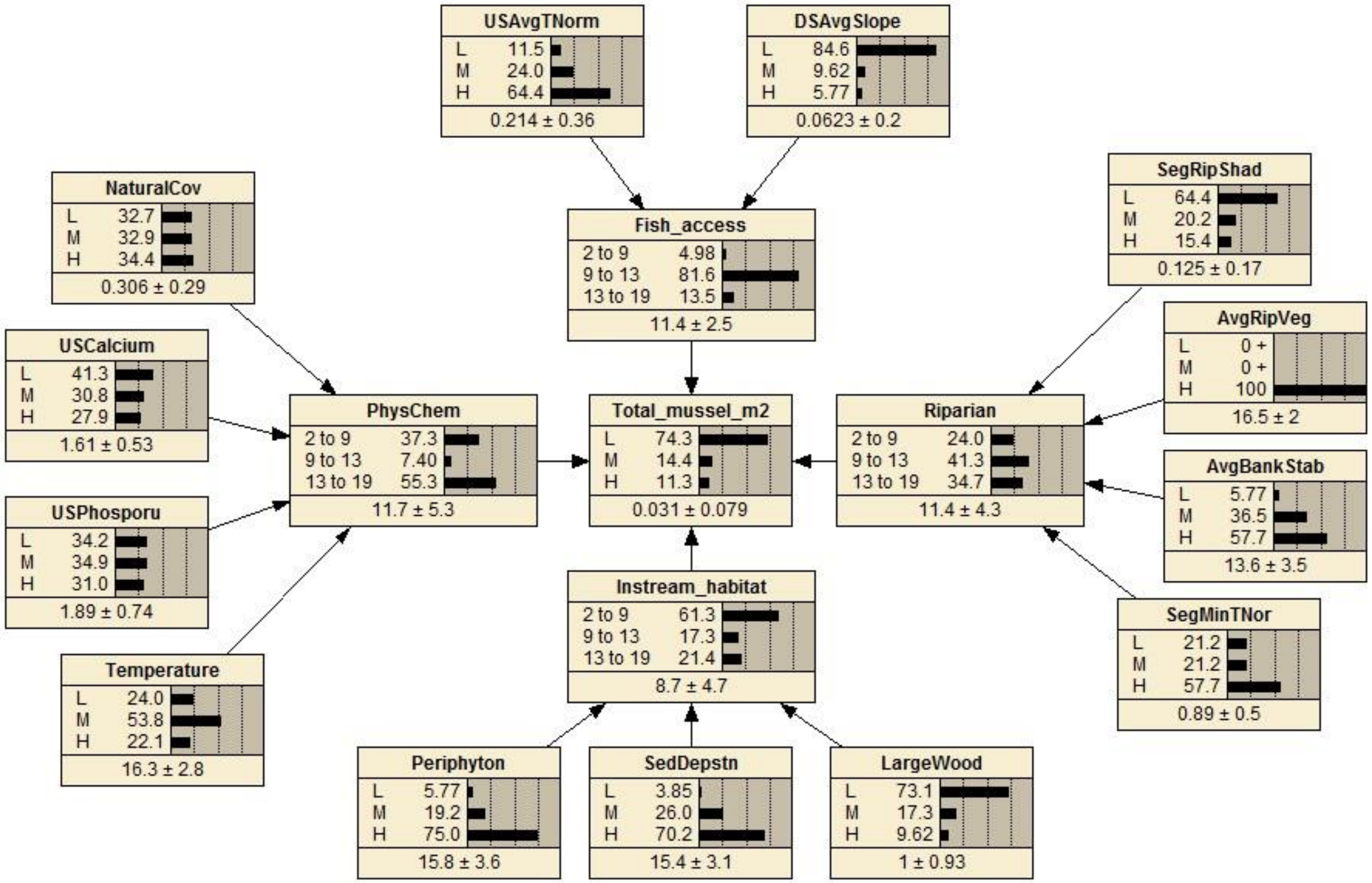

Figure 3: Bayesian Belief Network for two species of New Zealand freshwater mussel

Results

Bayesian Belief Networks

The ability of the tuna BBN (Fig. 2) to describe abundance of both species of eel in the training data was moderate. There was a 36.6% error rate, a logarithmic loss score of 0.42 (this ranges from 0 to infinity, with 0 the best possible score), a spherical payoff score of 0.78 (this ranges from 0 to 1, with 1 being the best possible score) and a Cohen's kappa of 0.65 (indicative of good model fit) (Landis and Koch 1977). However, the BBN did not perform well on 10% of the data left out of the model building (independent data); there was a 54.2% error rate, a log loss score of 2.45, a spherical payoff score of 0.34 and a Cohen's kappa of 0.21.

The architecture for the kākahi BBN is presented in Figure 3. The ability of the network to describe the training data was good. There was a 10.6% error rate, a logarithmic loss score of 0.22 (this ranges from 0 to infinity, with 0 the best possible score), a spherical payoff score of 0.92 (this ranges from 0 to 1, with 1 being the best possible score) and a Cohen's kappa of 0.80 (indicative of good model fit). However, the BBN did not perform well on independent data; there was a 46.2% error rate, a log loss score of 1.75, a spherical payoff score of 0.63 and a Cohen's kappa of 0.12.

Boosted Regression Trees

The BRT for kōura density had a CV correlation coefficient of 0.778 ± 0.066, with conductivity, stream width, substrate diversity, segment flow, flood size and distance to the coast explaining the highest percentage of density variation (Table 1). Kōura are more abundant in small streams (<1 m wide) within 200 km of the coast, that have high substrate diversity, low conductivity (<5 mS/m) and small floods (Table 1, Appendix 1).

E. menziesii were generally more abundant than *E. aucklandica* so the BRT for total mussel density was dominated by the former species. It had a CV correlation coefficient of 0.528 ± 0.063. *E. aucklandica* and *E. menziesii* had CV correlation coefficients of 0.431 ± 0.068 and 0.540 ± 0.068, respectively. Flood size, catchment area and deposited sediment were dominant predictor variables for both species of kākahi, whereas the presence of *Gobiomorphus huttoni* (redfin bully) and large wood were important for *E. menziesii* only, with water temperature, slope and stream width important for *E. aucklandica* only (Table 1, Appendix 1).

The longfin (*A. dieffenbachii*) and shortfin (*A. australis*) eel abundance model had a CV correlation coefficient of 0.803 ± 0.024 and 0.722 ± 0.031, respectively. Easting, altitude, segment slope and stream width were the best predictors of abundance (Table 1, Appendix 1). Shortfin eels were more abundant in open, low-slope streams, below 100 m a.s.l on the east coast, whereas longfin eels were more abundant in small streams with steeper slope on the west coast. The BRT for total tuna had a CV correlation coefficient of 0.675 ± 0.055 and was similar to the model for shortfin eels because of the overall higher abundance of shortfin eels at the study sites.

The BRT models for total tuna biomass were good with a CV correlation coefficient of 0.646 ± 0.042 and 0.647 ± 0.035, for shortfin and longfin eels, respectively (Table 1). Shortfin biomass was higher in small, high sediment, low water quality sites whereas longfin biomass was higher in small-to-medium sized streams with abundant kōura and high substrate diversity. BRT models of the biomass per individual tuna were not quite as good (Table 1), with larger shortfin eels in sites with lower flow variability and high deposited sediment levels, and larger longfin eels in bedrock streams with abundant kōura and diverse substrates.

