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Factors affecting the distribution of highly migratory species in New Zealand waters

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V. McGregor
P.L. Horn

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EXECUTIVE SUMMARY

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Distributional data from the New Zealand long-line fishery were fitted with BRT (Boosted Regression Tree) models using remote sensing datasets as predictors, to examine the extent to which large-scale biological and physical environmental forces might predict the potential distribution of highly migratory species.

While temporal and spatial variables and sea surface temperature were available, temperature at capture depth, chlorophyll-*a*, dissolved oxygen, and distance from a thermal front were not. Hence, the conclusions drawn here may comprise an incomplete explanation of what influences the species distributions.

BRT models were fitted to presence/absence data using the Binomial distribution and the number caught per set data using the Poisson distribution.

Predictive ability of all models was tested for each combination of species, response variable (presence/absence or number caught) and year. Predictive ability was found to range from poor to good, with models fitting to presence/absence generally better than those predicting the number caught.

Species that had either small datasets in terms of numbers caught or presences, or those with limited spatial distributions tended to have poorer predictive ability.

The species with the most predictive power in the Binomial models were albacore, big-eye tuna, butterfly tuna and long-snouted lancetfish. The species with the most predictive power in the Poisson models were butterfly tuna, mako shark, southern bluefin tuna and broadbill swordfish. Shortsnouted lancet fish had poor predictive ability in the Binomial and Poisson models. Big-eye tuna and yellowfin tuna had poor predictive ability in the Poisson models.

The predictive power was reduced when a model was applied outside the main range for a predictor variable of which it was fitted.

Variable effects were generally consistent for all models for each species. They sometimes became inconsistent where the data in one year were outside the range for one or more predictor variables in the other years.

The variables with the most influence in the Binomial models were sea surface temperature, latitude and subarea. The variables influencing the Poisson models varied greatly.

BRT models are usually fitted using temporal and environmental variables, and do not include spatial variables. Latitude and subarea were often selected as highly influential in these models and it is likely that these are a proxy for environmental variables.

1. INTRODUCTION

The new National Fisheries Plan for Highly Migratory Species (Ministry of Fisheries 2010) has identified the importance of using an ecosystem approach to fisheries management. In particular Objective 7 of the National Fisheries Plan for Highly Migratory Species aims to implement an ecosystem approach to fisheries management and aims to maintain food chain relationships and conserve trophic linkages.

The first steps in attempting to maintain food chain relationships and conserve trophic linkages were determining what they are, and what each species eats. The research reported here aimed to take distributional data and, using remote sensing datasets, examine the extent to which large-scale biological and physical environmental forces (i.e., at the scale of some kilometres resolution) influence the distribution of highly migratory species. The key database that formed the basis for this research was the data on the composition of the catch of highly migratory species from about 6500 surface longline sets, collected by observers between 1994 and 2012.

The research is part of a wider programme, in which we first established diet composition for the most abundant fish caught in the surface longline fishery, and evaluated whether there were any spatio-temporal patterns in diet (Horn et al. 2013). Then, in the research reported here, we assessed and determined potential linkages with wider biological and oceanographic characteristics and processes by examining the variance in univariate descriptors of the distribution of selected highly migratory species. The results of these analyses will indicate the feasibility of developing a focussed ecosystem model centred on Highly Migratory Species, their key prey species and the ecosystem resources needed to support their prey.

This document reports on Objective 3 of Project ZBD2011-01 "Evaluation of ecotrophic and environmental factors affecting the distribution and abundance of highly migratory species in New Zealand waters". Project objectives are as follows:

1. Assess the dietary composition of highly migratory teleosts and elasmobranchs using the data collected by the Observer Services.
2. Assess spatio-temporal patterns in dietary composition and changes in food utilisation with fish size.
3. Identify biological and physical environmental forces that can be used to explain highly migratory species distribution.
4. Develop an ecosystem model for the pelagic environment in New Zealand waters.

Objectives 1 and 2 were reported on by Horn et al. (2013). An examination of the results from Objectives 1–3 will determine whether it is viable to complete Objective 4, and, if so, what methods will be used to complete it.

2. METHODS

2.1 Fishery data

Information collected by observers on commercial surface longline vessels is stored in the centralised observer database (*cod*) administered by NIWA for the Ministry for Primary Industries (MPI). Sampling of individual surface longline sets involves the observers identifying and counting all longline catch brought on board the vessel during the time they are observing. The data available from *cod* for this analysis comprised information from 6515 observed surface longline sets collected between 25 March 1994 and 28 August 2012.

Information about commercial catch recorded by fishers on Tuna Longline Catch Effort Return (TLCER) forms is stored on the database (*warehou*) administered by MPI. For the current analysis, however, the Observer data was used in preference to TLCER data, because the commercial data tends to underestimate bycatch and catch of non-quota species because much of it is discarded at sea and not recorded (Francis et al. 2000). Several of the most abundant species were only introduced into the QMS in 2004 (e.g., southern bluefin and big-eye tunas, swordfish, mako, porbeagle and blue sharks, moonfish, Ray's bream), so QMS data on the distribution and abundance of these species would not be comprehensive or reliable.

An 'absence' for a species was where an observed set did not catch that species (the number observed for the species was zero). A presence for a species was where an observed set did catch that species (the number observed was greater than zero). The numbers of presences and absences for each species for each year are in Tables 1 and 2 respectively.

Table 1: Number of presences for each species for each year.

	Species code												
	ABR	**ALB**	**BIG**	**BTU**	**BWS**	**LAT**	**MAK**	**MOO**	**POS**	**RBM**	**STN**	**SWO**	**YFN**
1994	1	110	14	60	228	12	66	52	164	208	217	29	2
1995	0	137	26	72	260	49	84	90	228	260	258	20	31
1996	0	97	28	7	136	58	51	57	98	83	70	36	30
1997	0	222	53	117	400	99	154	190	286	293	304	124	71
1998	43	329	105	146	425	103	183	240	340	266	306	184	57
1999	12	284	31	164	381	63	144	160	348	294	335	172	22
2000	12	184	37	126	269	52	84	113	203	202	210	115	25
2001	99	261	77	72	271	139	142	152	122	145	134	182	92
2002	35	223	20	68	334	77	104	127	164	294	275	100	15
2003	69	460	131	86	545	138	185	211	225	350	316	121	112
2004	35	274	30	56	531	72	144	124	282	465	427	127	5
2005	16	255	36	55	311	84	131	120	160	219	214	130	18
2006	9	151	60	48	264	105	90	80	127	203	194	106	17
2007	26	358	80	99	404	192	184	213	252	293	292	184	21
2008	21	201	85	39	233	114	118	91	121	127	135	123	18
2009	58	255	97	98	395	130	171	136	230	308	284	137	7
2010	63	210	58	53	291	107	121	147	143	222	214	124	8
2011	21	205	76	60	315	104	152	112	168	212	229	162	2
2012	5	158	14	54	280	26	95	61	164	225	241	115	0

Table 2: Number of absences for each species for each year.

	Species Code												
	ABR	**ALB**	**BIG**	**BTU**	**BWS**	**LAT**	**MAK**	**MOO**	**POS**	**RBM**	**STN**	**SWO**	**YFN**
1994	237	128	224	178	10	226	172	186	74	30	21	209	236
1995	312	175	286	240	52	263	228	222	84	52	54	292	281
1996	140	43	112	133	4	82	89	83	42	57	70	104	110
1997	419	197	366	302	19	320	265	229	133	126	115	295	348
1998	397	111	335	294	15	337	257	200	100	174	134	256	383
1999	374	102	355	222	5	323	242	226	38	92	51	214	364
2000	265	93	240	151	8	225	193	164	74	75	67	162	252
2001	212	50	234	239	40	172	169	159	189	166	177	129	219
2002	315	127	330	282	16	273	246	223	186	56	75	250	335
2003	505	114	443	488	29	436	389	363	349	224	258	453	462
2004	506	267	511	485	10	469	397	417	259	76	114	414	536
2005	300	61	280	261	5	232	185	196	156	97	102	186	298
2006	266	124	215	227	11	170	185	195	148	72	81	169	258
2007	381	49	327	308	3	215	223	194	155	114	115	223	386
2008	214	34	150	196	2	121	117	144	114	108	100	112	217
2009	338	141	299	298	1	266	225	260	166	88	112	259	389
2010	238	91	243	248	10	194	180	154	158	79	87	177	293
2011	296	112	241	257	2	213	165	205	149	105	88	155	315
2012	275	122	266	226	0	254	185	219	116	55	39	165	280

For each set, available data included date, location (at the start of the set, to the nearest 0.1 degree of latitude and longitude), time at start of set and start of haul, number of hooks observed and the catch from them, and hook depth. Hook depth was derived for each longline set as the mean of the estimated maximum and minimum depths of hooks set, as recorded by the vessel skipper. The number of each species caught can be standardised as a catch per hook to give an index of relative abundance for that species at the location of the set. Rather than standardising, the BRT models were fitted to the number of each species caught, with the number of hooks offered as an explanatory variable. This approach avoids assuming a relationship between the number caught and the number of hooks, but allows for the relationship to exist. This was the approach also used for the Antarctic toothfish longline CPUE (catch per unit effort) (Hanchet et al. (2013)). Associated environmental parameters were applied to each set start date and location as described in Section 2.2. Each set was allocated to an area (one of four categories) and a sub-area (one of nine categories) as defined in Figure 1.

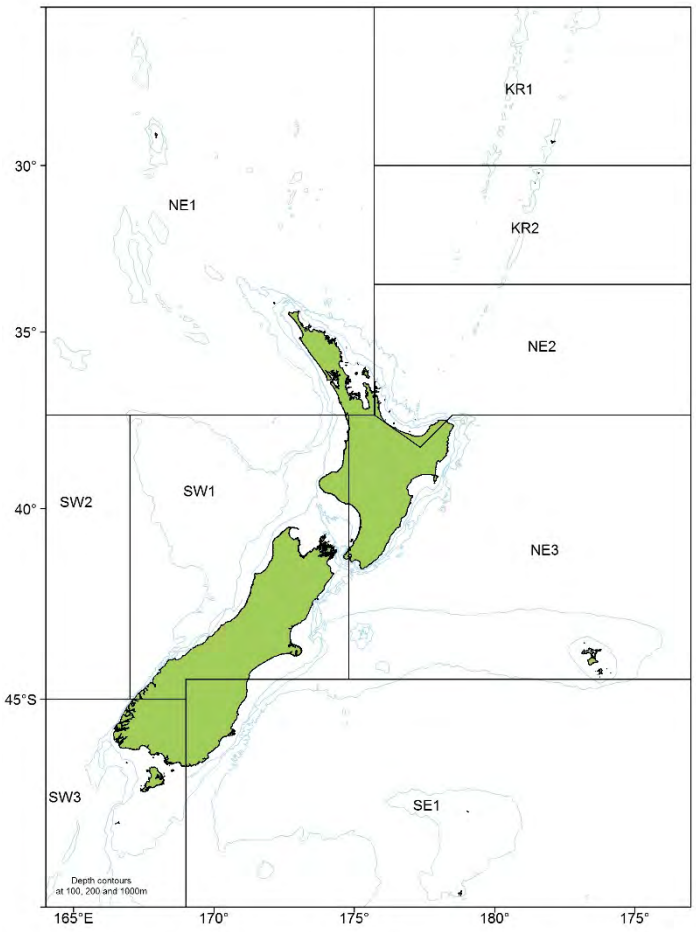


Figure 1: Subarea boundaries.

Distributional analyses are provided for the 13 species chosen for detailed dietary analyses by the Aquatic Environment Working Group. The set of species comprises the 14 most commonly caught species, excluding school shark.

2.2 Environmental data

A value of sea surface temperature (SST) for each landing location was derived from the Reynold's Optimum Interpolation (OI) Sea Surface Temperature Analysis. This analysis is produced daily on a ¼ degree grid. The analysis uses in situ and satellite SSTs plus SSTs simulated by sea ice cover. Before the analysis is computed, the satellite data is adjusted for biases using the method of Reynolds (1988) and Reynolds & Marsico (1993). A description of the OI analysis can be found in Reynolds & Smith (1994). The bias correction improves the large scale accuracy of the OI. The version used here (OI.v2) has an improved sea-ice simulation as described in Reynolds et al. (2002). The SST value relevant to the fisheries data was found by finding the nearest SST datapoint to the fisheries location for the same day. The ¼ degree SST grid means effectively 25 km resolution.

The sea surface height (SSH) values were found using an AVISO product for sea surface height (see http://www.aviso.oceanobs.com/en/altimetry.html). The product used was the reference version of the MADT (Maps of Absolute Topography) dataset. This is a spatially objectively-analysed (mapped) combination of 10-day repeat measurements of sea surface height anomaly with the Mean Dynamic Topography (MDT). The MDT is the part of mean SSH due to permanent currents, and so corresponds to the mean SSH minus the geoid. More information about the MDT used in SSALTO/DUACS system can be found on the AVISO web site at: http://www.aviso.oceanobs.com/en/data/products/auxiliary-products/mdt/. The SSH data are related to

the integrated density of the water at that point through the depth of the ocean; this is because less-dense water stands taller. Around New Zealand there is a north-south gradient in salinity that impacts SSH because saltier water is denser, with Subtropical Water (warm and salty) north of the Subtropical Front and Sub-Antarctic water (cold and fresh) south of the Subtropical Front. The nature of variability around New Zealand is that almost all of the variability in SSH results from changes in temperature. Thus, highs in SSH correspond to areas with higher mean temperatures, and vice versa.

The slopes in the sea surface result in currents that run along the lines of constant height, in the same way that winds flow along isobars in weather maps. This means that the estimates of MADT can also supply estimates of the surface current field. In this study, the magnitude of the current was extracted for comparison with the fisheries data. The MADT mapped height and velocity products have resolutions of 0.2–0.3° of latitude, 0.33° of longitude, and 7 days. The SSH and current speed values relevant to the fisheries data were determined by finding the nearest datapoint to the fisheries location on the nearest day.

Because moon phase is known to influence the feeding behaviour of some pelagic species, including southern bluefin tuna and Ray's bream (Kemps et at. 1998, Horn et al. 2013), the date-time of fish capture was referenced to moon phase as follows. The mean lunar cycle of 29.5 days was divided into four equal bins, each about 7.4 days long using a moon phase calculator at: http://www.timeanddate.com. Bin 1 was the 7.4 days centred on the actual date-time of the full moon, bin 2 encompassed the 7.4 days around the third quarter, bin 3 encompassed new moon, and bin 4 the first quarter.

2.3 Data analyses

A powerful method that is gaining widespread support for extrapolation of the distribution of a single species (or single group of species) is the statistical technique of boosted regression trees (BRT: Leathwick et al. 2006). We used a set of predictor variables (Table 3) to explain the variance in univariate descriptors of distribution of each HMS species using BRT. Models for presence-absence (binomial) and for number caught (Poisson) were investigated (Pinkerton et al. 2010) based on catch and effort data from the *cod* database.

Table 3: Data used for these analyses, with descriptions of variable names.

	Data	Description
Fishing	fishing_event_key	Unique combination of trip_no and set_no *(not offered as a predictor variable)*
	duration	Time (in hours) between start of set and start of haul
	hook_depth	Average estimated depth (m) of hooks set
	hook_no	Number of hooks set on the longline
Location	start_latitude	Latitude at start of set
	start_longitude	Longitude at start of set
	area	Gross area split (four areas: KR, NE, SE, SW)
	sub_area	More refined area split (nine areas)
Time/date	set_date	Date longline was set
	set_time	Start time of set (24 hr clock, decimalised)
	time_haul	Start time of haul
	haul_date	Date haul started
	haul_month	Month haul started
	haul_yr	Year haul started
Environmental	SST	Sea surface temperature
	SST_anomaly	Sea surface temperature anomaly
	SSH	Sea surface height (cm)

	SSH_mag_uv	Surface current (cm/second)
	moon_ph	Moon phase (four bins, each about 7.4 days long)
Catch by species		*Number of this species caught on this longline set*
	ABR	Shortsnouted lancetfish
	ALB	Albacore
	BIG	Big-eye tuna
	BTU	Butterfly tuna
	BWS	Blue shark
	LAT	Longsnouted lancetfish
	MAK	Mako shark
	MOO	Moonfish
	POS	Porbeagle shark
	RBM	Ray's bream
	STN	Southern bluefin tuna
	SWO	Broadbill swordfish
	YFN	Yellowfin tuna

The Boosted Regression Trees (BRT) modelling technique is a method used for modelling single response variables using several predictors (Leathwick et al. 2006; Ridgeway 2006; De'ath 2007; Elith et al. 2008). BRT is an ensemble method, meaning that a large number of relatively simple models, in this case, binary regression trees, are combined and averaged to give a model that generally outperforms traditional multivariate fitting methods in terms of the explanatory power of the resulting model (Friedman & Meulman 2003; Hastie et al. 2001). BRT automatically fits complex, non-linear interactions between variables. The fitting of a BRT model is controlled by three factors: (1) the learning rate; (2) the tree complexity (how many independent variables can interact to determine each split); (3) the number of trees that are used. These parameters, and the cross-validation method explained below, were chosen so as to generate models with a high degree of generality because we want to potentially use the fitted model to extend spatial predictions of species presence or abundance into unsampled areas (Hastie et al. 2001). The relative importance of predictor variables was calculated as developed by Friedman (2001), and implemented in the R-gbm library (Ridgeway 2006).

For each BRT model developed, the optimal learning rate (*lr*), tree complexity (*tc*) and number of trees (*nt*) were selected using a step-wise process as described in Elith et al. (2008).

To test the predictive power of the models, a separate model was developed for each year, from 1994 to 2012, and each of the 13 species. For each model, the data for species s were selected, then the data for year y removed. The model was fitted to the resulting dataset. This model was then used to predict the response variable in the data for year y, species s. The resulting fitted values were compared with the observed values. The predictive ability of a model was assessed by analysing various plots and calculating the predictive deviance, as defined by Elith et al. (2008). A smaller predictive deviance indicates that a model has greater predictive power. A plot of fitted versus observed values was created for each model. If the model fitted well, the points were close to the line $y = x$. Plots were also created on the New Zealand map to show spatially the observed responses and the fitted responses. For the presence-absence (Binomial) models, each point is coloured according to the fitted probability of a presence. These were compared to the plot of observed presences and absences. For the number present (Poisson) models, separate maps are presented for observed data and fitted data, with the colour of each point indicating the number present. These figures are presented in Appendix C and key figures are also in the Results section.

For each predictor variable, its relative contribution (influence) was calculated as developed by Friedman (2001). This, and the consistency of a variable effect as viewed in the partial dependence plots were used to assess a variable's usefulness and reliability in the model.

3. RESULTS

3.1 Selecting controlling factors and assessing predictive power

Initially, all models were fitted using *tc*=2 and *tc*=3, which corresponds to allowing either one level interactions (e.g. SST × depth) or two level interactions (e.g. SST × depth × moon phase). The calculated predictive deviance for each model for a species with *tc*=2 and *tc*=3 were compared, with an increase in the predictive deviance required to justify increasing the *tc* from 2 to 3. Increasing the *tc* to 4 was not considered due to minimal improvements resulting from increasing from 2 to 3. For the SWO Poisson models, there was sufficient improvement in predictive ability to justify using *tc*=3. For all other models, *tc*=2 was sufficient.