Table 1: Results of BRT models for 5 mahinga kai species in the Waikato Region, including the six most important variables in predicting the target species (first row), the percent variation explained (second row) and the critical threshold for higher density or biomass (third line) (more detail for the latter is in Appendix 1). Note: FRE3 = flow 3 times median flow; Pr = probability

	Training data correl.	Cross-validated data correl.	Standard error for CV correl.	Variables that explain the most variation in the data, the percentage they explain and critical threshold of greater x (where x is the number in the third row)					
Kōura relative abundance	0.997	0.778	0.066	Conductivity (mS/m)	Width (m)	Substrate diversity	Segment flow (m^3/sec)	Mean annual flood size (m^3/sec)	Distance to coast (km)
				16.76	10.64	5.97	5.65	5.17	4.42
				< 5	< 1	> 5	< 0.05	< 3	< 200
Echyridella aucklandica	0.631	0.431	0.068	Temperature (°C)	Downstream maximum slope (°)	Mean annual flood size(m^3/sec)	Catchment area (km^2)	Modelled sediment (g/m^2)	Width at MALF (Mean Annual Low Flow (m)
				21.69	17.72	15.89	8.52	8.52	6.36
				< 14	< 3	> 20	> 5000000	< 1	> 5
Echyridella menziesii	0.787	0.54	0.068	Redfin bully (Pr)	Mean annual flood size (m^3/sec)	Large wood	Catchment area (km^2)	Deposited sediment (g/m^2)	Upstream calcium (g/m^3)
				11.89	11.42	9.82	8.33	7.7	7.58
				> 0.65	> 10	> 5	> 5000000	> 15	> 2
Total mussel	0.768	0.528	0.063	Redfin bully (Pr)	Mean annual flood size (m^3/sec)	Temperature (°C)	Catchment area (km^2)	Large wood (%)	Width at MALF (m)
				14.68	13.34	10.01	9.1	8.15	6.29
				> 0.65	> 10	< 14	> 5000000	> 5	> 5
Shortfin eel relative abundance	0.953	0.722	0.031	Downstream maximum slope (°)	Altitude (m a.s.l.)	Segment riparian shade (Proportion)	Upstream calcium (g/m^3)	Easting (NZMG)	Substrate diversity
				11.08	6.83	5.01	4.69	4.53	4.51

				< 4	< 100	< 0.2	> 2	> 1820000	< 2
Longfin relative abundance	0.959	0.803	0.024	Easting (NZMG)	Gradient (°)	Segment slope (°)	Width (m)	FRE3 (m^3/sec)	Catchment area (km^2)
				30.67	10.06	7.4	6.49	3.74	3.7
				< 175000	> 3	> 2.5	< 1	> 18	< 1000000
Total eel relative abundance	0.963	0.675	0.055	Altitude (m a.s.l)	Easting (NZMG)	Downstream maximum slope (°)	Segment CLUES nitrogen (ppb)	Large gravel (%)	Width (m)
				8.27	5.78	5.12	5.04	4.68	4.38
				< 100	1750000 < x < 1820000	< 2	> 2	> 50%	< 1
Shortfin eel total biomass	0.891	0.646	0.042	MCI	Dissolved ogygen (%)	Segment Clues nitrogen (ppb)	Depth (m)	Modelled sediment (g/m^2)	Nitrate nitrogen (mg/l)
				11.22	6.25	5.66	5.58	5.51	3.74
				< 85	< 82%	> 3	< 0.12	> 80	> 1.25
Longfin eel total biomass	0.964	0.647	0.035	Kōura density	Width (m)	Channel width (m)	Sample year	Segment flow variability	Substrate diversity
				20.47	9.09	5.78	3.44	2.81	2.81
				> 50	< 2	< 2	> 2013	> 0.24	> 5.5
Shortfin eel biomass / individual	0.692	0.608	0.067	Segment flow variability	Mean annual flood size (m^3/sec)	Modelled sediment (g/m^2)	Emergent exotic macrophytes (%)	Total phosphorous (mg/L)	Segment flow variability
				16.84	15.08	12.28	6.52	5.59	5.48
				< 0.02	< 1	> 90	> 50	> 0.055	< 0.1

Longfin eel biomass / individual	0.72	0.469	0.06	Bedrock (%)	Segment riparian shade (proportion)	Kōura abundance	Kōura density	Large gravel (%)	Substrate diversity
				12.41	8.61	8.51	6.53	5.93	3.84
				> 30	< 0.2	> 120	> 30	< 20	> 5.5

Discussion

The Boosted Regression Trees (BRT) performed better at modelling the focal species than the Bayesian Belief Networks (BBN) despite the BBNs being developed with variables selected *a priori* as potentially the most important for determining the abundance of the target species. The advantage of the BRTs is that they can select from the full suite of potential predictor variables in the specific dataset, rather than from a smaller, discretised list of potentially important variables. The logistical requirements of BBN construction essentially limit their ability to flexibly model the data. Furthermore, discretisation is difficult with many biological variables as they are continuous (Death *et al.* 2015).

As highlighted in the introduction, the BBNs are extremely useful for communicating the casual pathways of environmental influences on species populations, but if the actual predictive ability of the models is low then their educational merit is moot. It would be better to construct a diagram of the casual pathways once the important environmental drivers have been determined with a BRT. However, if mutual participation in the modelling is critical for buy-in, this approach may not provide a useful modelling tool for incorporating traditional knowledge.

Previous predictive spatial models of fish and invertebrate species for New Zealand rivers have focused on predicting presence/absence of those species at a specific site (Joy and Death 2002, 2004; Leathwick *et al.* 2005, 2008a, 2008b; Crow *et al.* 2014). However, for management of a food resource it is likely to be more important to identify sites where abundance is above a certain threshold rather than whether there is a high probability of finding a particular species. There are no current models for kākahi or kōura, but there are for both species of tuna. There is a weak relationship ($F_{1,48278}$ = 41478, P < 0.001, r^2=0.46 and $F_{1,48278}$ = 3133, P < 0.001, r^2=0.06) between the predicted abundance of the two species of tuna from the BRT model and the probability of finding the species at a site from the Crow *et al*. (2014) presence/absence model (Fig. 4). Thus, a high probability of finding tuna does not necessarily translate into there being a high abundance of tuna at a site. It would therefore seem far more sensible to focus on modelling abundance of a species rather than presence/absence for managing traditional food resources.

Table 2: Important variables in predicting target mahinga kai species in the Waikato Region grouped as to whether they are able to be managed of not. A “?” designates it may be challenging to manage

	Kōura numbers	**Kākahi numbers**	**Tuna numbers**	**Tuna biomass**
Can be managed	Substrate diversity	Deposited sediment	Segment riparian shade	Segment riparian shade
	? Conductivity	Large wood	Substrate diversity	? DO percent
		Temperature		Large gravel
		? Redfin bullies		Substrate diversity
		? Width MALF		Nitrate
				Total Phosphorous
				Deposited sediment
				? MCI
Beyond influence	Distance to coast	Catchment area	Altitude	Bedrock
	Mean annual flood size	Downstream maximum slope	Downstream maximum slope	Channel width
	Segment flow	Mean annual flood size	Easting	Depth
	Width	Upstream calcium	FRE3	
			Gradient	Emergent exotic macrophytes
			Segment slope	Kōura density
			Upstream Calcium	Mean annual flood size
			Catchment area	Sample year
			Width	Segment flow variability
				Segment low flow
				Width

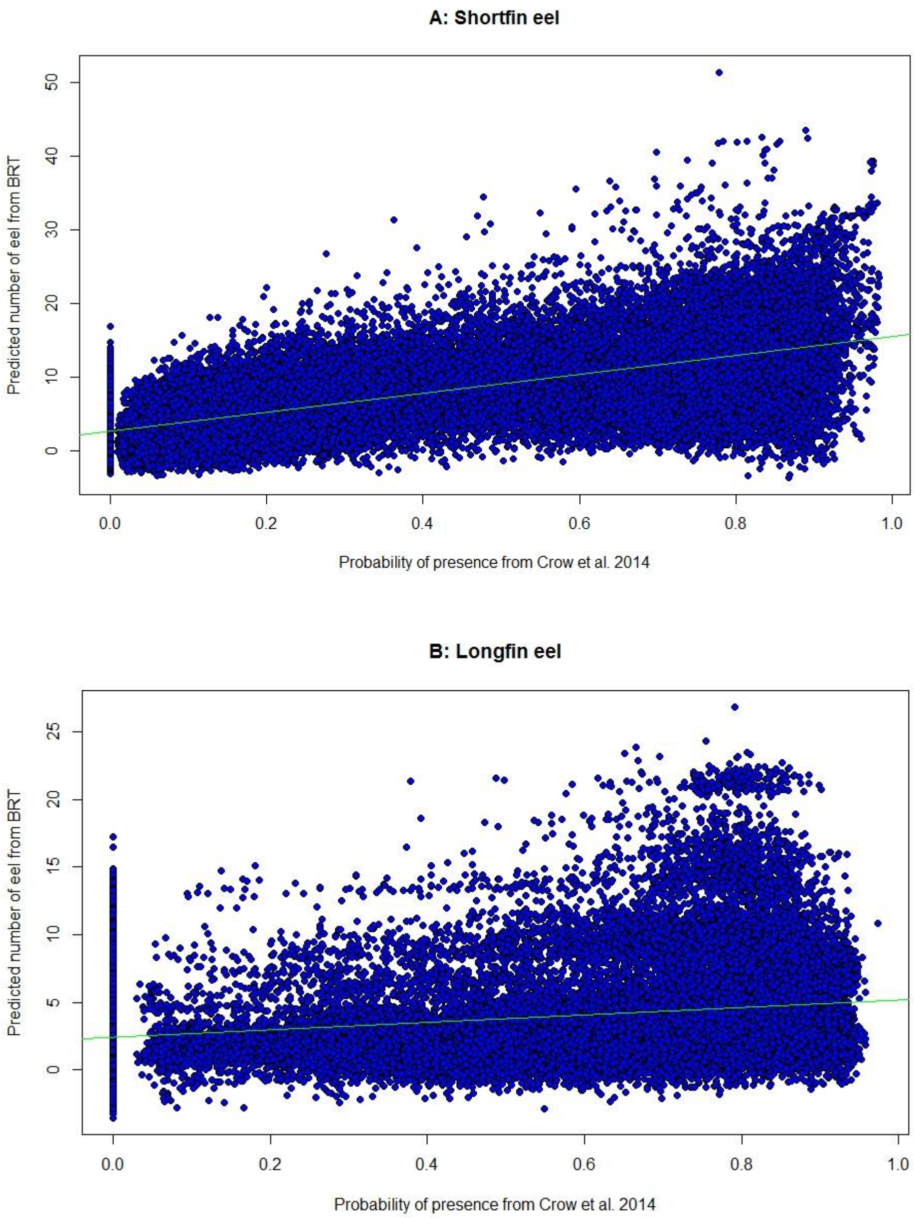

Figure 4: Plot of predicted abundance of (A) shortfin eel and (B) longfin eel from the BRT model against the probability of finding the species at that site from the Crow et al. (2014) presence/ absence model

Perhaps of most interest to indigenous peoples, from the perspective of food resources, is the total biomass and/or size of individual animals. Here there seems to be more variables that could potentially be manipulated to increase biomass including various measures of water quality, substrate and sediment deposition (Table 2). Again, these models of biomass may be far more useful for resource management of mahinga kai than the current presence/absence predictive models. Two issues that remain unresolved for more accurate models, particularly for biomass, include accounting for commercial (tuna only), recreational and/or customary harvest pressure, for which there are no data. Clearly, managing a resource without any records or estimates of harvest is extremely difficult. In small streams commercial harvest pressure may be low, but the impact, even if only decadal, may be quite severe for population biomass recovery. We also used electrofishing data collected by the local environment agency rather than the more traditional harvest technique of netting. Electrofishing is not as effective in deep water where larger eels are found in wadeable streams during the day. It is more effective in shallower streams where there tend to be fewer large eels because of the shallower conditions. However, netting is a passive technique suited to deeper water that catches proportionally larger eels from a larger spatial area. Furthermore, nets for traditional harvest may also be baited drawing from an even larger area. Finally, there are no models that assess the condition of the target species. Many tangata whenua (local people) have commented to us that while tuna may still be present, many are often now not suitable for consumption because of high parasite loads (R Death, pers comm.).

The utility of both modelling approaches to assist indigenous aspirations for directly managing traditional food resources may be limited because most of the important environmental drivers of species abundance are characteristics of environmental drivers beyond the ability of iwi to manage (e.g. location, altitude, flood regimes, catchment area and stream slope; Table 2). For example, kōura BRT models were strongly influenced by conductivity and substrate diversity, while kākahi models were influenced by the abundance of redfin bully, which prefer good water quality and unimpeded sea access, the presence of large wood and deposited sediment levels. There are some notable exceptions where local scale drivers were identified, however (Table 2), but only riparian shade and substrate diversity could be manipulated to affect tuna density; ironically, increasing density (predominantly for shortfin eels) is linked with declines in both these measures.

Conclusions

It can often be challenging for government agencies to develop resource management plans related to traditional food gathering sites and species as the knowledge of those sites may have been lost or be difficult to collect. Predictive abundance models of key species may offer potential for government agencies to take account of indigenous people’s aspirations at sites with high resource value even when that knowledge is lost or unavailable. They can also provide a mechanism for discussing the opportunities for environmental management actions to affect those populations, especially if all parties have been involved in the collection of data and model development, and construction of model architecture.

So are artificial intelligence models useful for traditional management of freshwater food resources? They can certainly provide objective and accurate models for linking target species with key environmental drivers from a large range of potential variables. However, these drivers may not necessarily be those that can be managed and/or those that have previously been held to be important, particularly when the scale of the model may differ from that of traditional management actions. They will, however, provide a useful starting point for conversations and/or management strategies for these species. While artificial intelligence models may seem to be a very powerful and useful tool, if people are not comfortable with their use or their predictions then they will no longer be useful. We found that developing that comfort can be challenging and to take quite some time. We also found that visual presentation of the findings at locations where participants can verify the outcomes based on their own knowledge greatly helps with their acceptance of the results.