For each *tc*, the optimal learning rate (*lr*) and number of trees (*nt*) were found by decreasing *lr* and increasing *nt* until either the minimum predictive deviance was found (full description of this method in Elith et al. (2008)) or the limit was exceeded for either *lr* or *nt*. The limits set were 0.0005 for *lr* and 2000 for *nt*. The resulting values are in **Error! Reference source not found.**. As all models exceed the limit of 2000 for *nt,* the most extreme cases (BTU Poisson and RBM Poisson) were rerun with a limit of 10 000 for *nt.* The improvement in terms of predictive ability are insufficient to warrant the additional number of trees (Figure 2).

Predictive power of the models varies between species and whether it is the count data or presence/absence data being modelled. Four of the species (ALB, BIG, BTU and LAT) had fair-good predictive power across all Binomial (presence/absence) models (**Error! Reference source not found.**). For these species, the Binomial models can be used with reasonable confidence. There are some cases where the models should not be used; ABR had poor-fair predictive power in the Binomial models and poor predictive power in the Poisson (count) models, and BIG and YFN both had poor predictive power in the Poisson models. The rest of the models have poor-good or poor-fair predictive ability, and while they can be of use, the possibility of poor predictive ability from them should be remembered.

The deviance explained is generally higher for the Poisson models than the Binomial models, even though the Binomial models fit the data better based on visual analysis of the comparison plots.

Table 4: Summary of Binomial (a) and Poisson (b) models for each species. The blue rows indicate models with sufficient predictive power such that the variable effects were analysed. A darker shade of blue indicates greater predictive power based on analysis of comparison plots (as follows in the remainder of this section.

a.)

Binomial (presence/absence) models

Species	*tc*	*lr*	*nt*	*Predictive ability*	*Proportion deviance explained*	*Number of presences*	*Number of absences*
ABR	2	0.05	220	Poor-fair	0.49	530	5 990
ALB	2	0.02	245	Fair-good	0.36	4 370	2 140
BIG	2	0.01	2300	Fair-good	0.58	1 060	5 460
BTU	2	0.01	3000	Fair-good	0.22	1 480	5 040
BWS	2	0.01	2550	Poor-good	0.23	6 270	240
LAT	2	0.02	2600	Fair-very good	0.58	1 720	4 790
MAK	2	0.01	2350	Poor-fair	0.25	2 400	4 110
MOO	2	0.02	2250	Poor-fair	0.16	2 480	4 040
POS	2	0.05	2600	Poor-fair	0.25	3 830	2 690
RBM	2	0.02	3000	Poor-good	0.51	4 670	1 850
STN	2	0.02	2300	Poor-good	0.64	4 660	1 860
SWO	2	0.02	2250	Poor-fair	0.41	2 290	4 220
YFN	2	0.01	3000	Poor-good	0.68	550	5960

b.)

Poisson (number caught)

Species	*tc*	*lr*	*nt*	*Predictive ability*	*Proportion deviance explained*	*Number caught*
ABR	2	0.02	2750	Poor	0.65	2 240
ALB	2	0.05	5050	Poor-fair	0.83	85 020
BIG	2	0.05	2550	Poor	0.75	3 760
BTU	2	0.05	2800	Poor-good	0.50	3 140
BWS	2	0.05	7800	Poor-fair	0.56	166 060
LAT	2	0.05	3200	Poor-good	0.80	12 370
MAK	2	0.04	2400	Fair	0.45	5 610
MOO	2	0.05	3100	Poor-fair	0.57	7 820
POS	2	0.05	5900	Poor-fair	0.51	16 100
RBM	2	0.05	6950	Poor-fair	0.66	106 050
STN	2	0.05	6750	Poor-good	0.62	43 670
SWO	3	0.02	2850	Poor-good	0.63	7 750
YFN	2	0.02	2500	poor	0.83	3 210

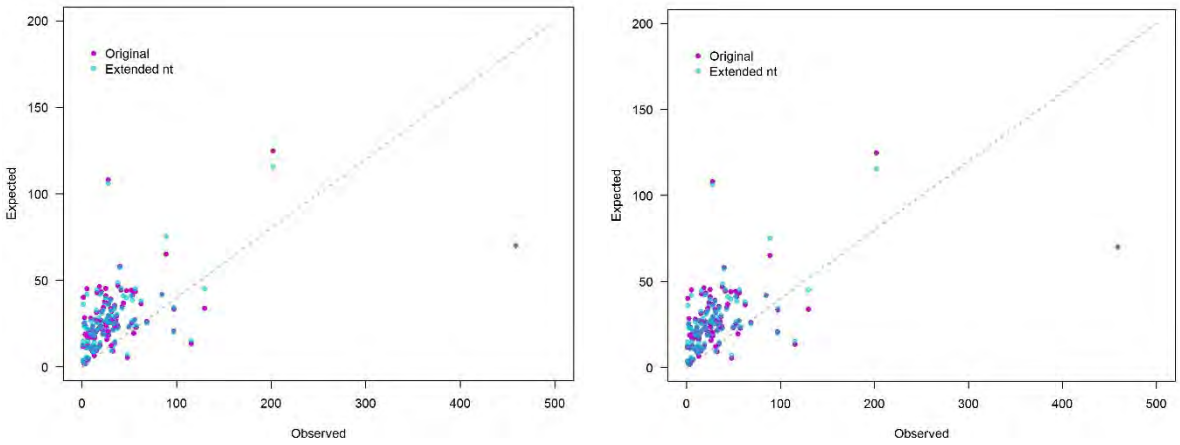


Figure 2: Observed and predicted counts of BWS (left) and RBM (right) for each year/subarea bin with the original limit of 1000 trees and the extended limit of 10 000 trees.

3.1.1 ABR

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 decreases the predictive deviance in the 2010 model (Figure 3), but is almost the same in all other models. For both *tc*=2 and *tc*=3, most of the predictive deviance in the 2010 model is coming from subarea NE1, and while there appears to be a significant drop in predictive deviance in Figure 3, the difference is unnoticeable in Figure 4. It is not likely that further increasing the *tc* would significantly improve predictive ability and for the remainder of the analyses *tc*=2 has been used for all ABR Poisson models.

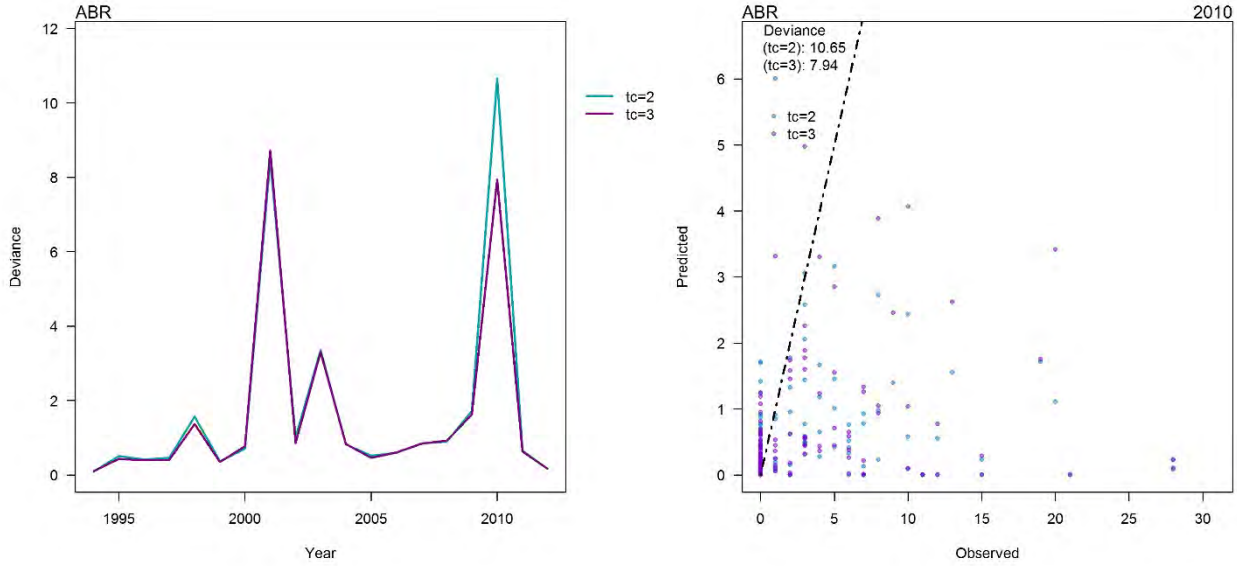
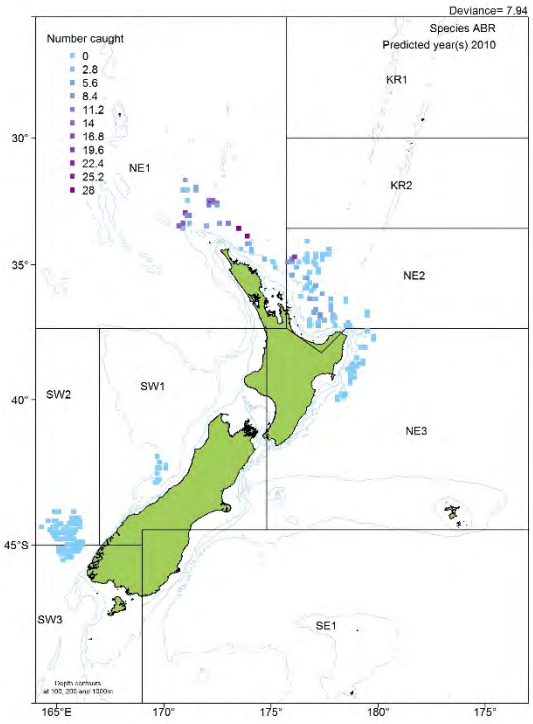
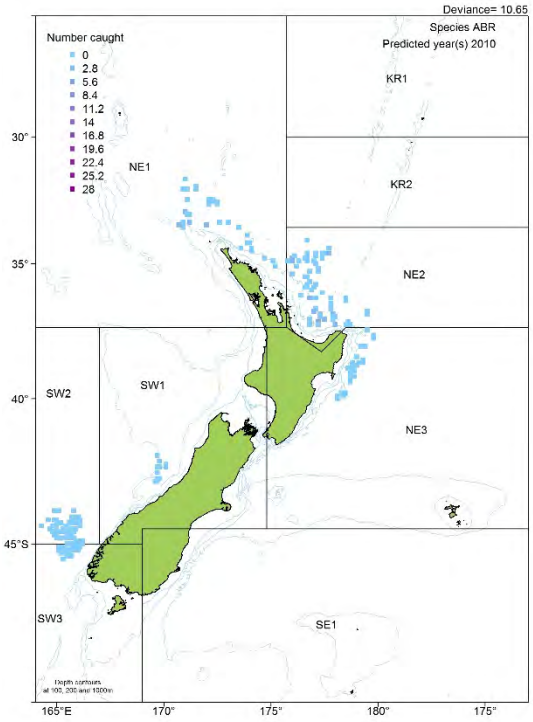


Figure 3: Predictive deviance for Poisson model using tree complexity of 2 and 3 across all years (left) and for the 2010 model (right) for species ABR.

a.) Observed



b.) Predicted (*tc*=2)



c.) Predicted (*tc*=3)

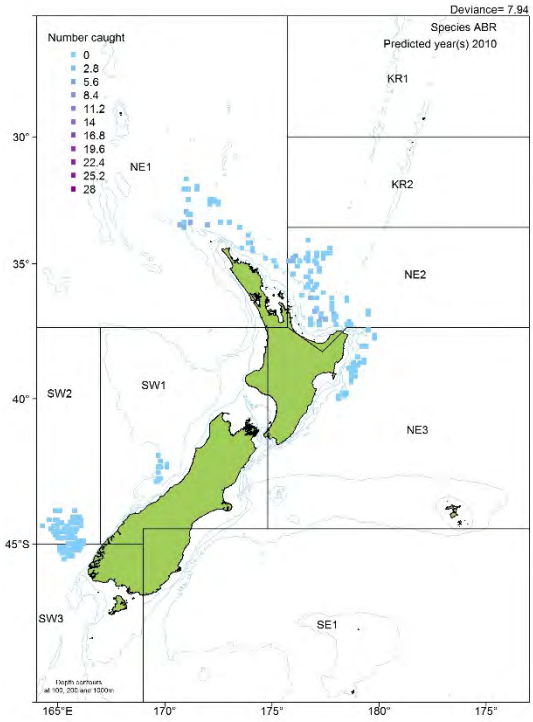


Figure 4: Observed (a) and predicted using tc=2 (b) and tc=3 (c) numbers of ABR caught with the 2010 Poisson model.

Binomial

Increasing the *tc* from 2 to 3 causes little change in the predictive deviance in all models, with slight increases or decreases in some (Figure 5). It is not likely that further increasing the *tc* would significantly improve the predictive ability and for the remainder of the analyses *tc*=2 has been used for all ABR Binomial models.

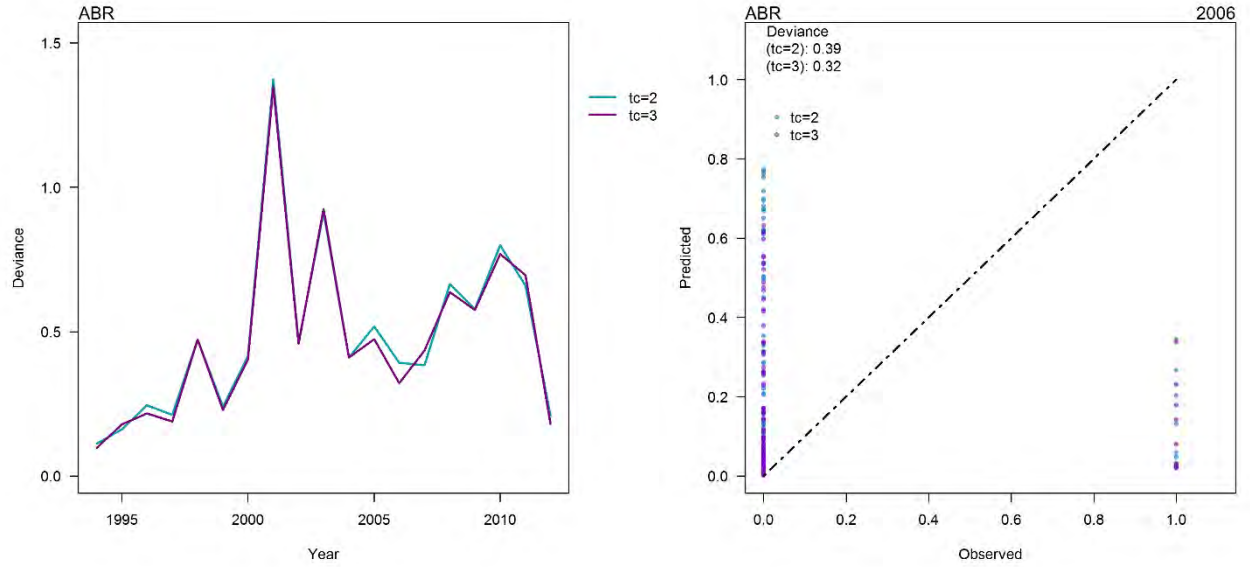


Figure 5: Predictive deviance for Binomial model using tree complexity of 2 and 3 across all years (left) and for the 2006 model (right) for species ABR.

Predictive ability

Poisson

The predictive ability was generally poor (Figures 6 and 7). The models omitting year 2001, 2003 or 2010 had the highest predictive deviance (Figure 3). In all these years, the predicted numbers caught were almost entirely unmatched with the observed in both location and numbers (Figures 8, 9 and 11). The 1999, 2005 and 2010 models had three of the lowest predictive deviances. The predicted numbers caught using the 1999 model were similar to those observed (Figure 7), but the 2012 model (Figure 12) and the 2005 model (Figure 10) had fairly poor predictability. Due to poor predictive ability, and hence irrelevance of the models, no further analyses are presented for ABR Poisson models.

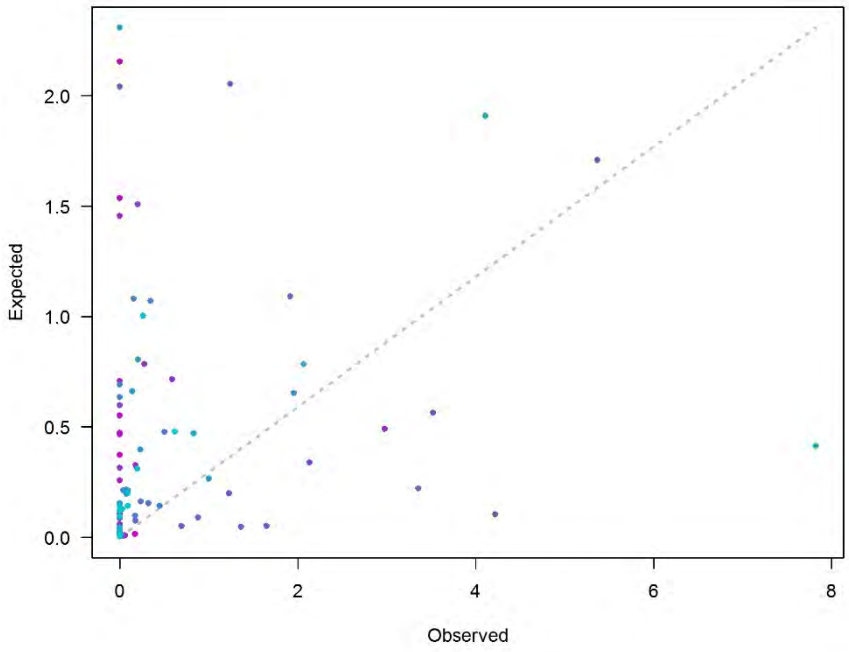


Figure 6: Observed and predicted counts from ABR Poisson models for each year/subarea bin. Green dots are tc=2, purple dots are tc=3.

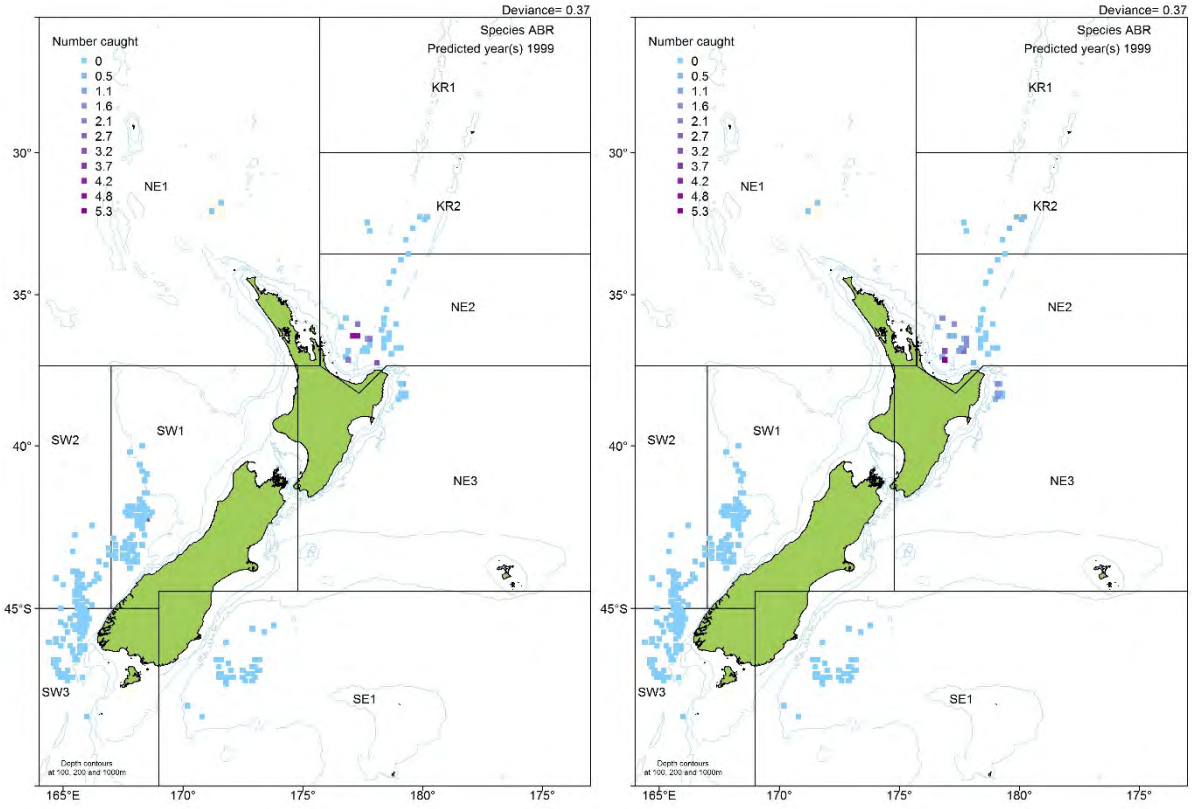


Figure 7: 1999 Poisson model observed (left) and predicted (right) numbers of ABR caught.