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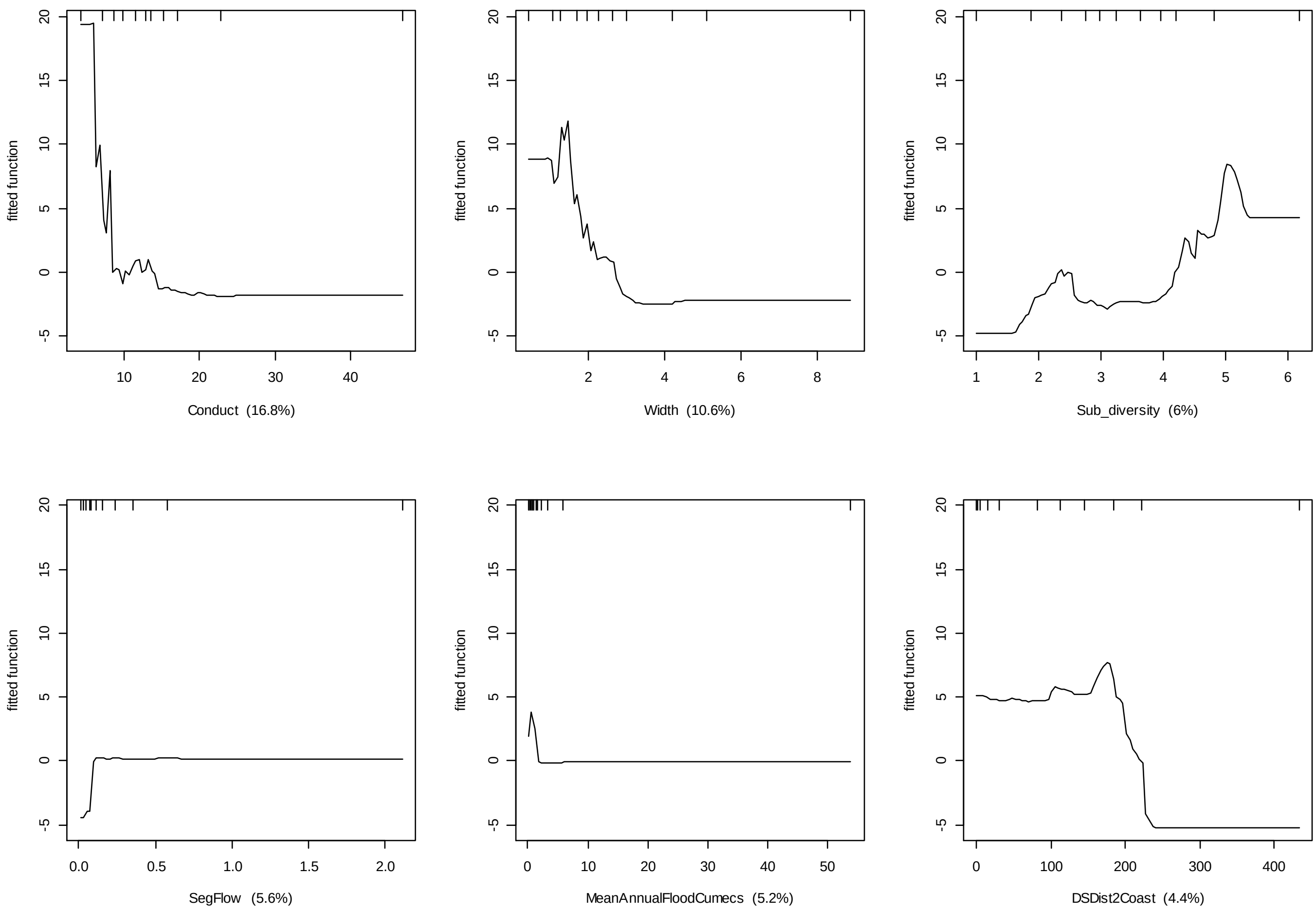
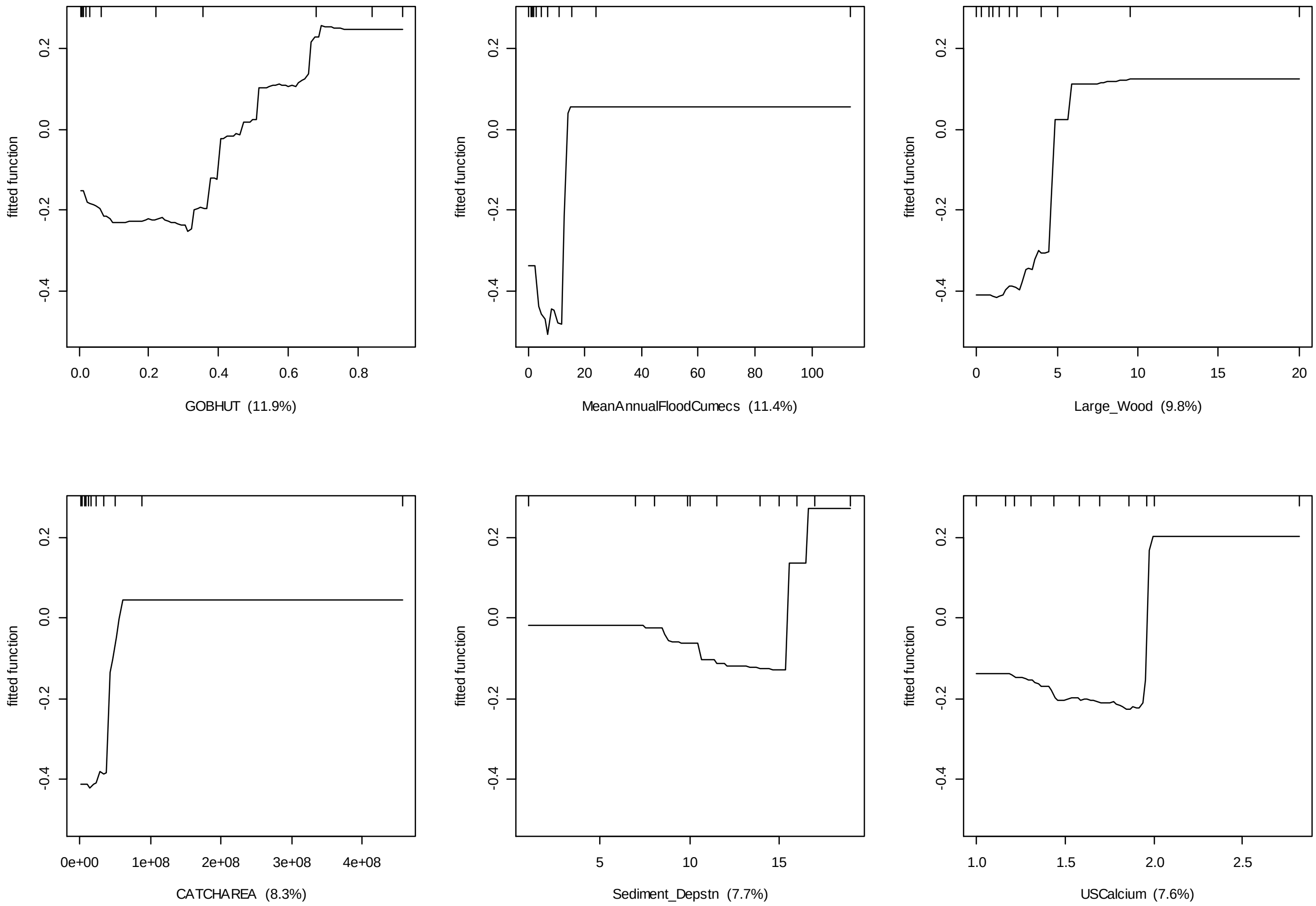
Appendix 1

Six partial plots from the most important predictor variables (in order of decreasing importance) in BRT models for:

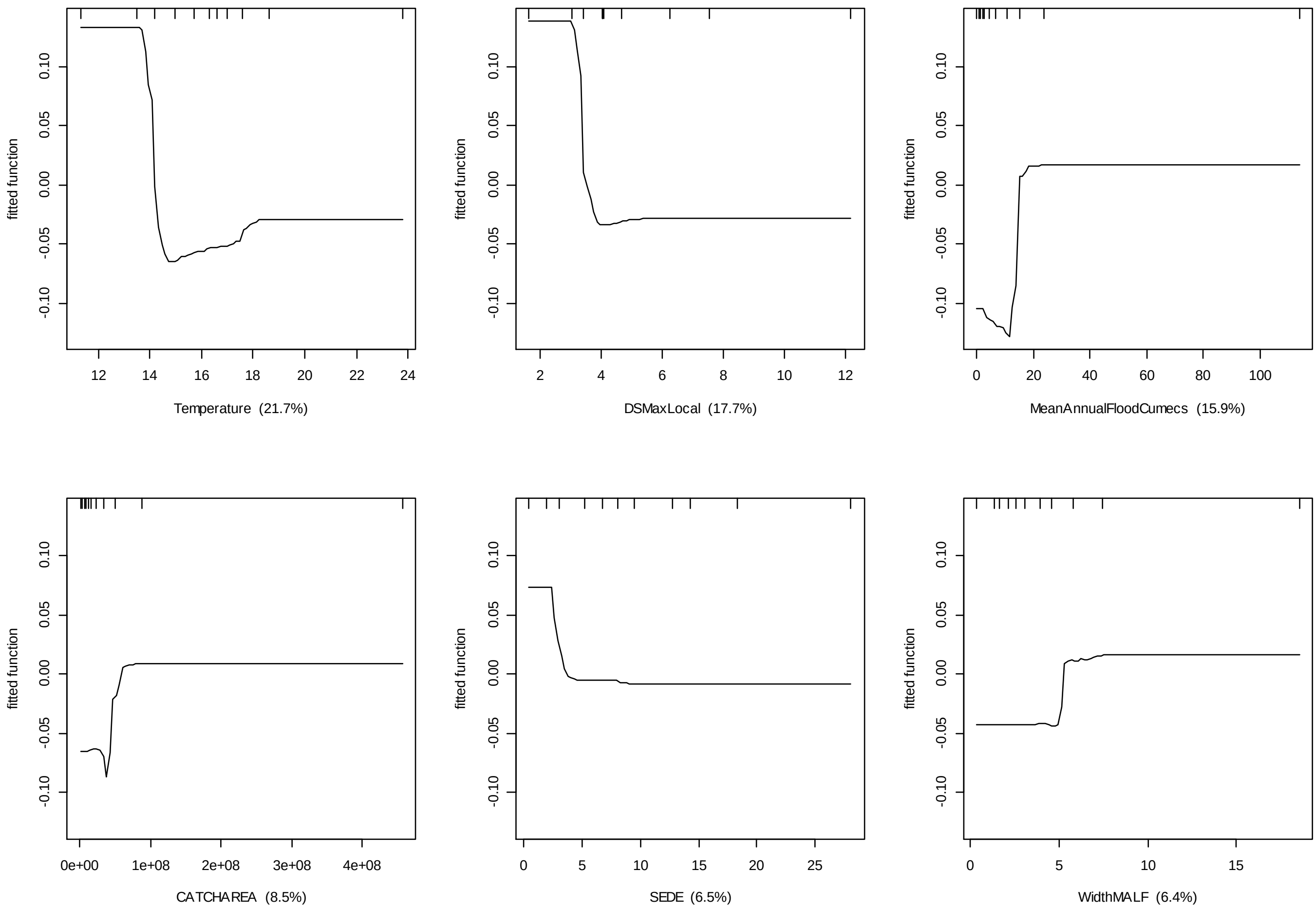
A) Kōura density per m^2



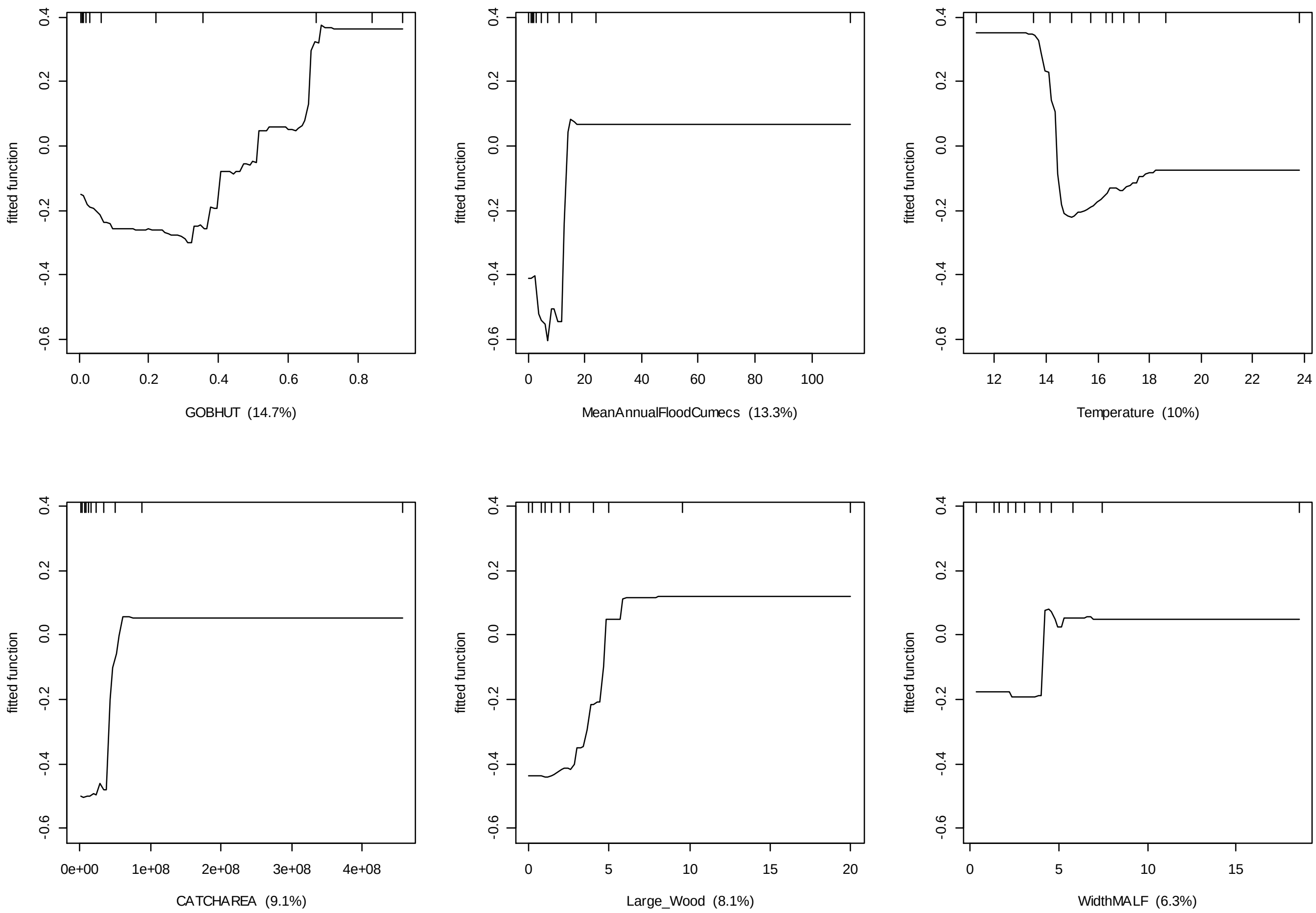
B) *Echyridella menziesii* density per m^2