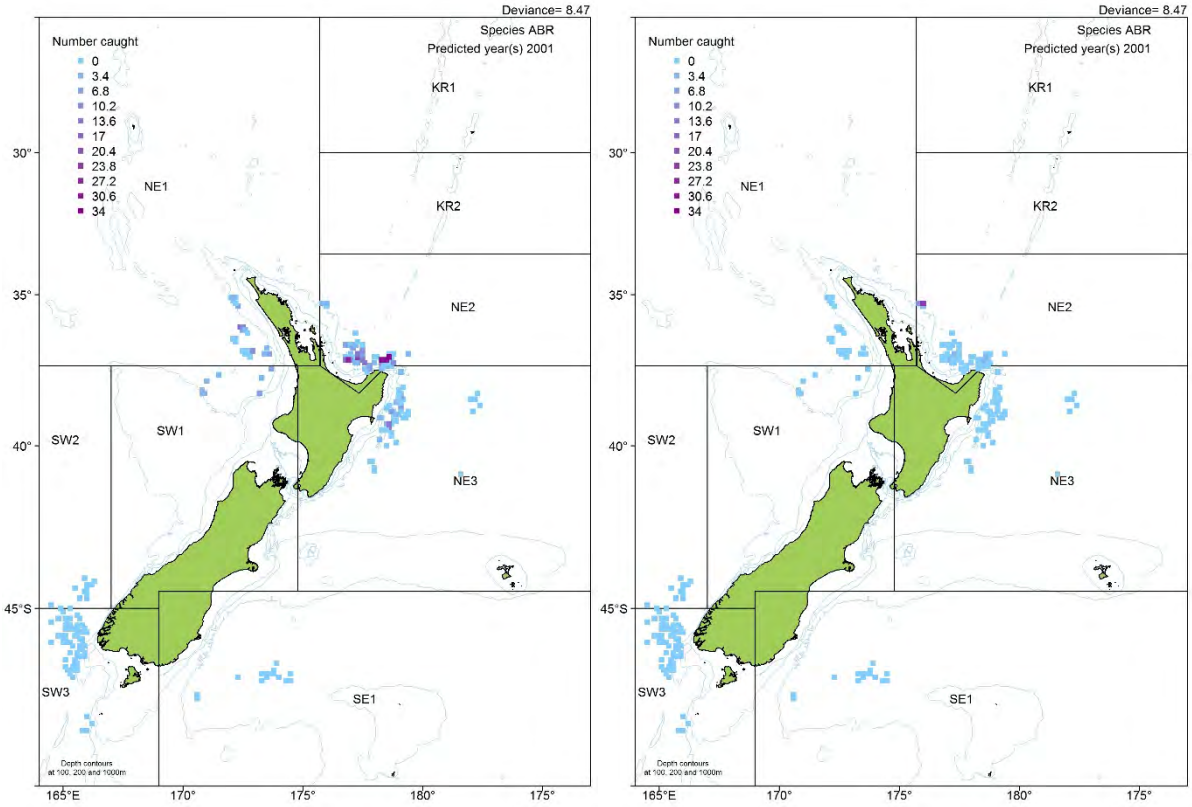


Figure 8: 2001 Poisson model observed (left) and predicted (right) numbers of ABR caught.

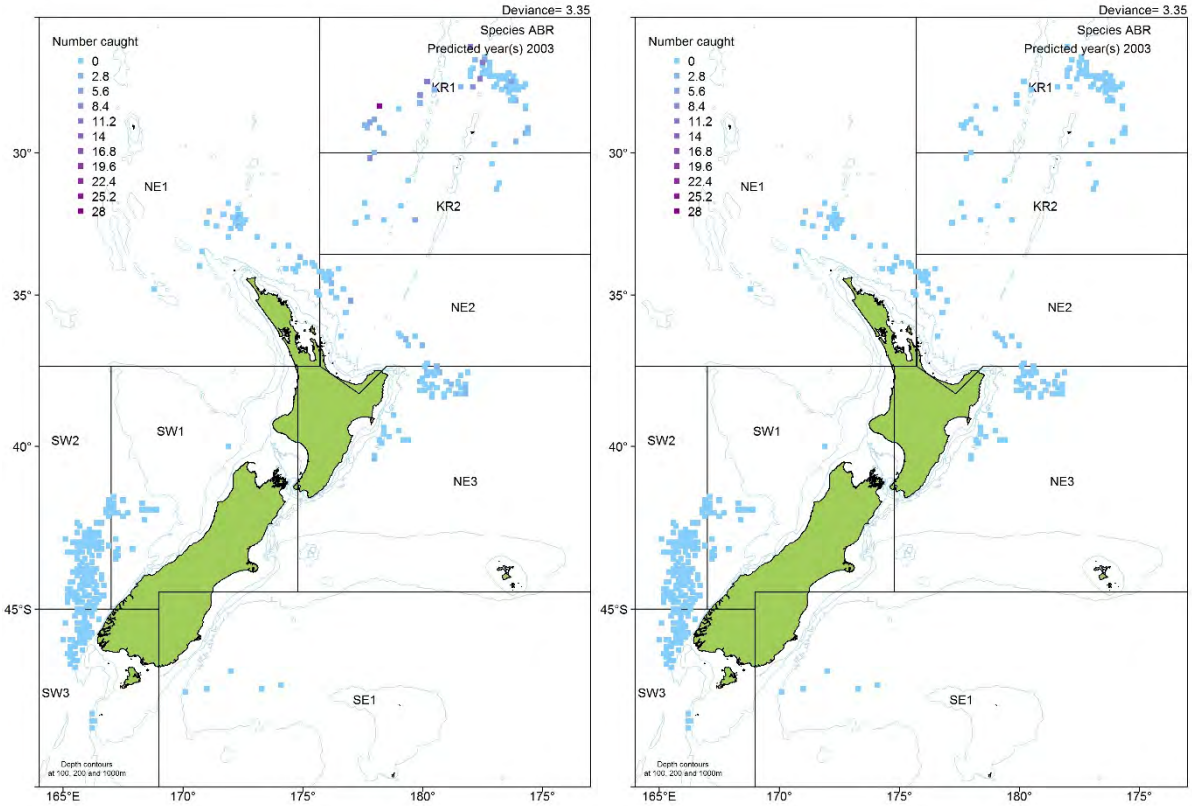


Figure 9: 2003 Poisson model observed (left) and predicted (right) numbers of ABR caught.

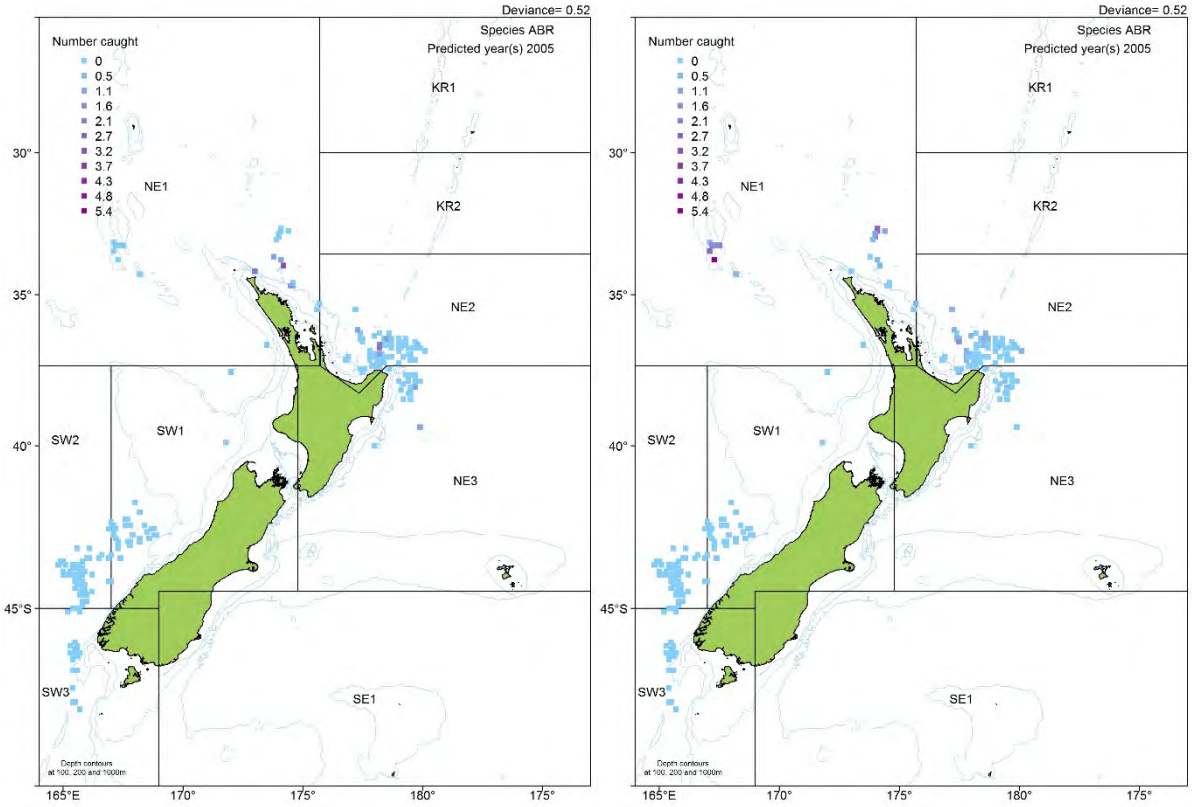


Figure 10: 2005 Poisson model observed (left) and predicted (right) numbers of ABR caught.

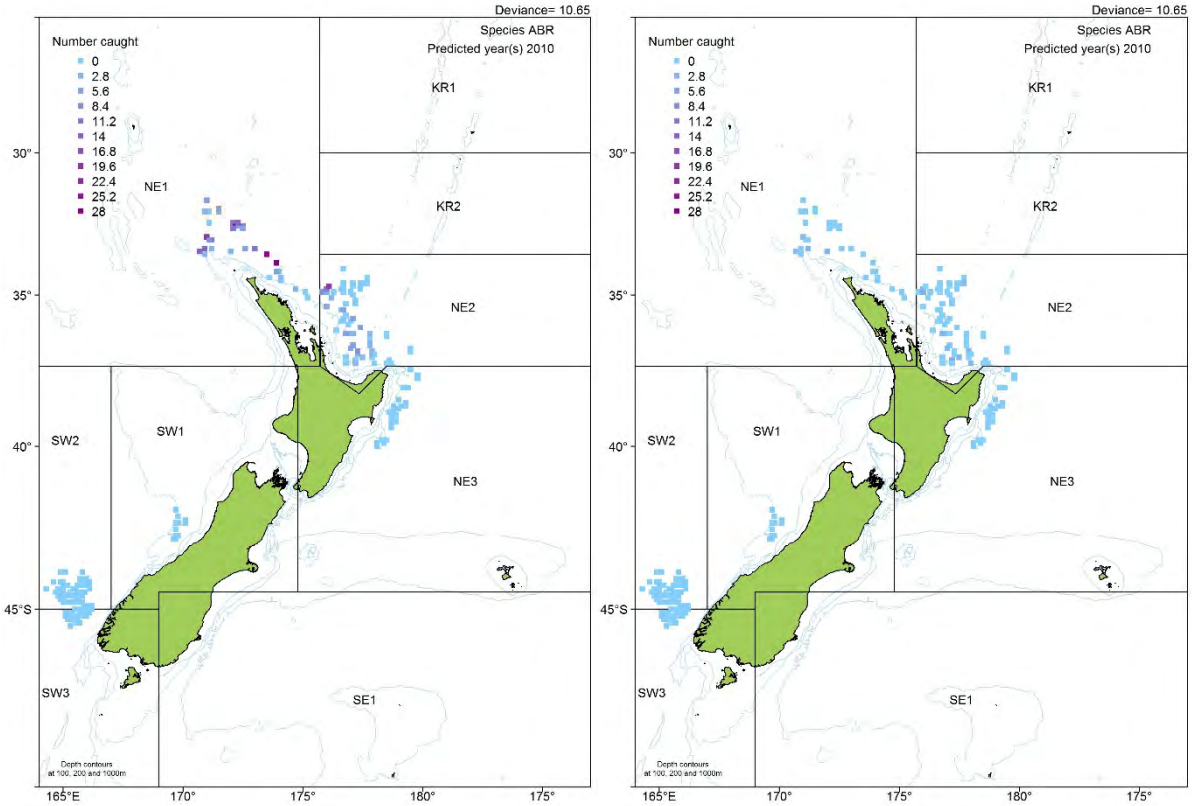


Figure 11: 2010 Poisson model observed (left) and predicted (right) numbers of ABR caught.

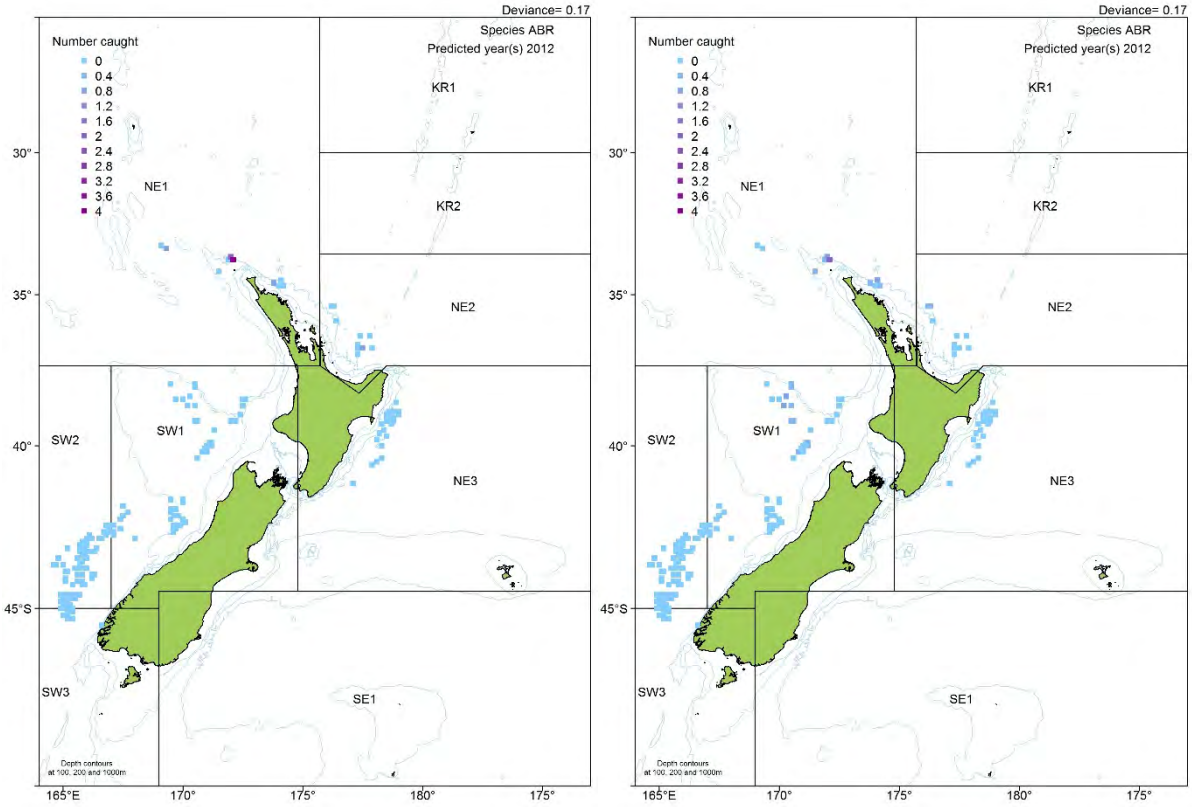


Figure 12: 2012 Poisson model observed (left) and predicted (right) numbers of ABR caught.

Binomial

The predictive ability was generally poor (Figure 13), but fair in models predicting 1999, 2009 or 2011 data (Figures 15, 18 and 19). With the exception of these years, the predicted presence and absences were almost entirely unmatched with the observed (e.g. Figures 14, 16 and 17).

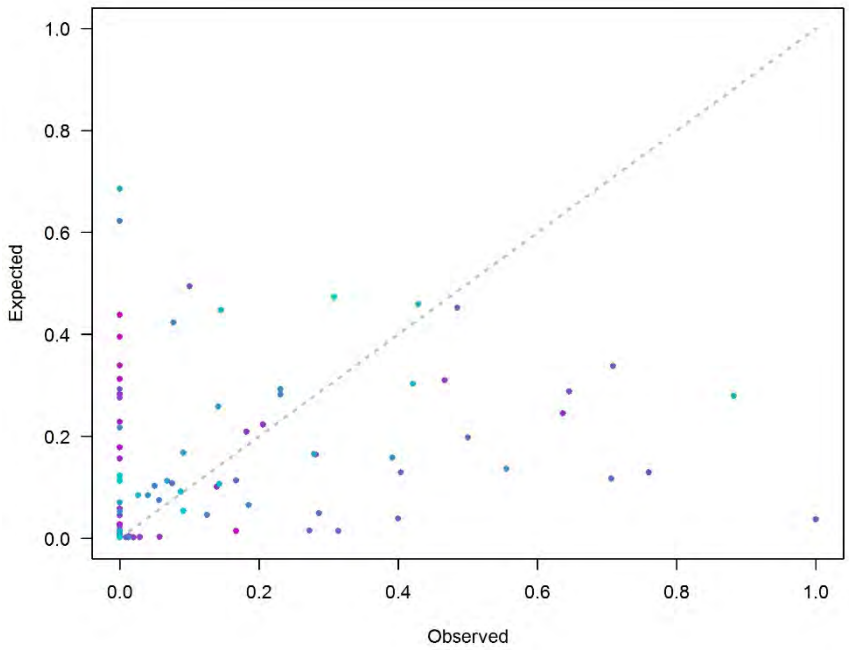


Figure 13: Observed and predicted probability of the presence of ABR for each year/subarea bin.