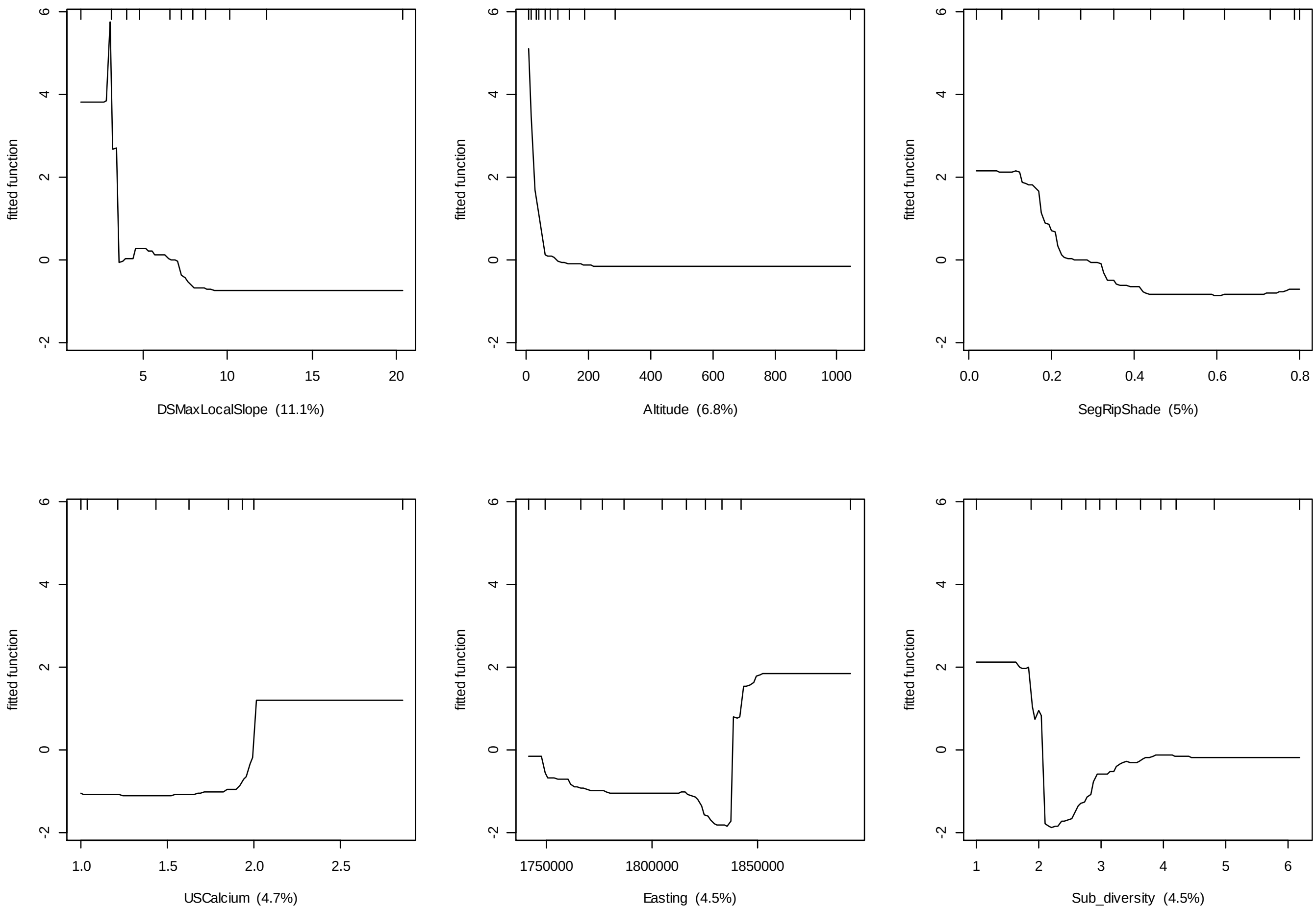
C) *Echyridella aucklandica* density per m^2



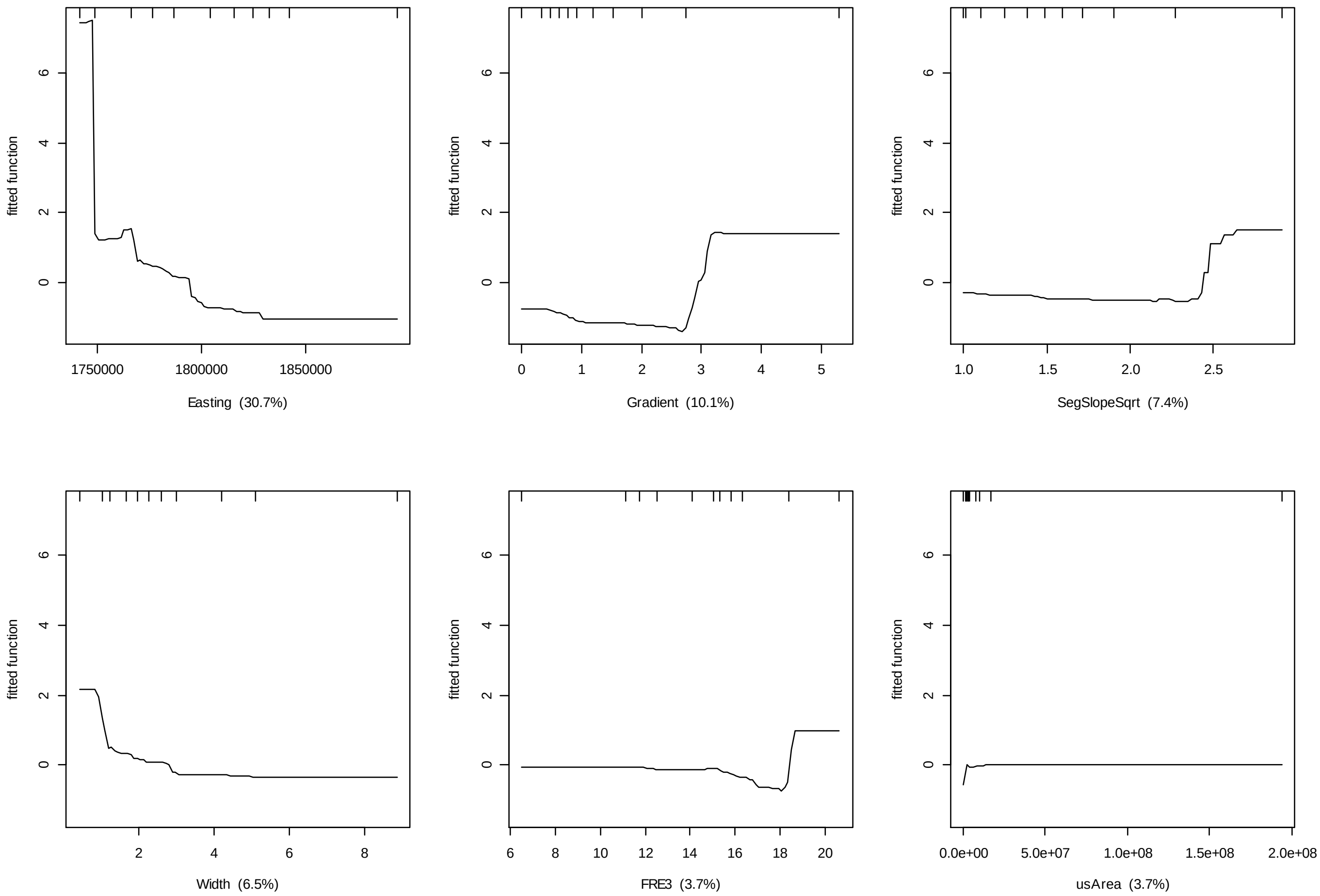
D) Total mussel density per m^2



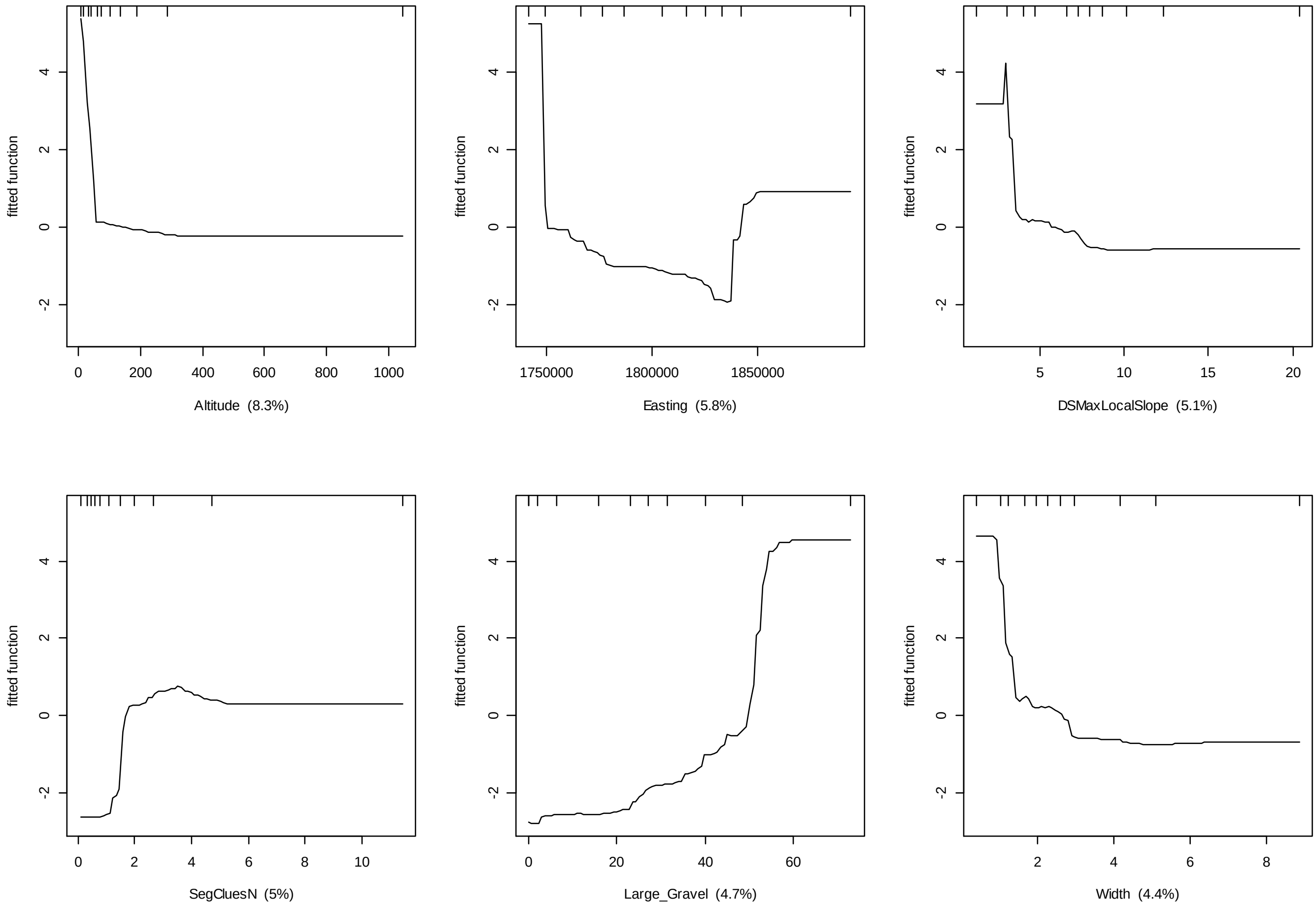
E) Shortfin eel density per m^2



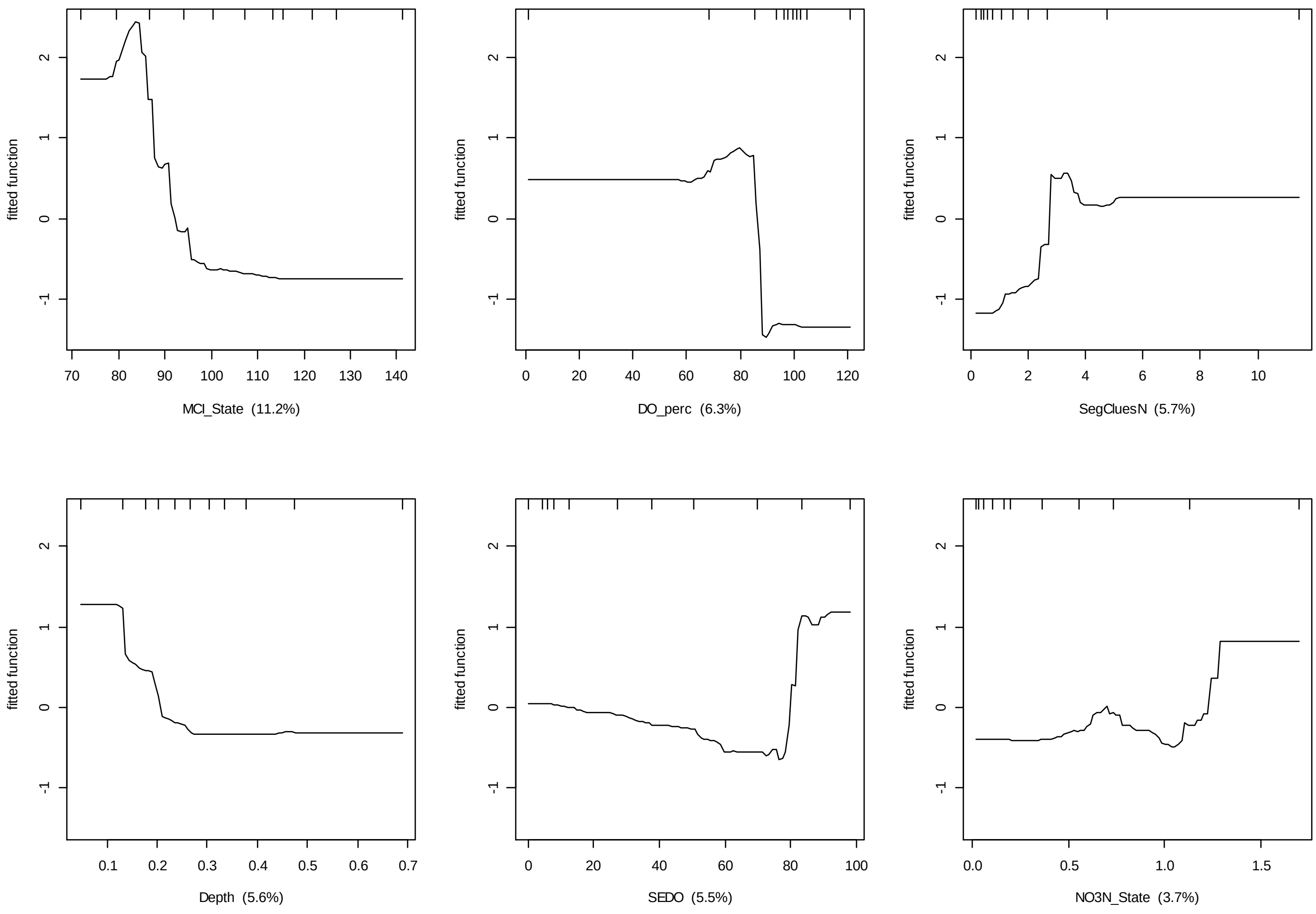
F) Longfin eel density per m^2



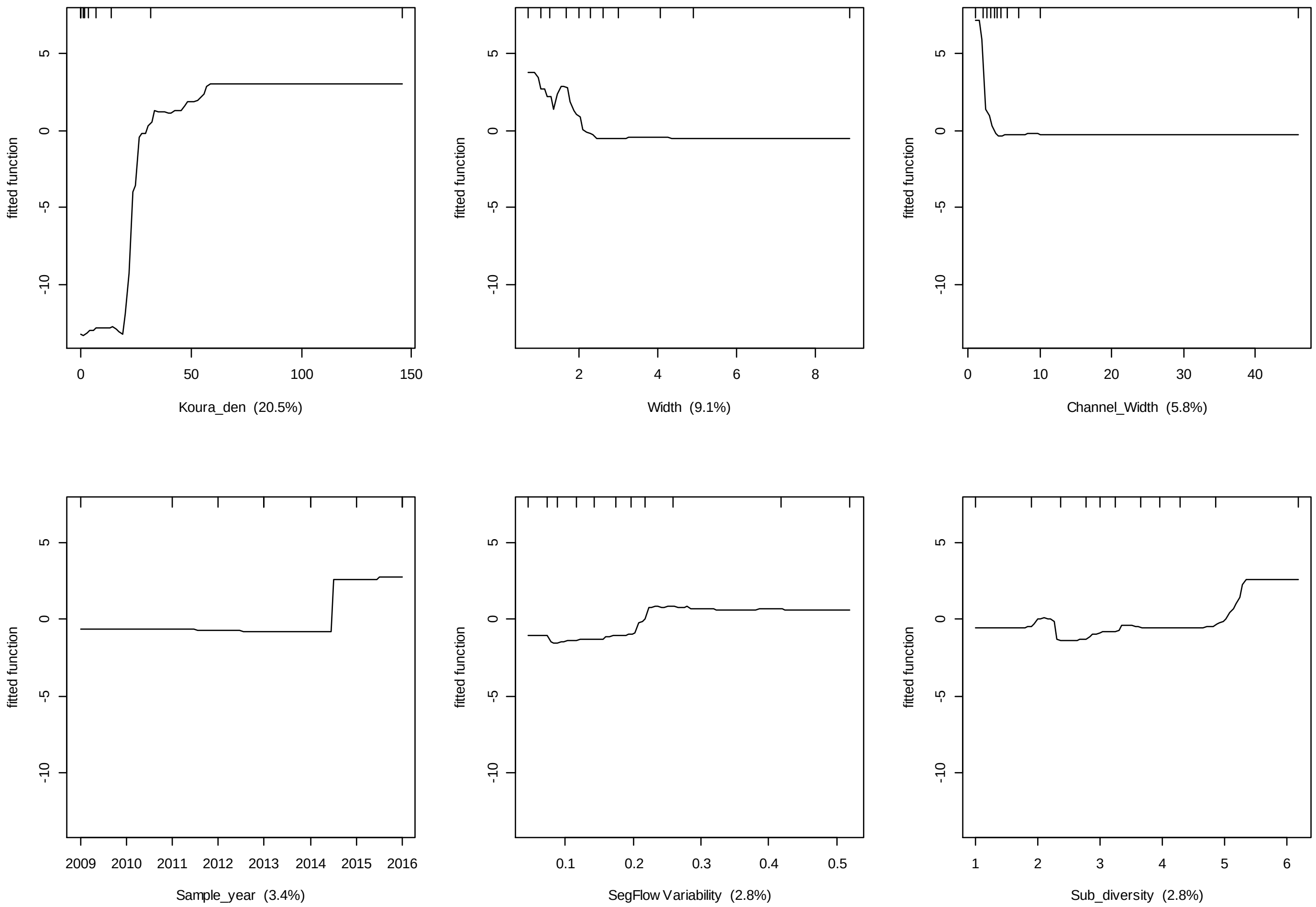