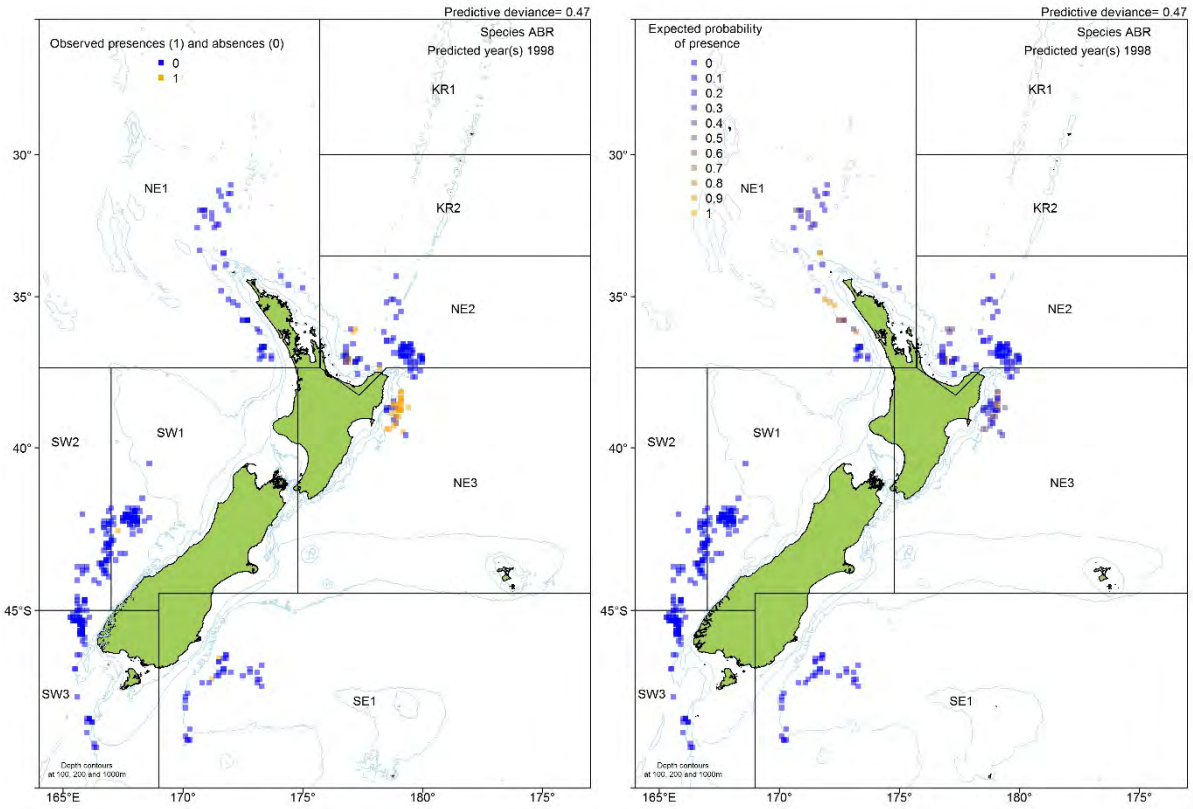


Figure 14: 1998 Binomial model observed (left) and predicted (right) ABR presence/absence.

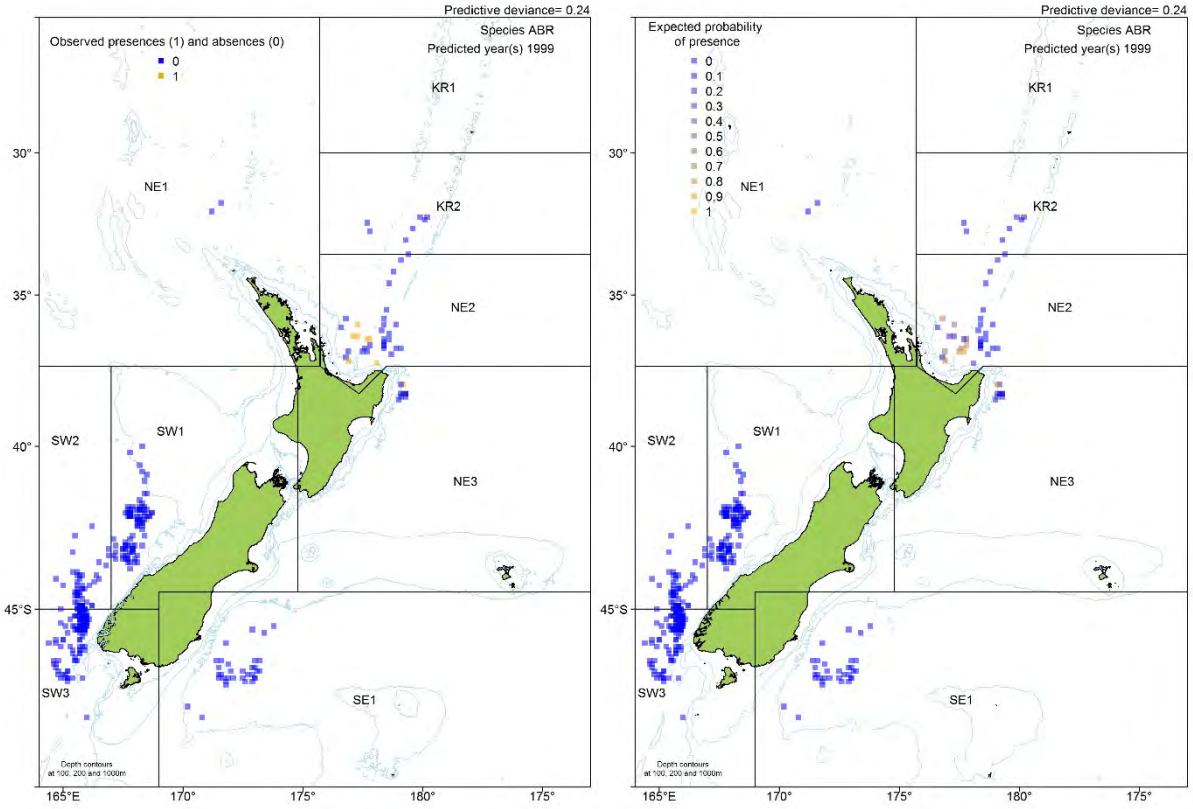


Figure 15: 1999 Binomial model observed (left) and predicted (right) ABR presence/absence.

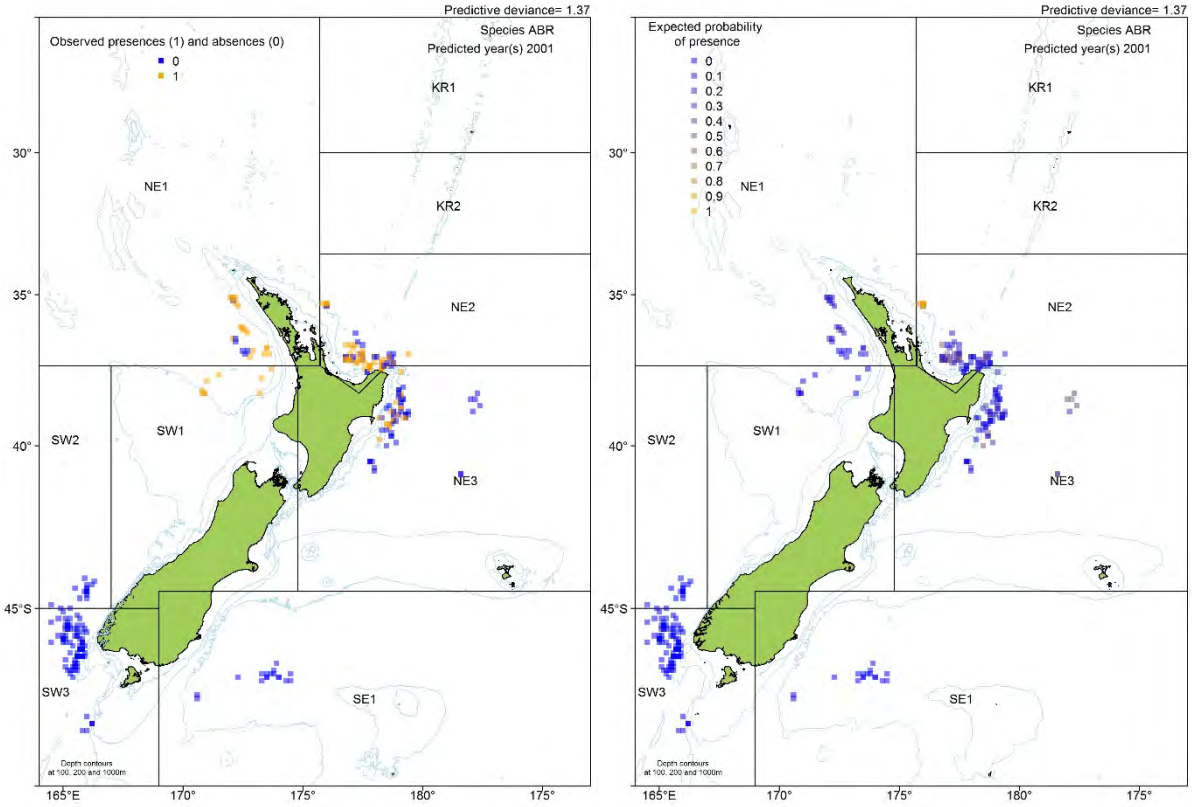


Figure 16: 2001 Binomial model observed (left) and predicted (right) ABR presence/absence.

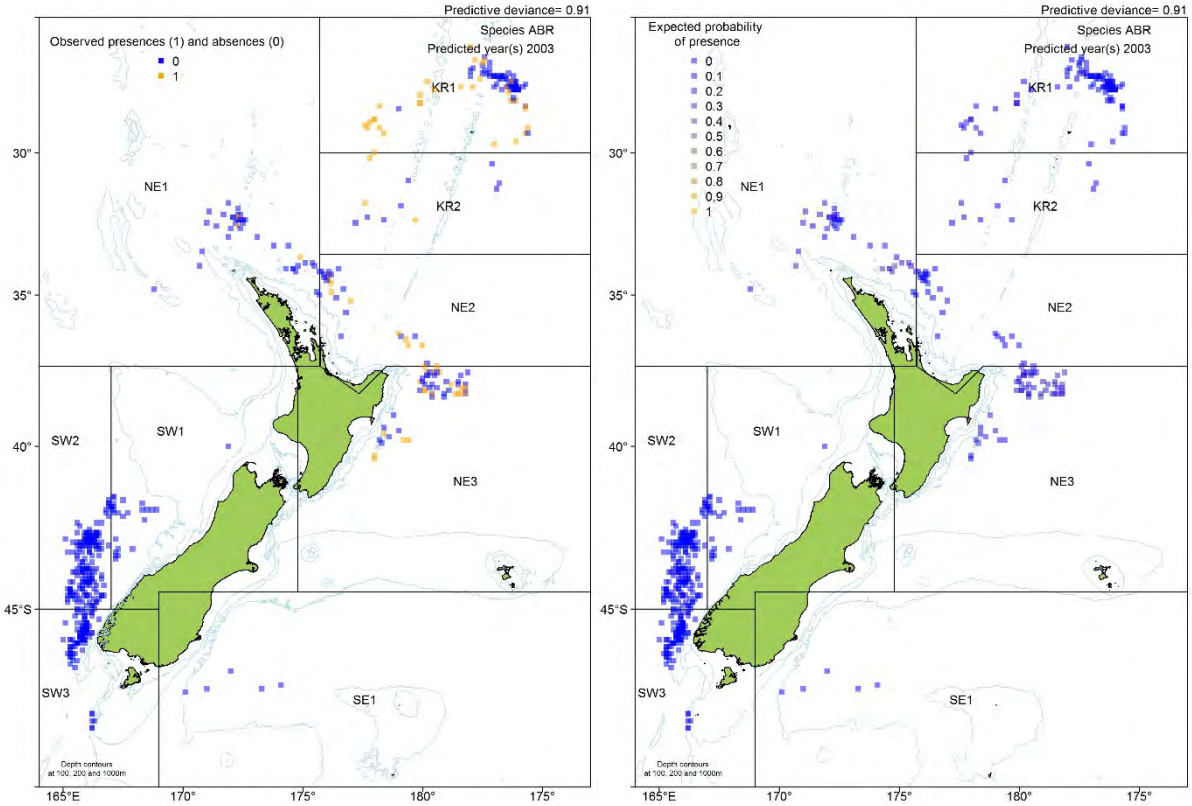


Figure 17: 2003 Binomial model observed (left) and predicted (right) ABR presence/absence.

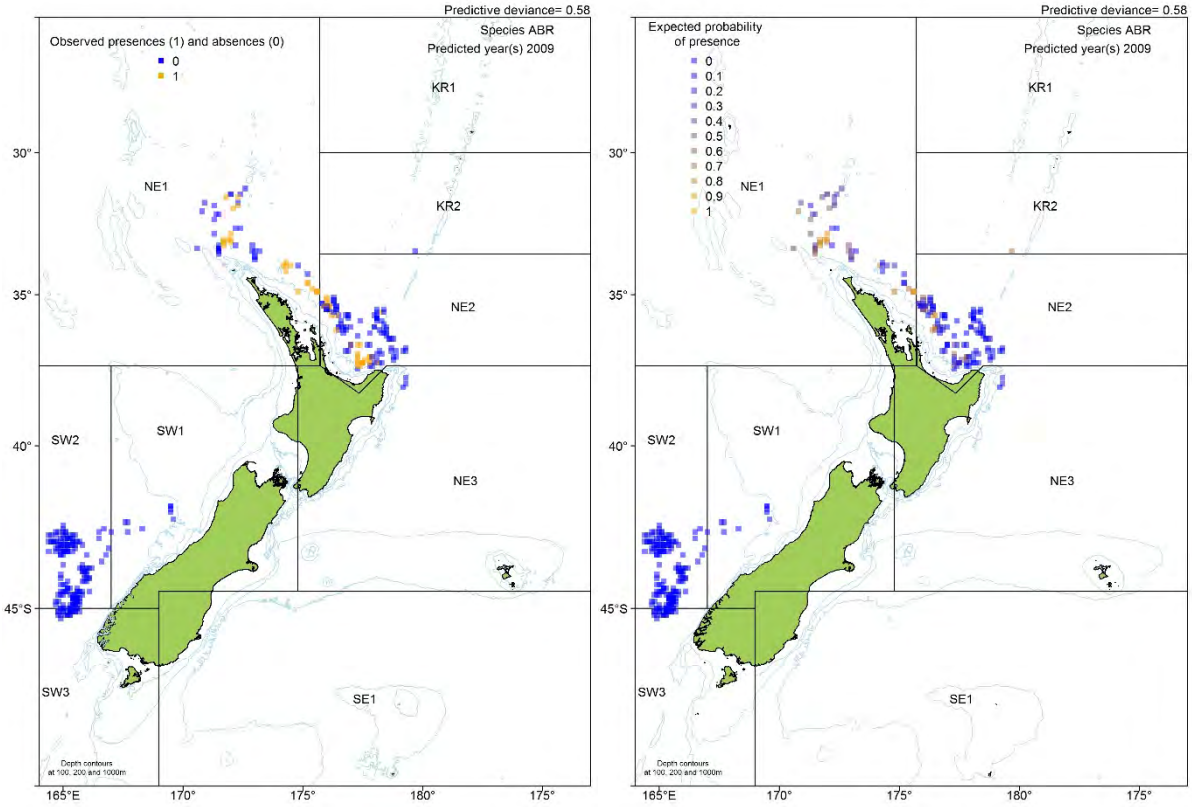


Figure 18: 2009 Binomial model observed (left) and predicted (right) ABR presence/absence.

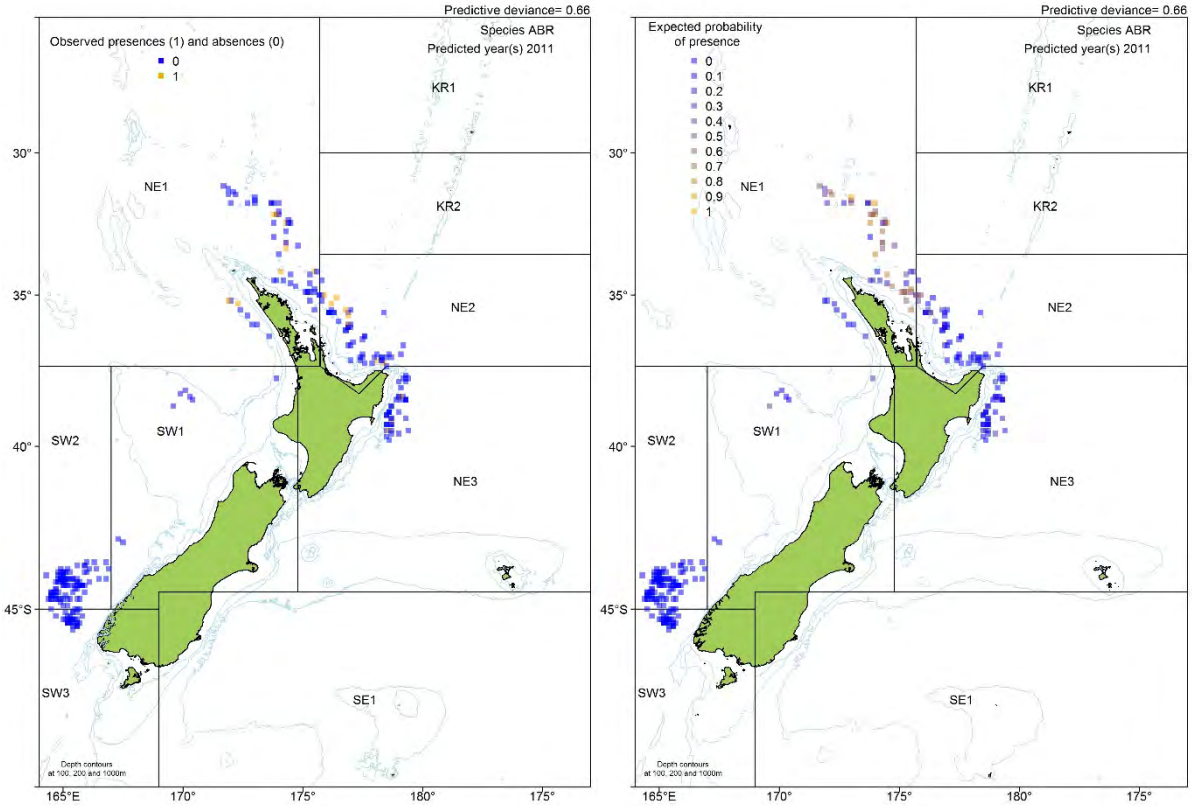


Figure 19: 2011 Binomial model observed (left) and predicted (right) ABR presence/absence.

3.1.2 ALB

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 actually increased the predictive deviance noticeably in the 2003 model (Figure 20). The 2003 data had more points in the KR1 subarea than the other years. The model fitted using *tc*=3 was perhaps over fitting to the data from the other years, causing it to be too specific and hence a poorer predictor for the 2003 data than the *tc*=2 model, especially in subarea KR1 (Figure 21). It was not likely that increasing the *tc* would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all ALB Binomial models.

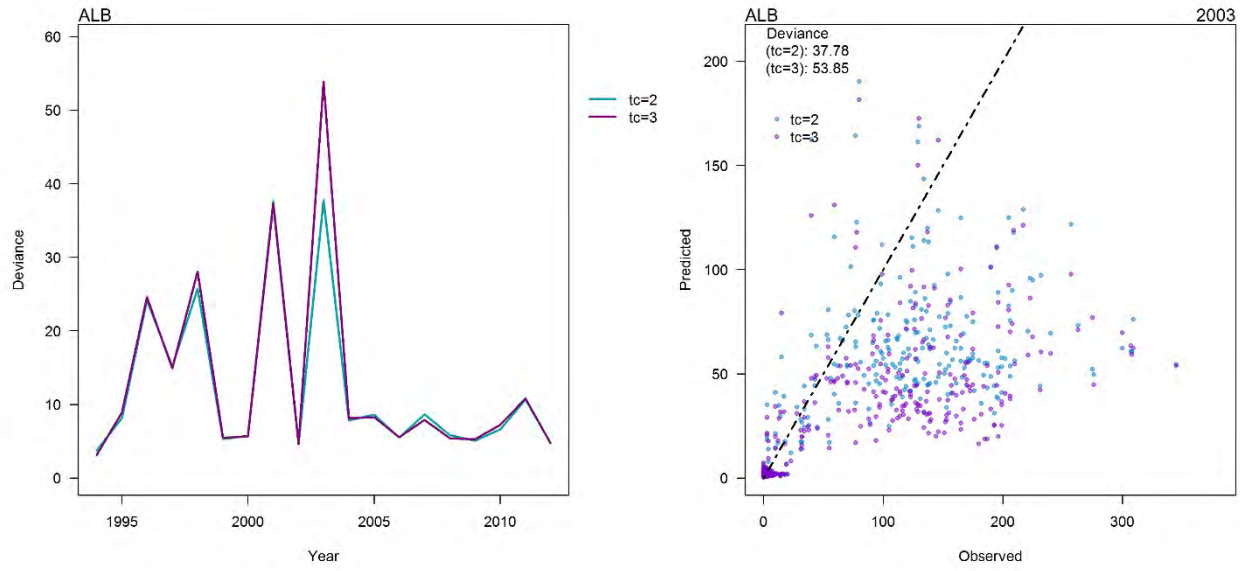
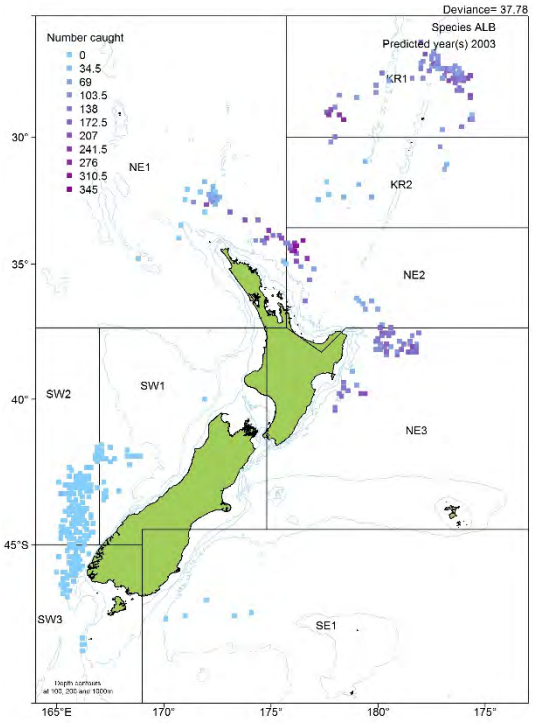
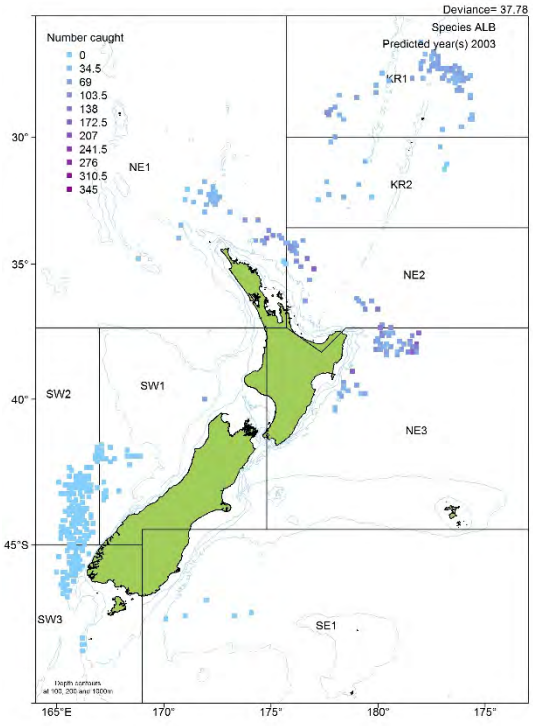


Figure 20: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2003 model (right) for species ALB.

a.) Observed



b.) Predicted (*tc*=2)



c.) Predicted (*tc*=3)

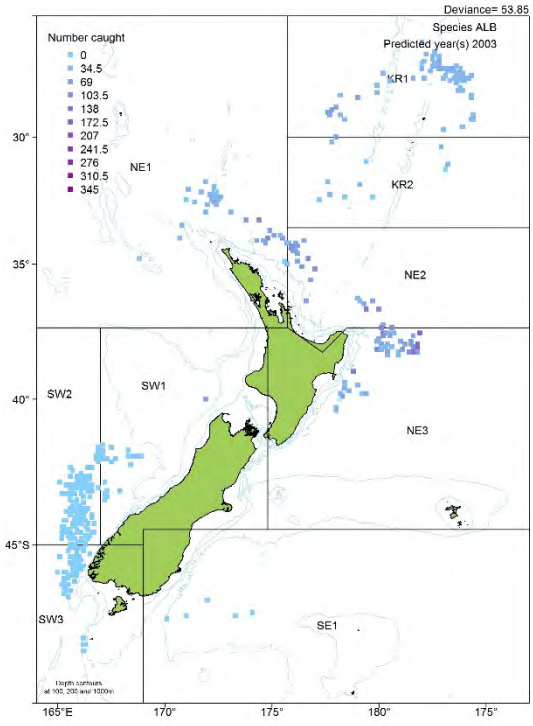


Figure 21: Observed (a) and predicted using tc=2 (b) and tc=3 (c) numbers of ALB caught with the 2003 Poisson model.

Binomial

Increasing the *tc* from 2 to 3 actually increased the predictive deviance slightly in the 2000 and 2007 models, but otherwise caused little change (Figure 22). It was not likely that increasing the *tc* further would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all ALB Binomial models.

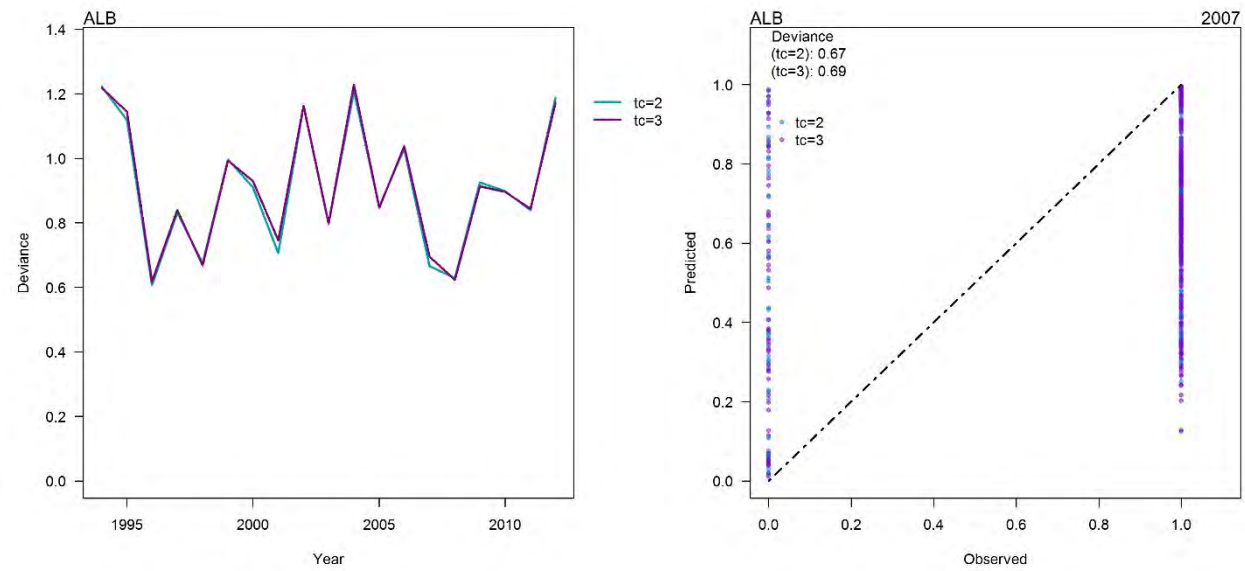


Figure 22: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2003 model (right) for species ALB.

Predictive ability

Poisson

The predictive ability was generally fair in many of the models (Figure 23), although quite underestimated in several. The models omitting year 1996, 1998, 2001 or 2003 had the highest deviance (Figure 22). In all these years, the predictions underestimated the numbers caught, but the locations of positive numbers caught were fairly well matched with those observed (Figures 24, 25, 26 and 27). The 2012 model had one of the lowest predictive deviances. In this model, the predicted numbers caught were higher in subarea NE3 than the observed numbers caught, lower in SW1 and well matched in the other areas.

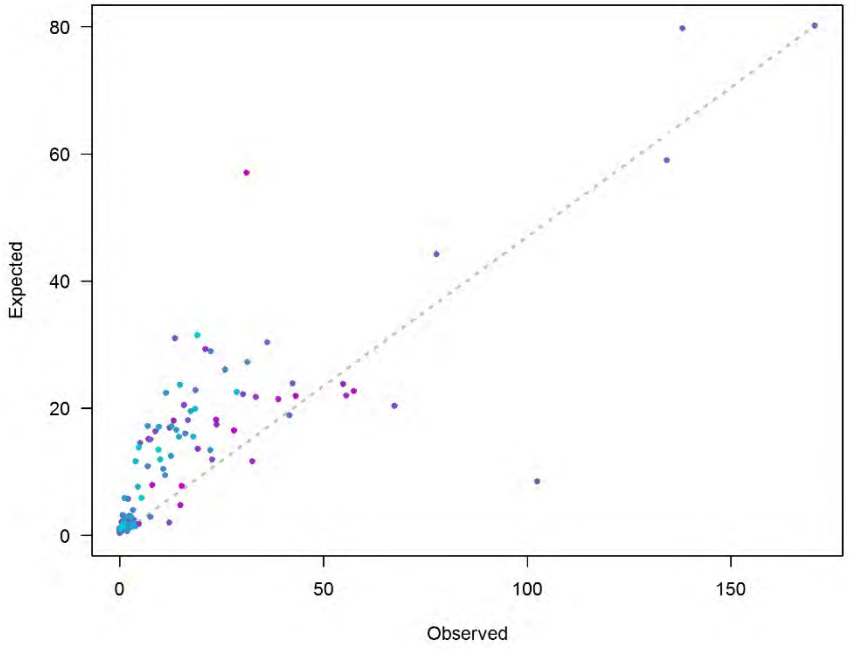


Figure 23: Observed and predicted counts of ALB for each year/subarea bin.

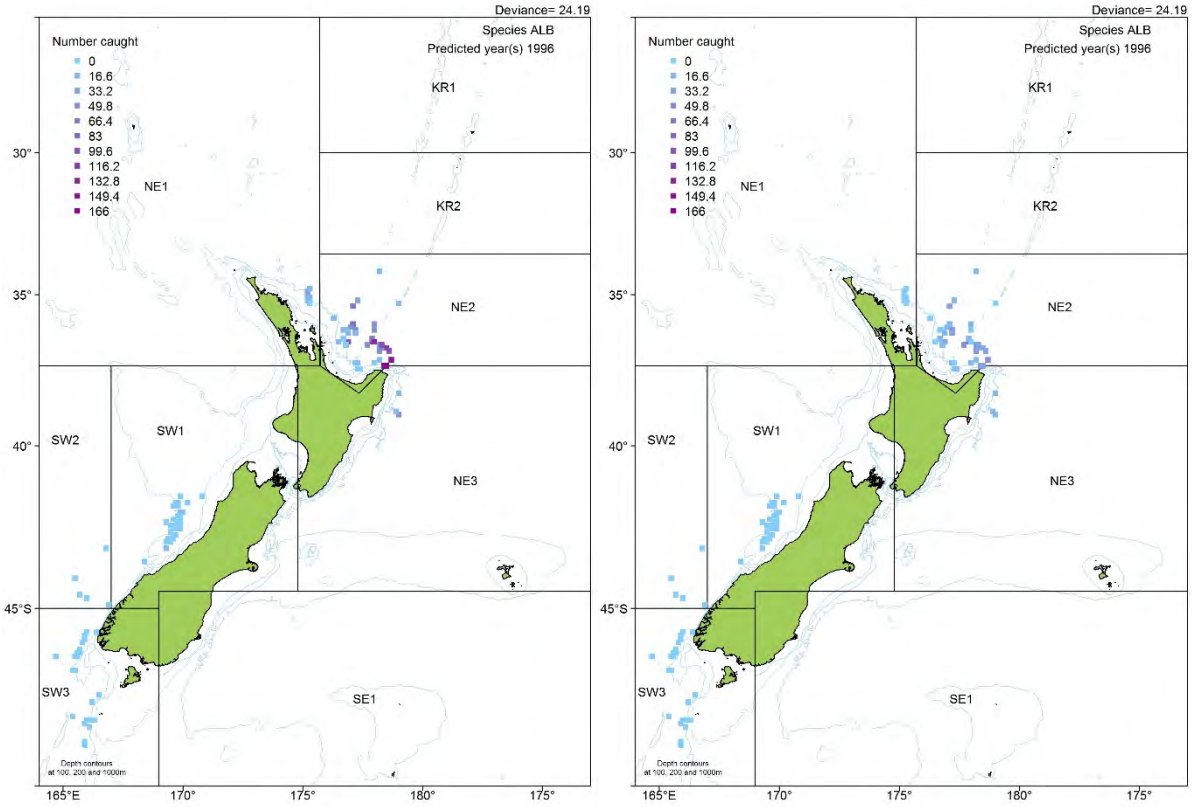


Figure 24: 1996 Poisson model observed (left) and predicted (right) numbers of ALB caught.

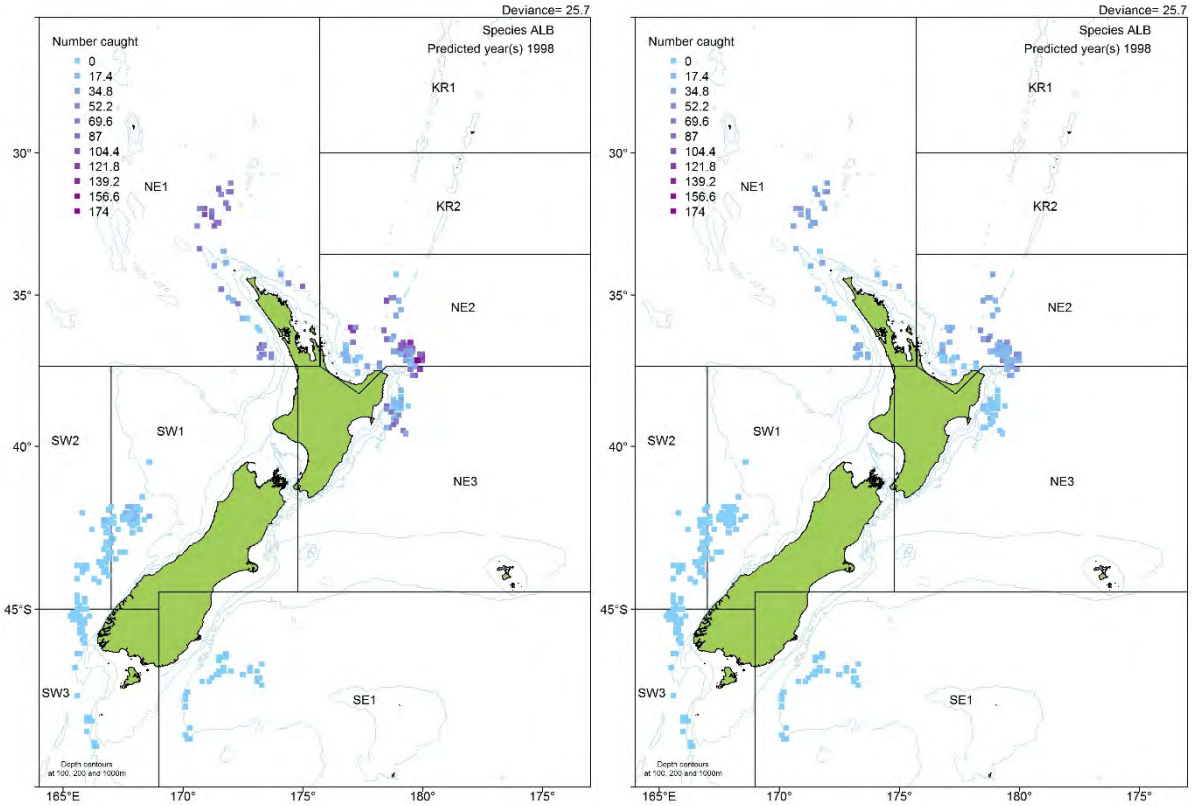


Figure 25: 1998 Poisson model observed (left) and predicted (right) numbers of ALB caught.

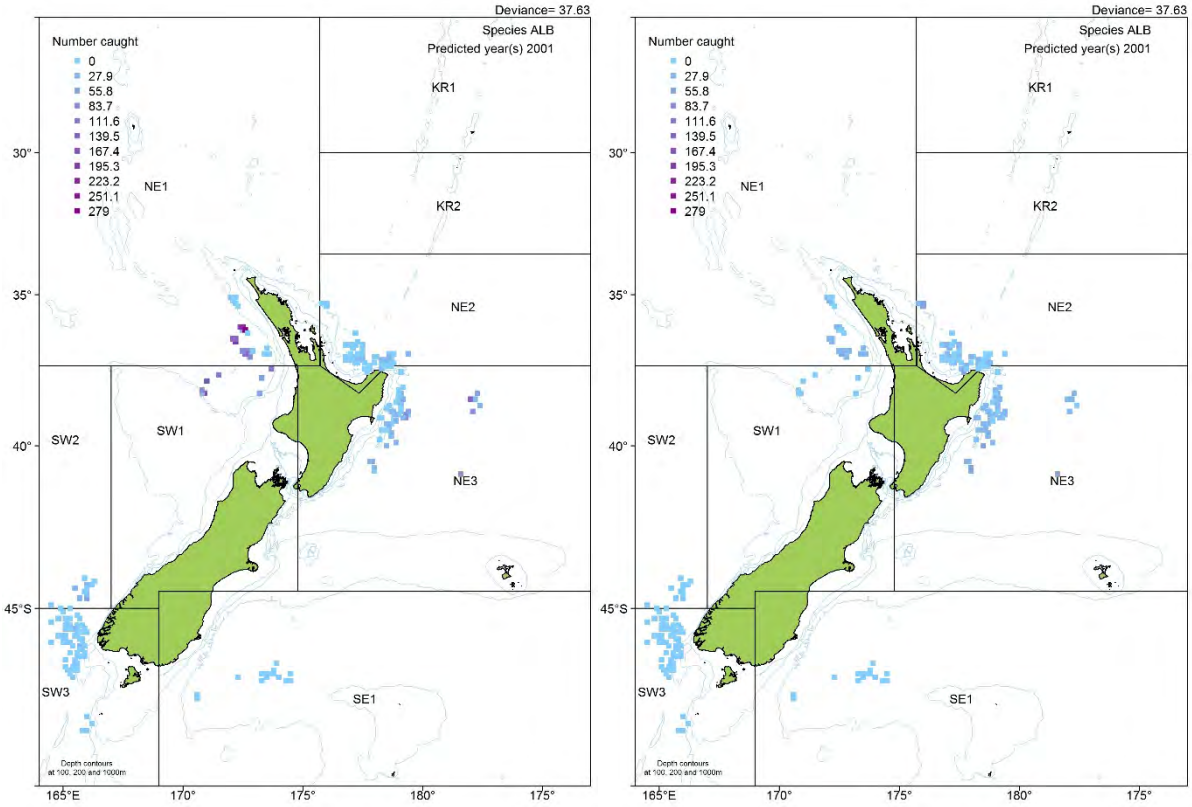


Figure 26: 2001 Poisson model observed (left) and predicted (right) numbers of ALB caught.