G) Total eel density per m^2



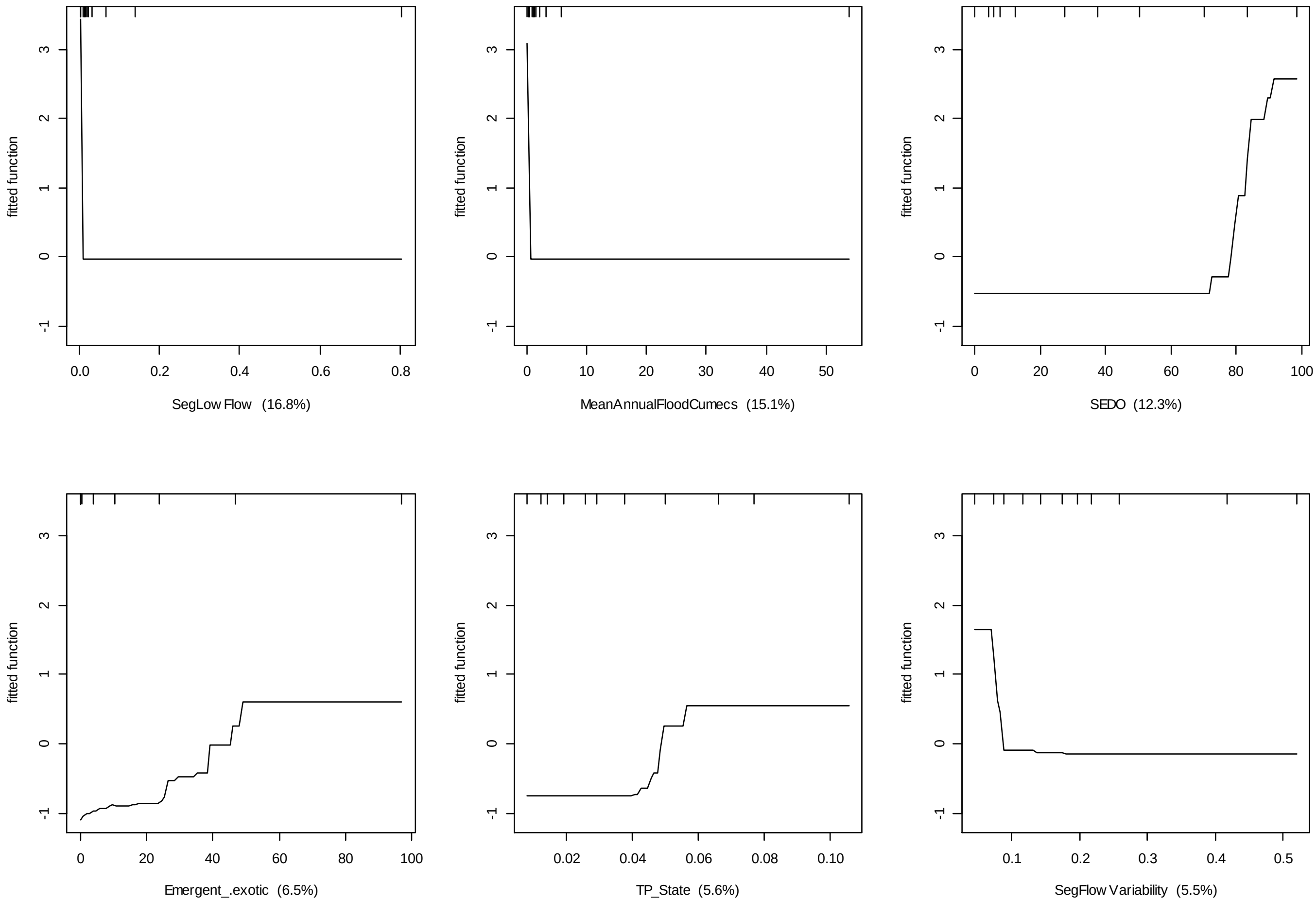
H) Shortfin eel total biomass per m^2



I) Longfin eel total biomass per m^2



J) Shortfin eel biomass per individual fish



K) Longfin eel biomass per individual fish