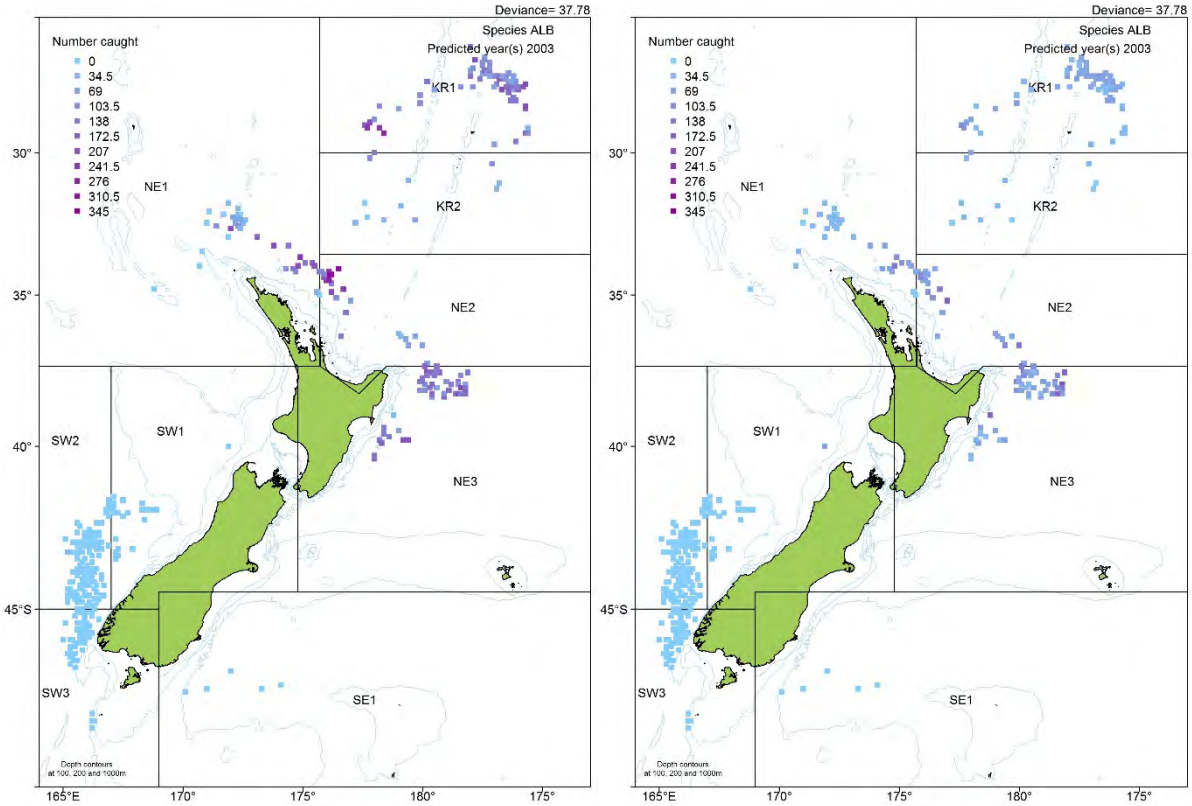


Figure 27: 2003 model observed (left) and predicted (right) numbers of ALB caught.

Binomial

The predictive ability was fair across most models and good in some (Figure 28). Where there were a few absences off the north east coast of New Zealand, these were often mis-predicted as presences (Figures 29 and 30). This could be a latitude effect, as latitude was the second most influential predictor variable for all the ALB binomial models (see Figure 141).

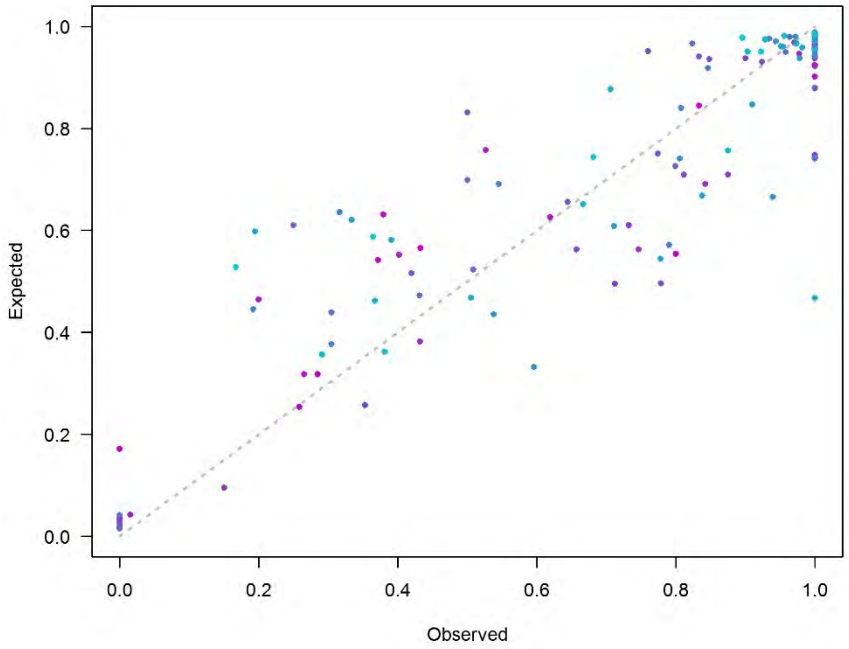


Figure 28: Observed and predicted probability of the presence of ALB for each year/subarea bin.

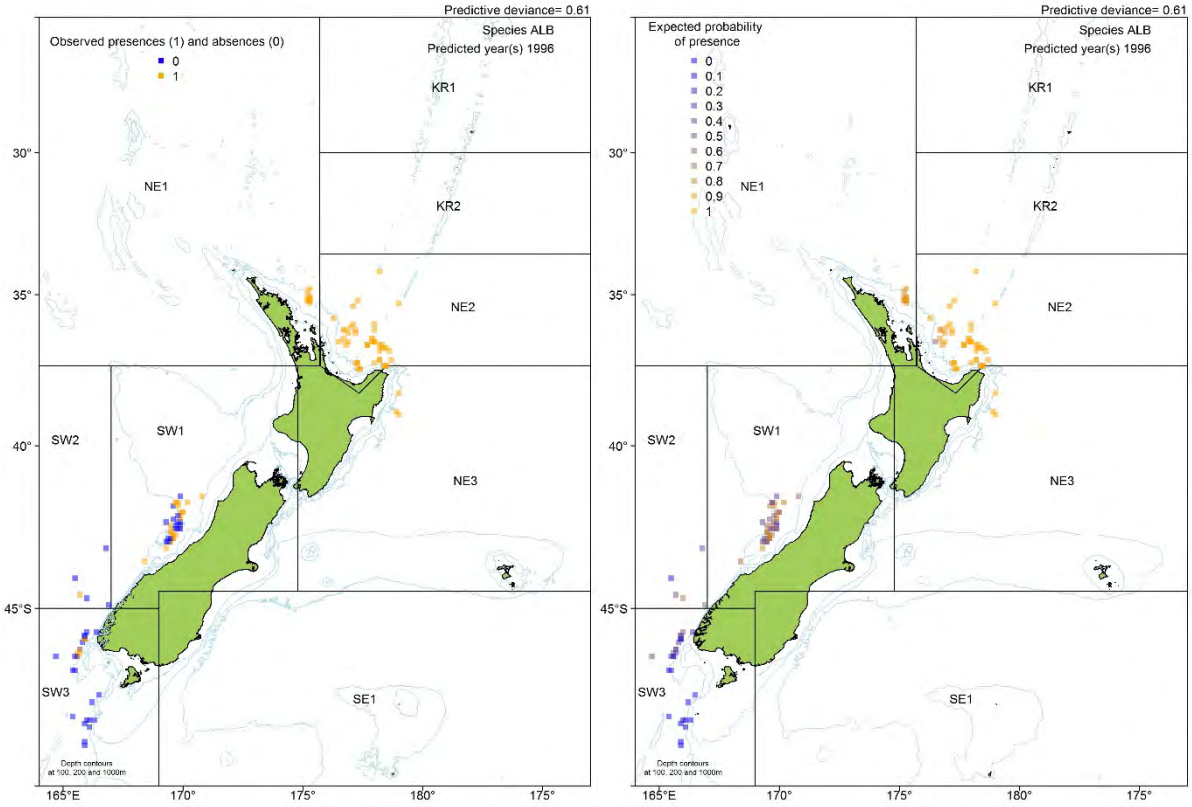


Figure 29: 1996 Binomial model observed (left) and predicted (right) presence/absence of ALB in the catch.

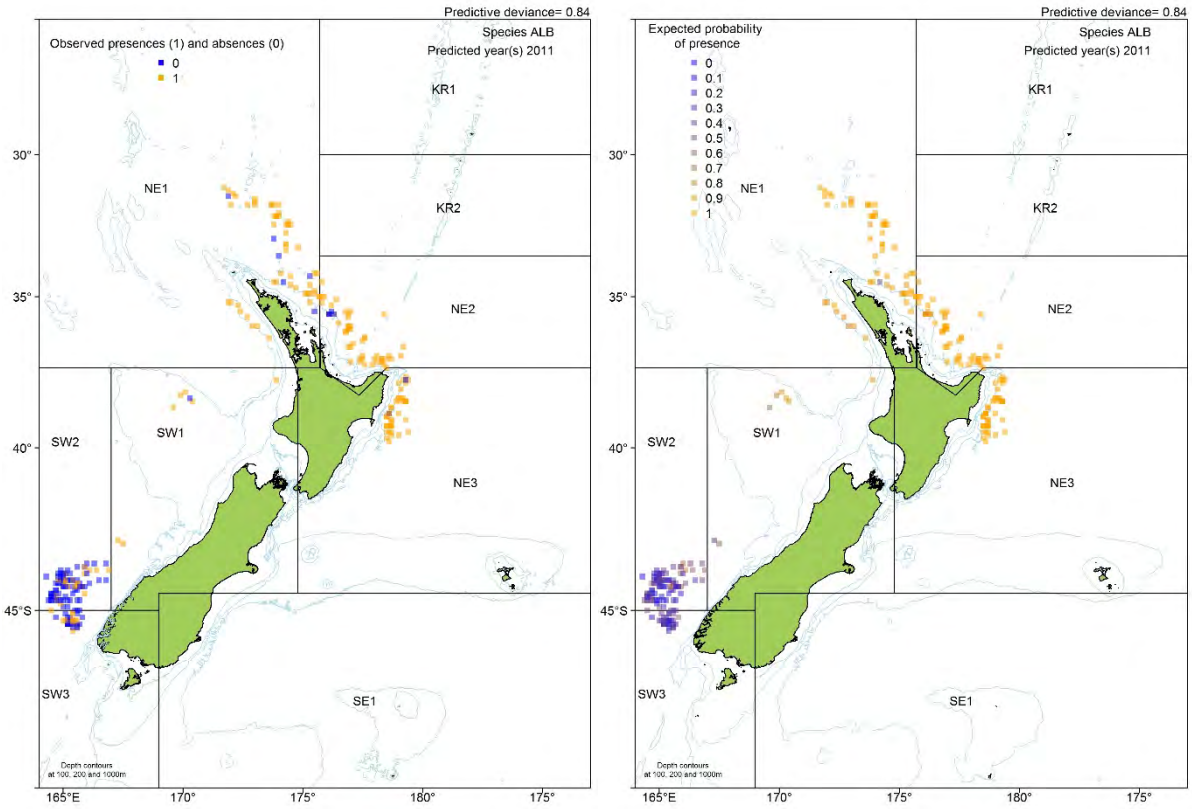


Figure 30: 2011 Binomial model observed (left) and predicted (right) presence/absence of ALB in the catch.

3.1.3 BIG

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 decreased the predictive deviance in the 2003 model (Figure 31), but made no difference to the other models. It was not likely that increasing the *tc* would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all BIG Binomial models.

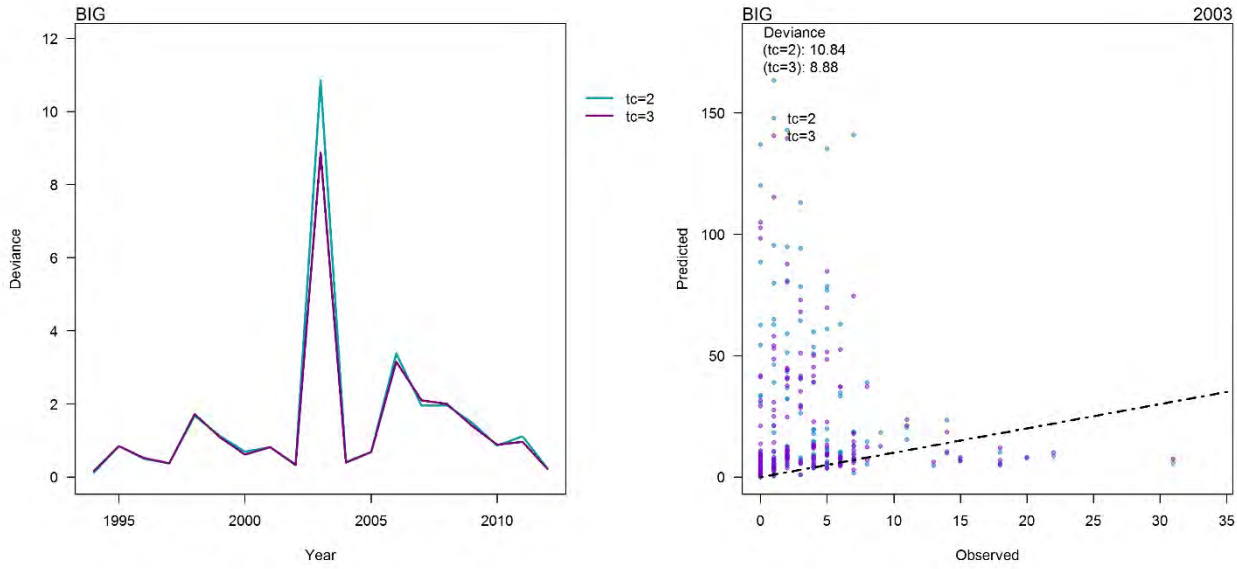


Figure 31: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2003 Poisson model (right) for species BIG.

Binomial

Increasing the *tc* from 2 to 3 made little change to the predictive deviance of the models (Figure 32). It was unlikely that increasing the *tc* further would improve predictive ability and *tc*=2 has been used for the remainder of the analyses for all BIG Binomial models.

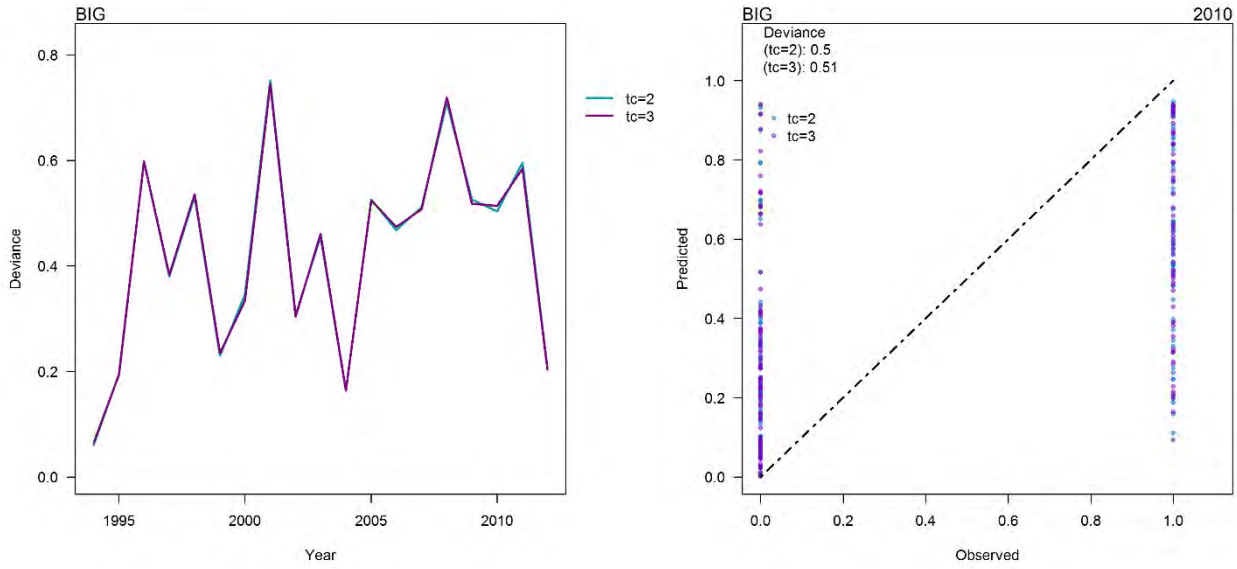


Figure 32: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2003 Binomial model (right) for species BIG.

Predictive ability

Poisson

The predictive ability was a mixture of fair and poor (Figure 33). The models omitting year 2003, 2006 or 2007 had the highest predictive deviance (Figure 32). In all these years, the observed numbers caught were not well predicted (Figure 35, 37 and 38). The 2007 model slightly underestimated numbers in subarea NE1, the 2003 model overestimated the numbers caught in subarea KR1, and the 2002 model slightly overestimated in subarea NE1. The 2002, 2004 and 2012 models had three of the lowest predictive deviances. The predicted numbers caught using all these models were fairly well matched to those observed (Figure 34, 36 and 39).

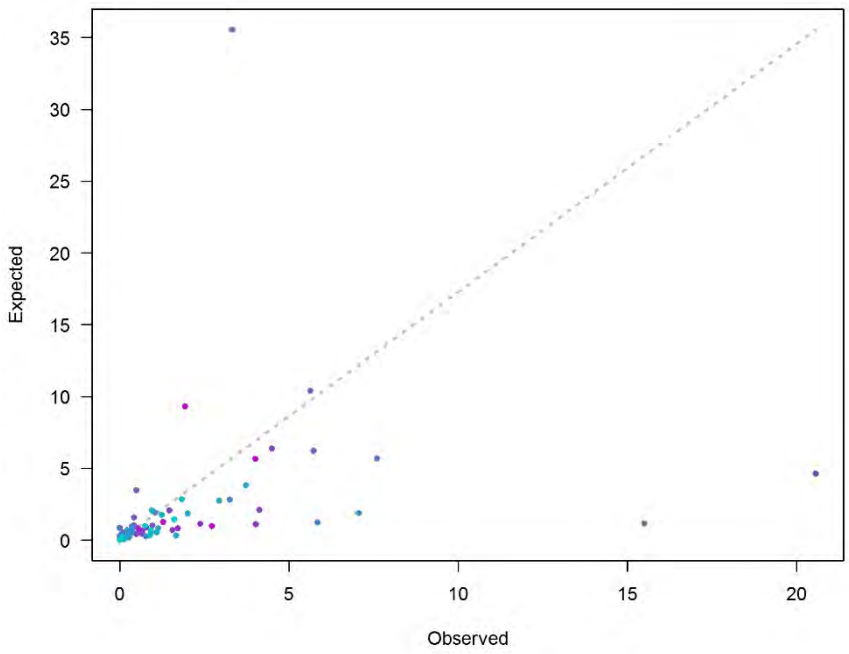


Figure 33: Observed and predicted counts of BIG for each year/subarea bin.

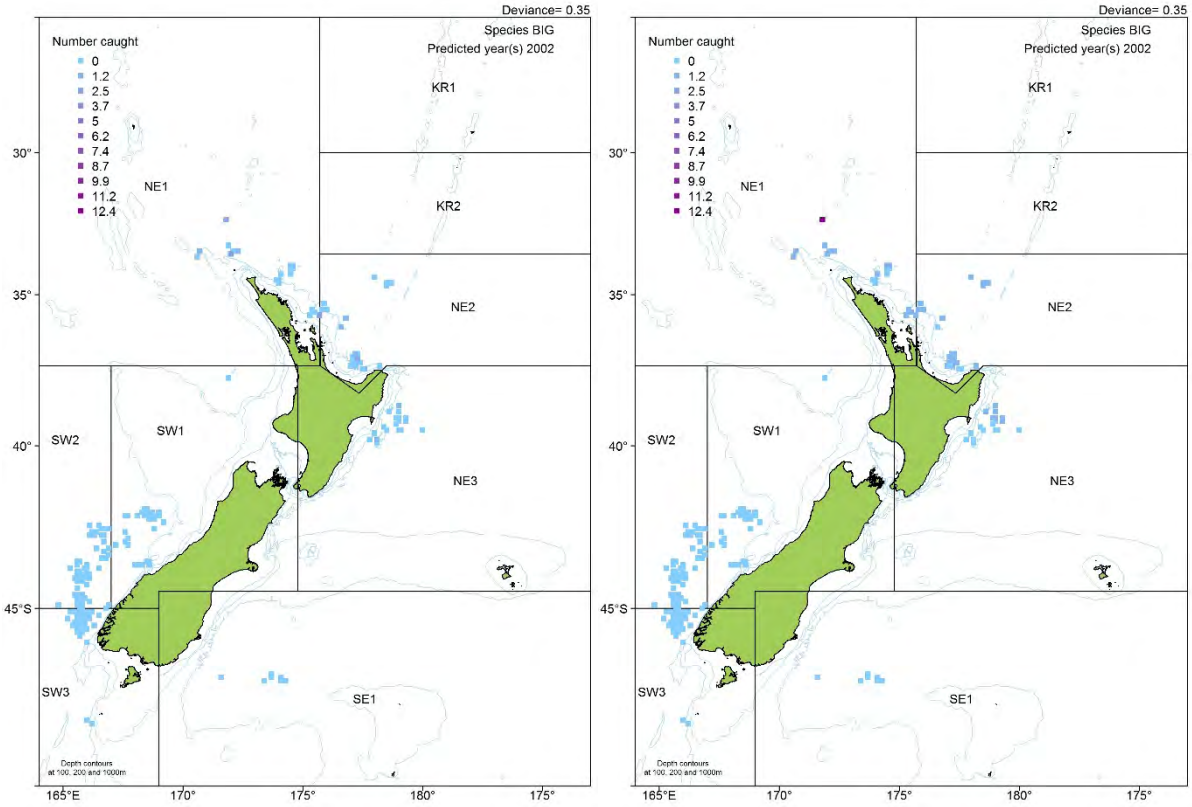


Figure 34: 2002 Poisson model observed (left) and predicted (right) numbers of BIG caught.

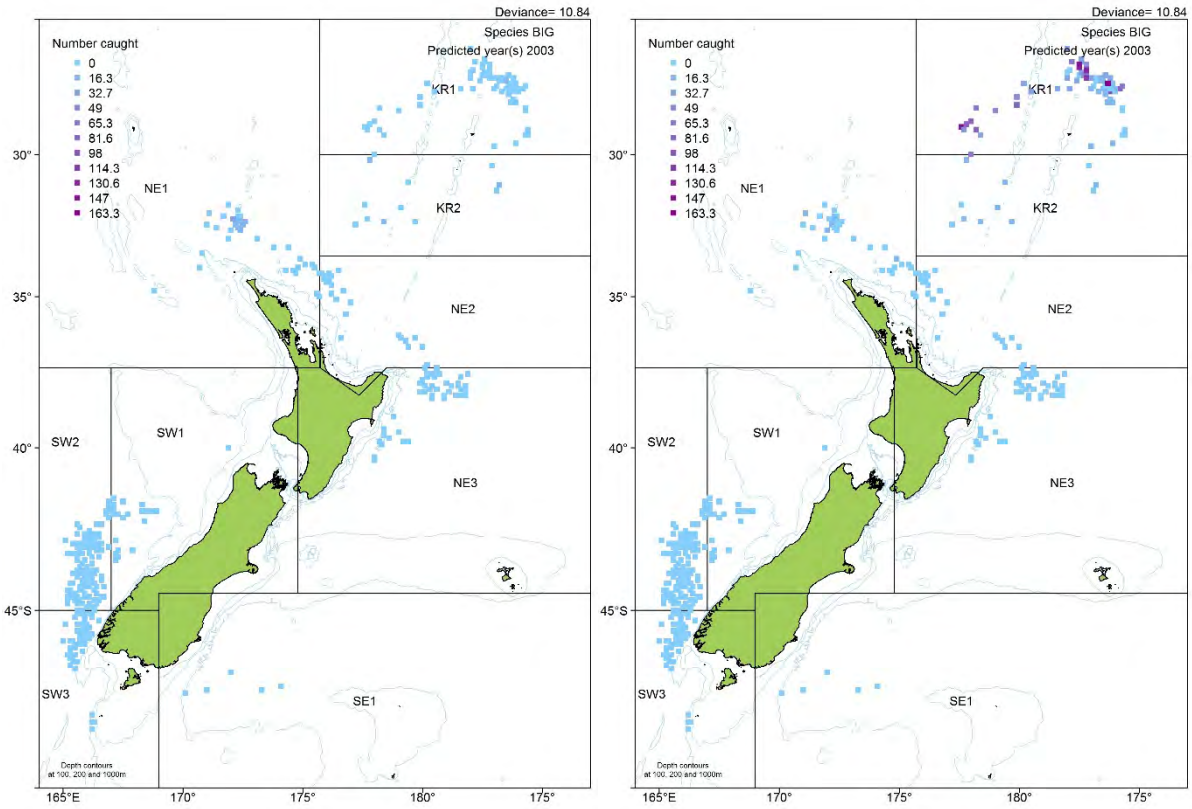


Figure 35: 2003 Poisson model observed (left) and predicted (right) numbers of BIG caught.

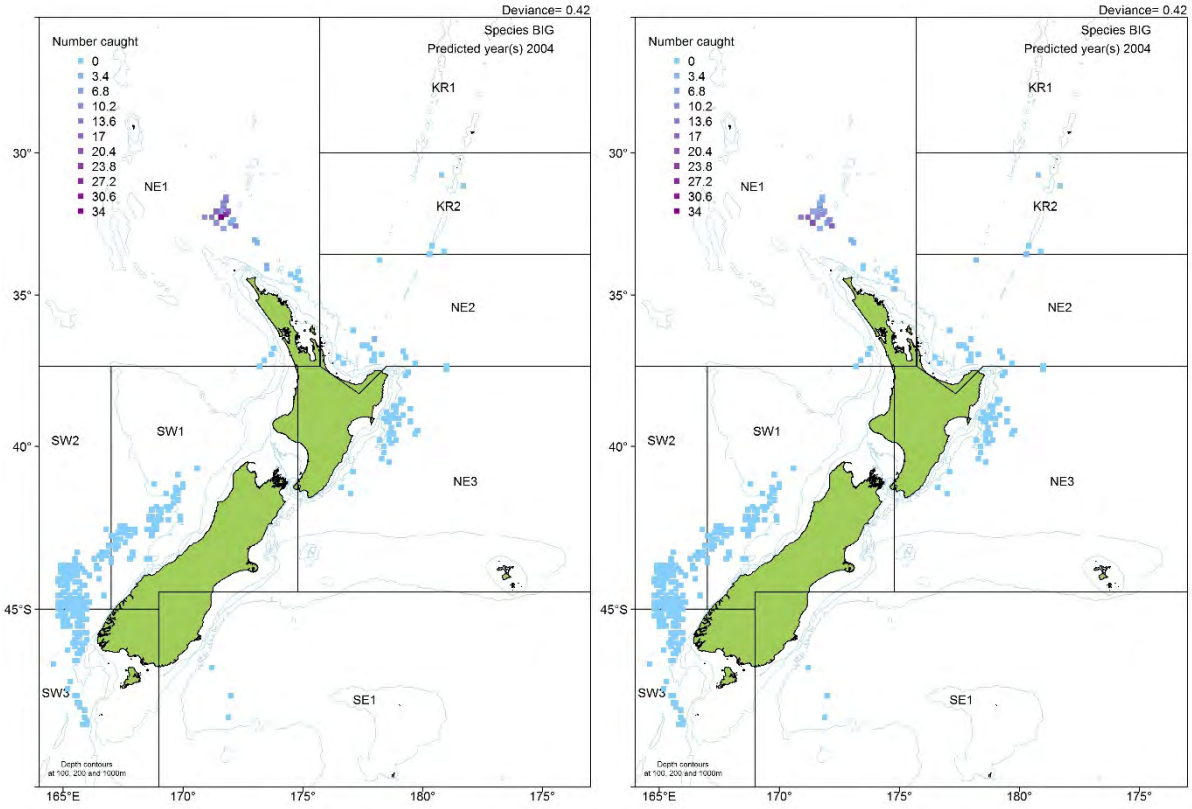


Figure 36: 2004 Poisson model observed (left) and predicted (right) numbers of BIG caught.

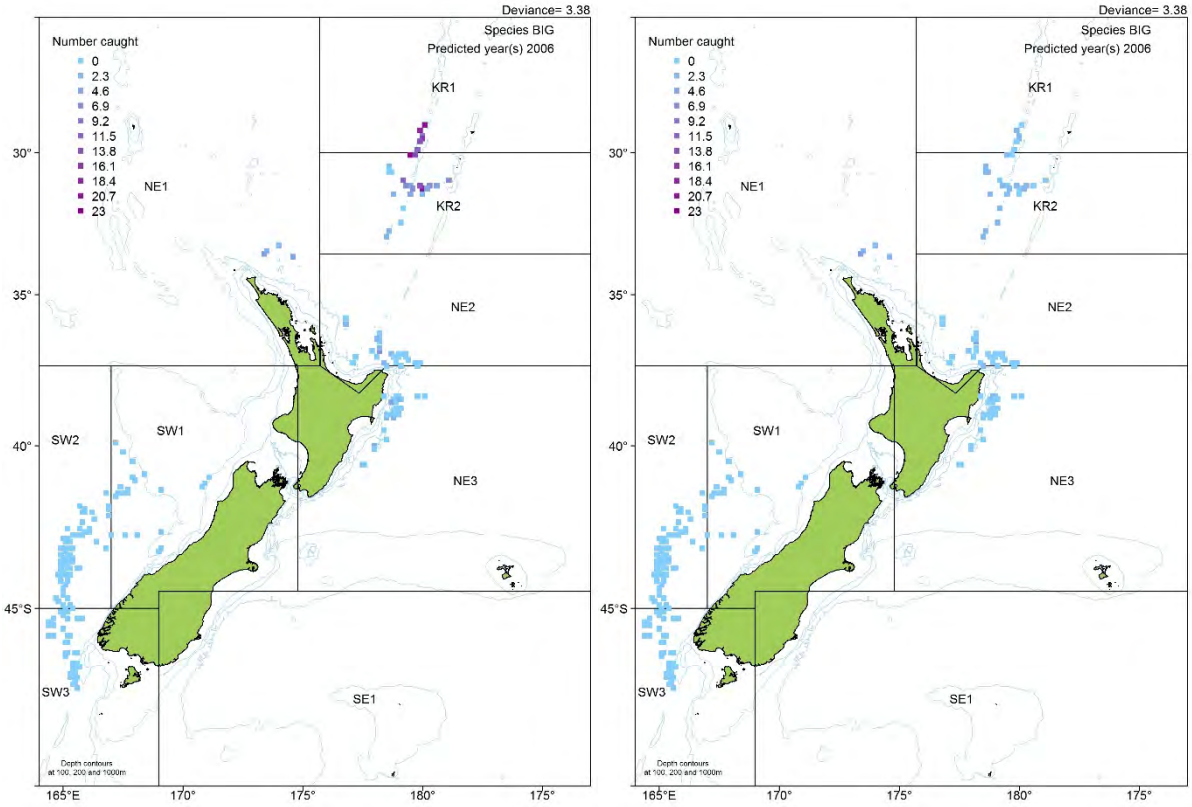


Figure 37: 2006 Poisson model observed (left) and predicted (right) numbers of BIG caught.

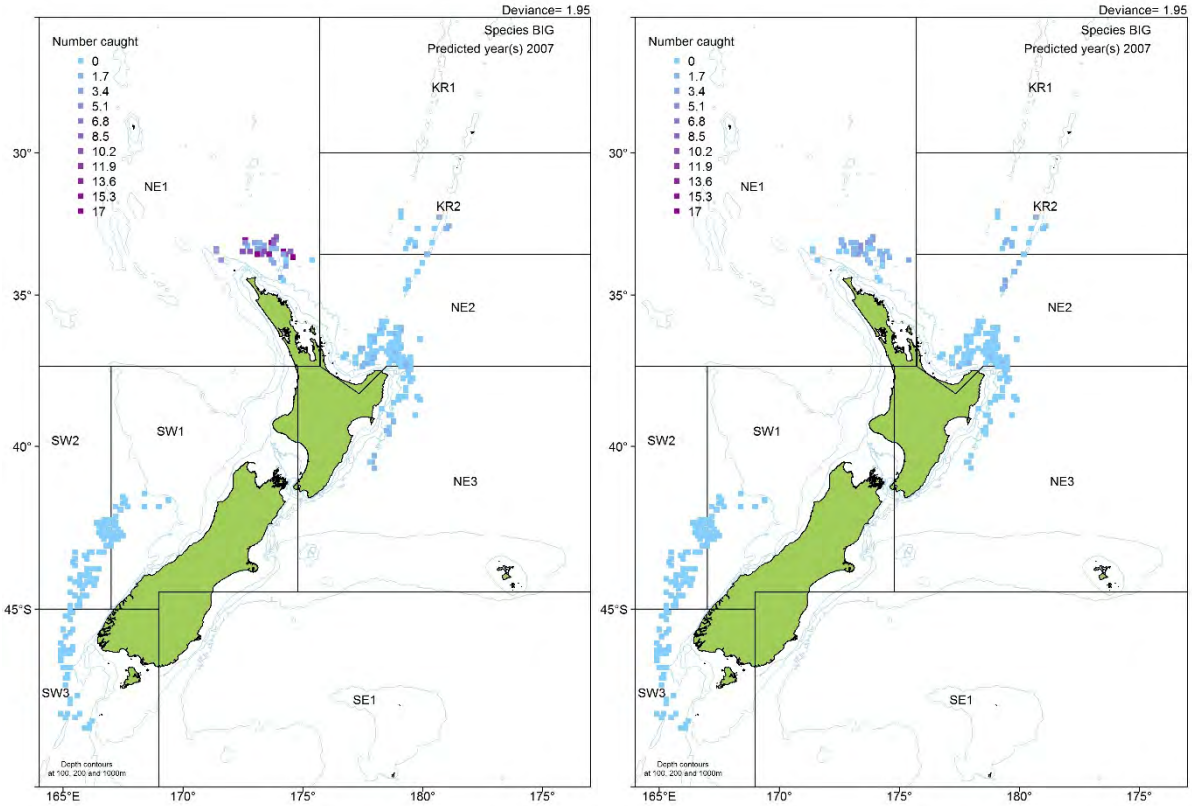


Figure 38: 2007 Poisson model observed (left) and predicted (right) numbers of BIG caught.

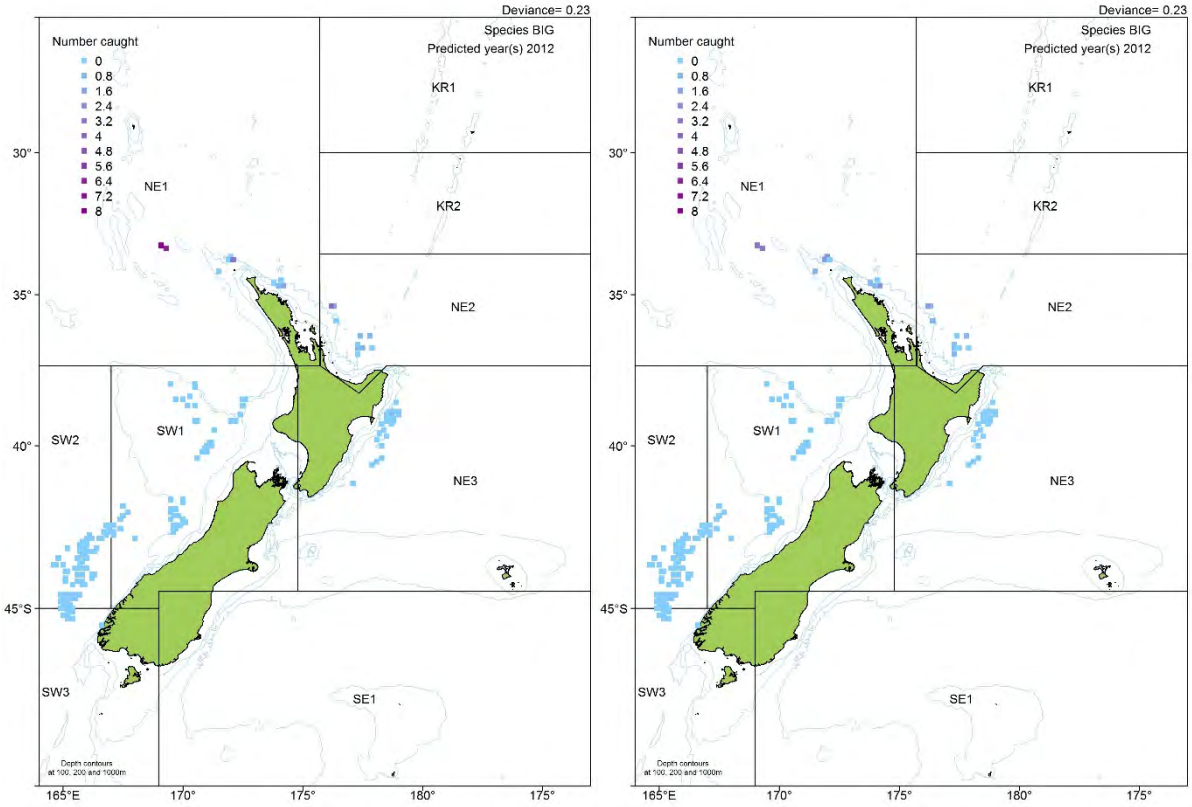


Figure 39: 2012 Poisson model observed (left) and predicted (right) numbers of BIG caught.

Binomial

The predictive ability was fair to good across all models (Figure 40). Two of the models had some poor predictive ability; the model fitted to year 2000 had some false misses in subarea NE1 (Figure 41), and the model fitted to year 2003 had some false hits off the north east coast and in subarea KR1 (Figure 42).

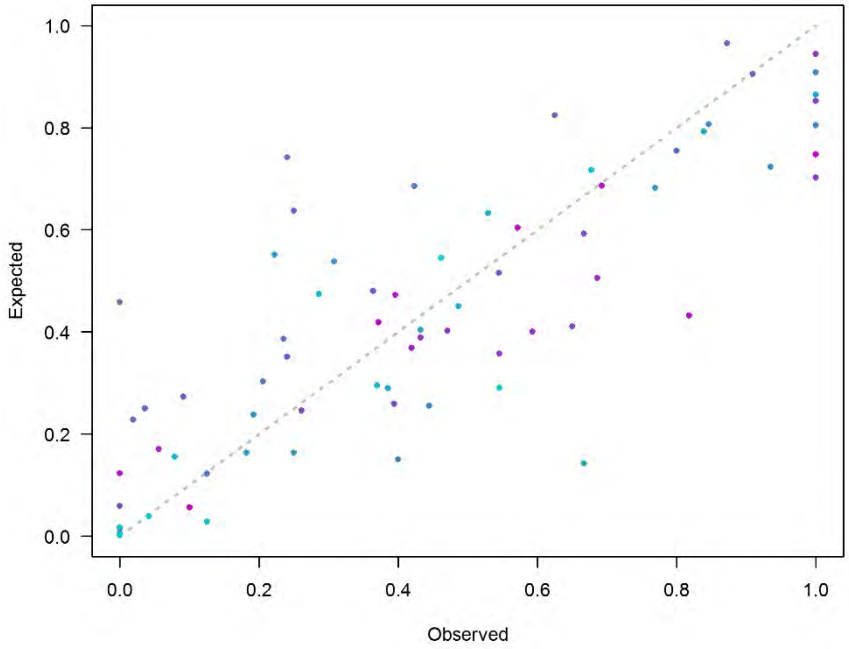


Figure 40: Observed and predicted probability of the presence of BIG for each year/subarea bin.

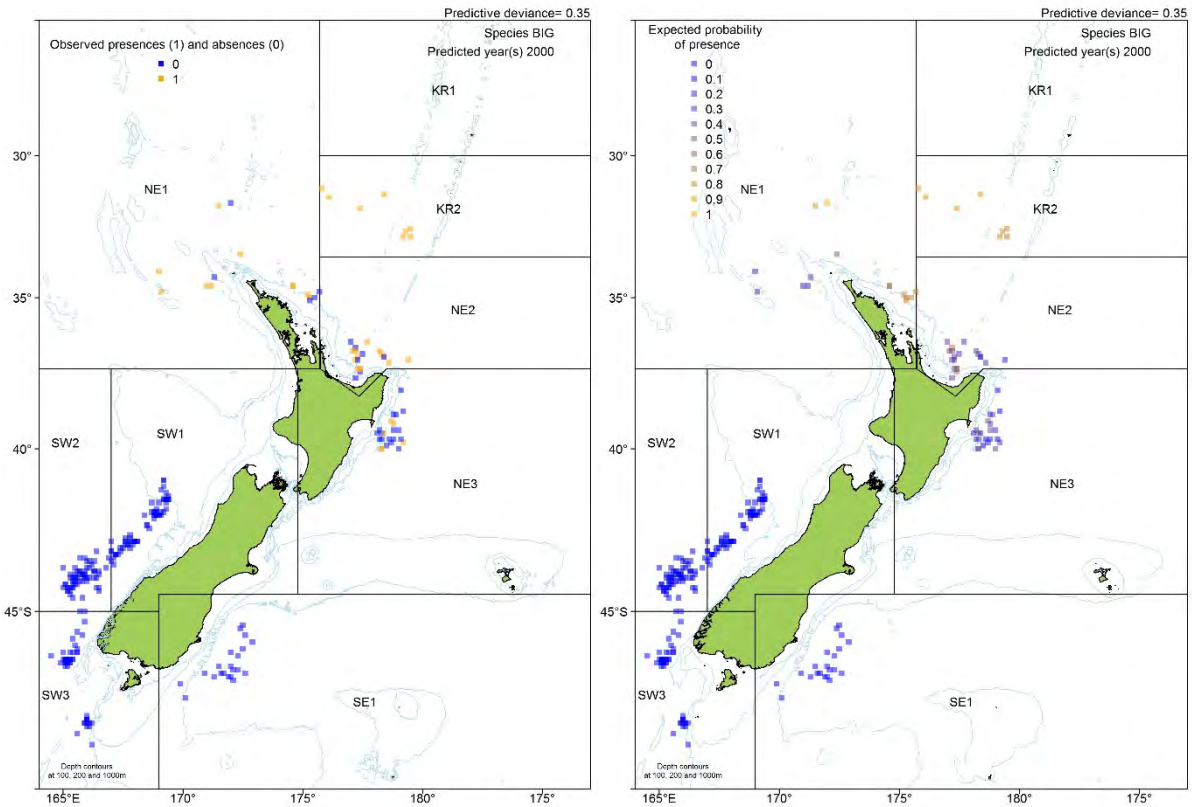


Figure 41: 2000 Binomial model observed (left) and predicted (right) presence/absence of BIG in the catch.

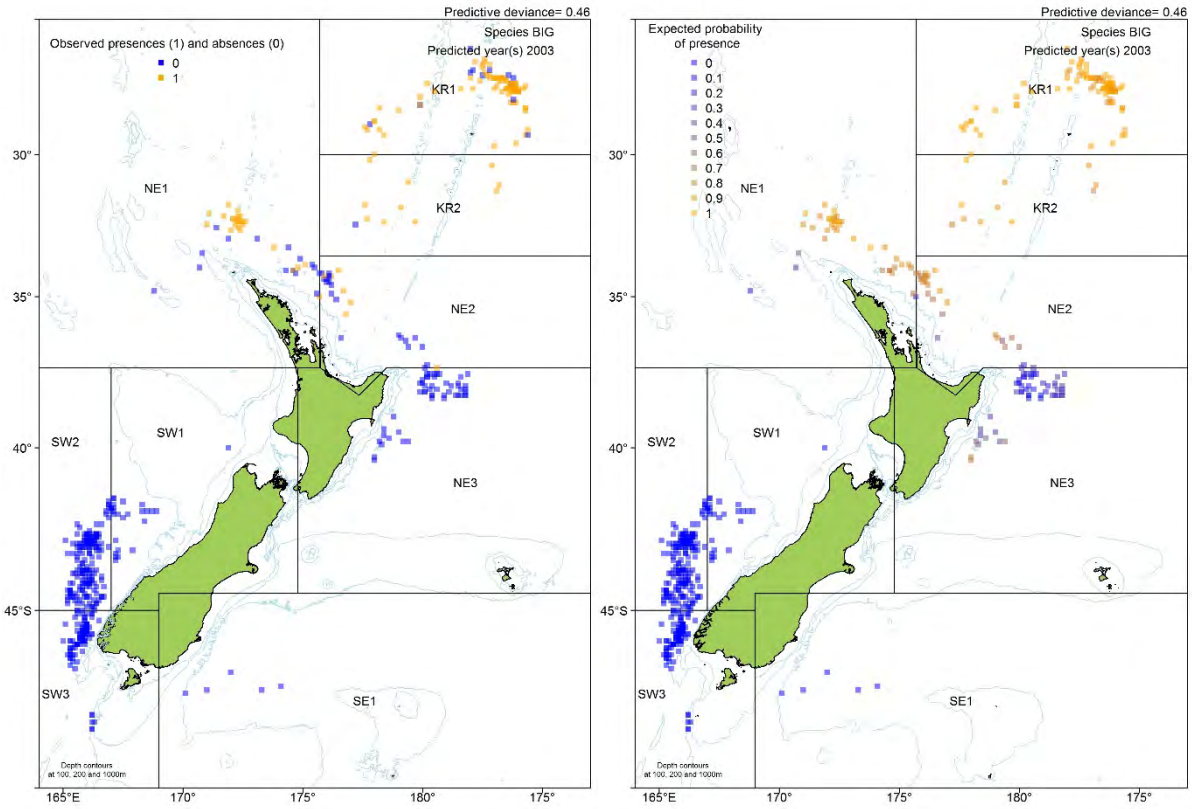


Figure 42: 2003 Binomial model observed (left) and predicted (right) presence/absence of BIG in the catch.

3.1.4 BTU

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years, with slight increases or decreases in some models (Figure 43). It was not likely that increasing the *tc* would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all BTU Binomial models.

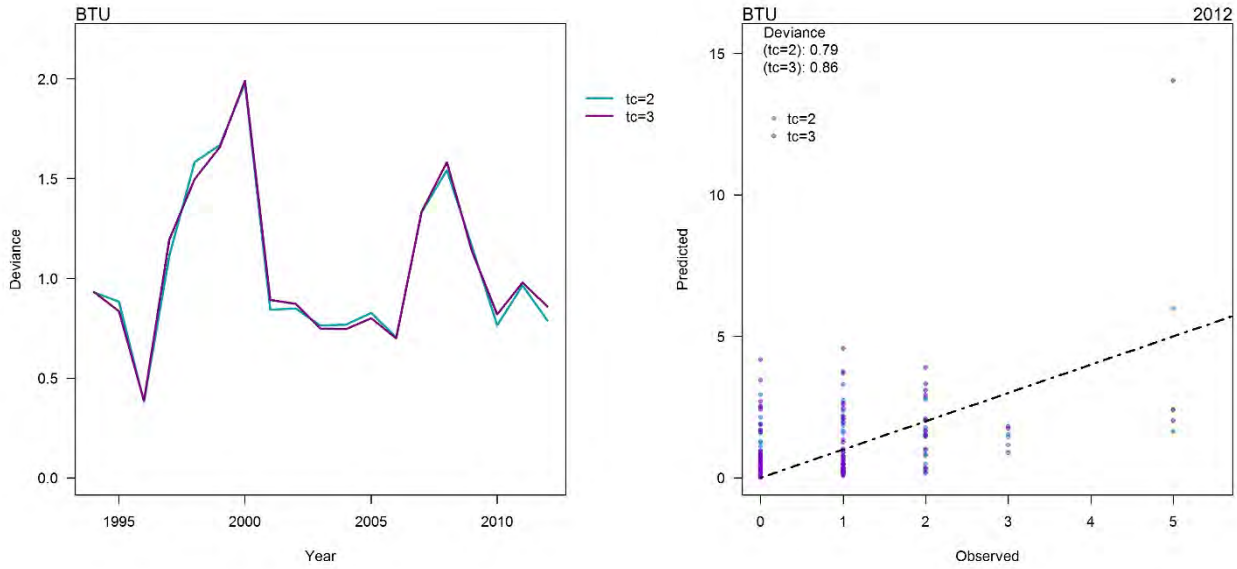


Figure 43: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2012 Poisson model (right) for species BTU.

Binomial

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance, with a very slight decrease in 2012 (Figure 44). It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all BTU Binomial models.

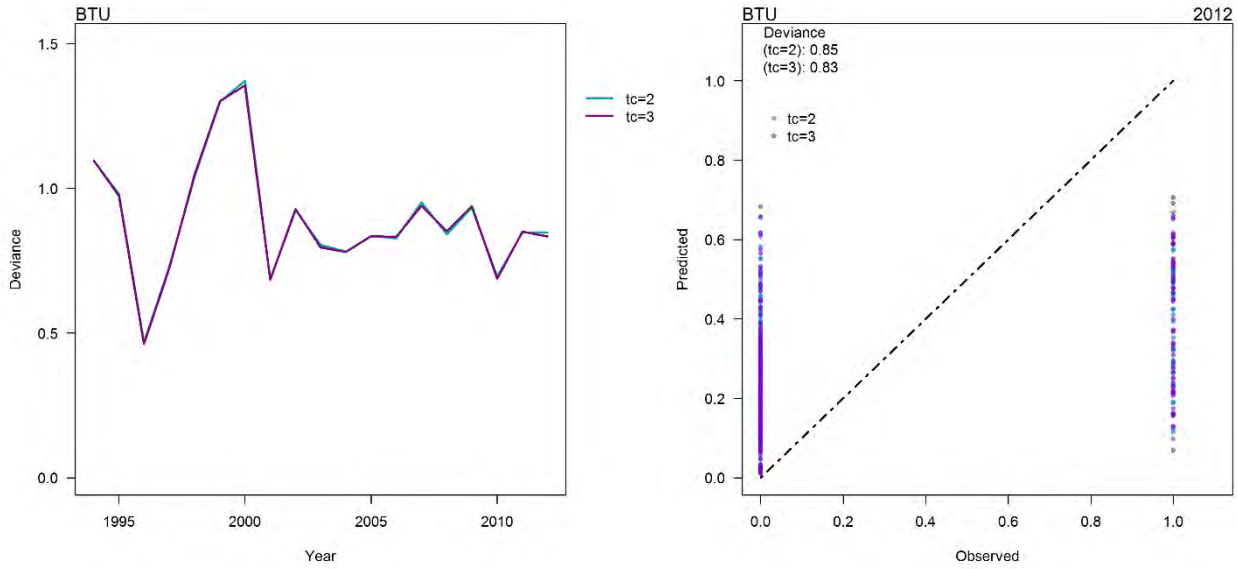


Figure 44: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2012 Binomial model (right) for species BTU.

Predictive ability

Poisson

The predictive ability was fair in most models (Figure 45) but quite poor in the 2008 and 2009 models (Figures 48 and 49) and quite good in the 1997 and 2001 models (Figures 46 and 47). The 2008 and 2009 models both underestimated the numbers caught.

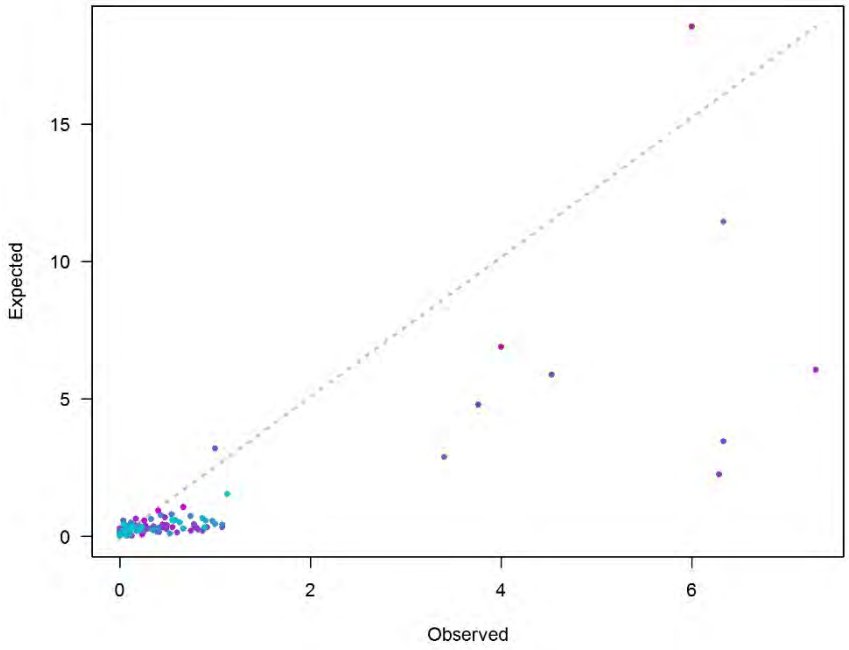


Figure 45: Observed and predicted counts of BTU for each year/subarea bin.

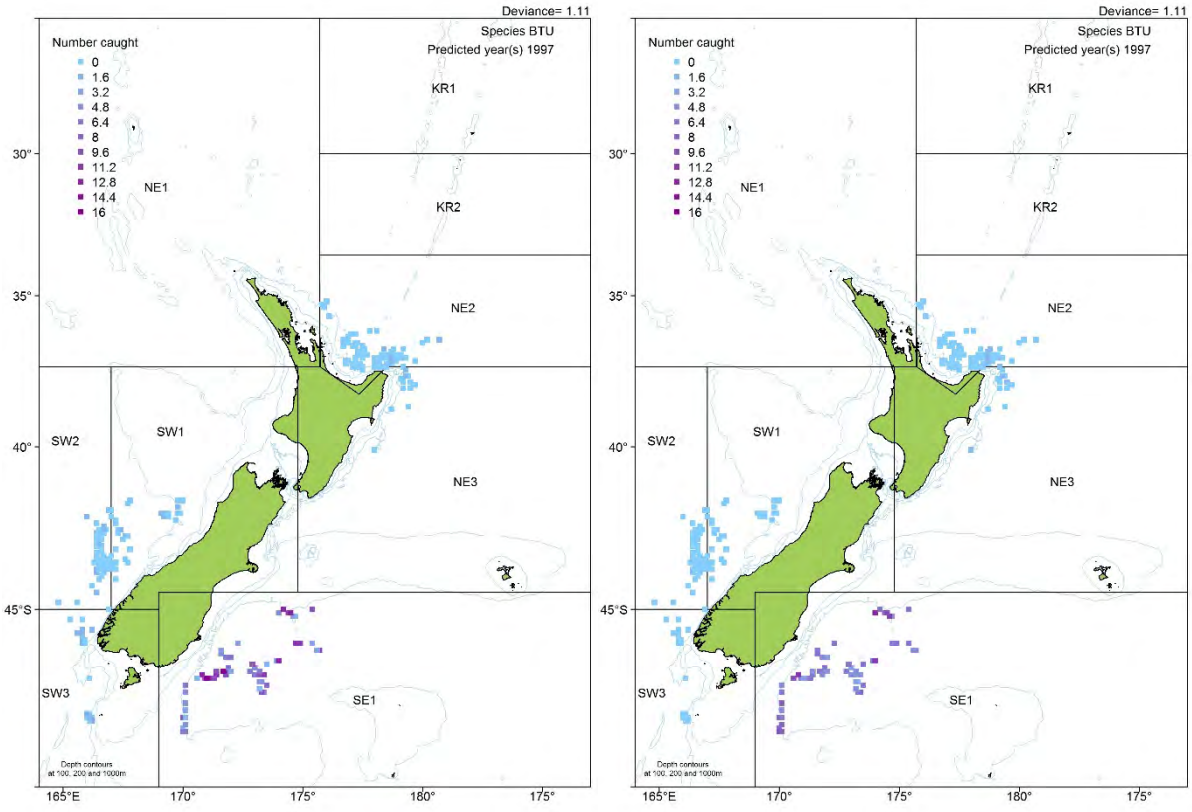


Figure 46: 1997 Poisson model observed (left) and predicted (right) numbers of BTU caught.

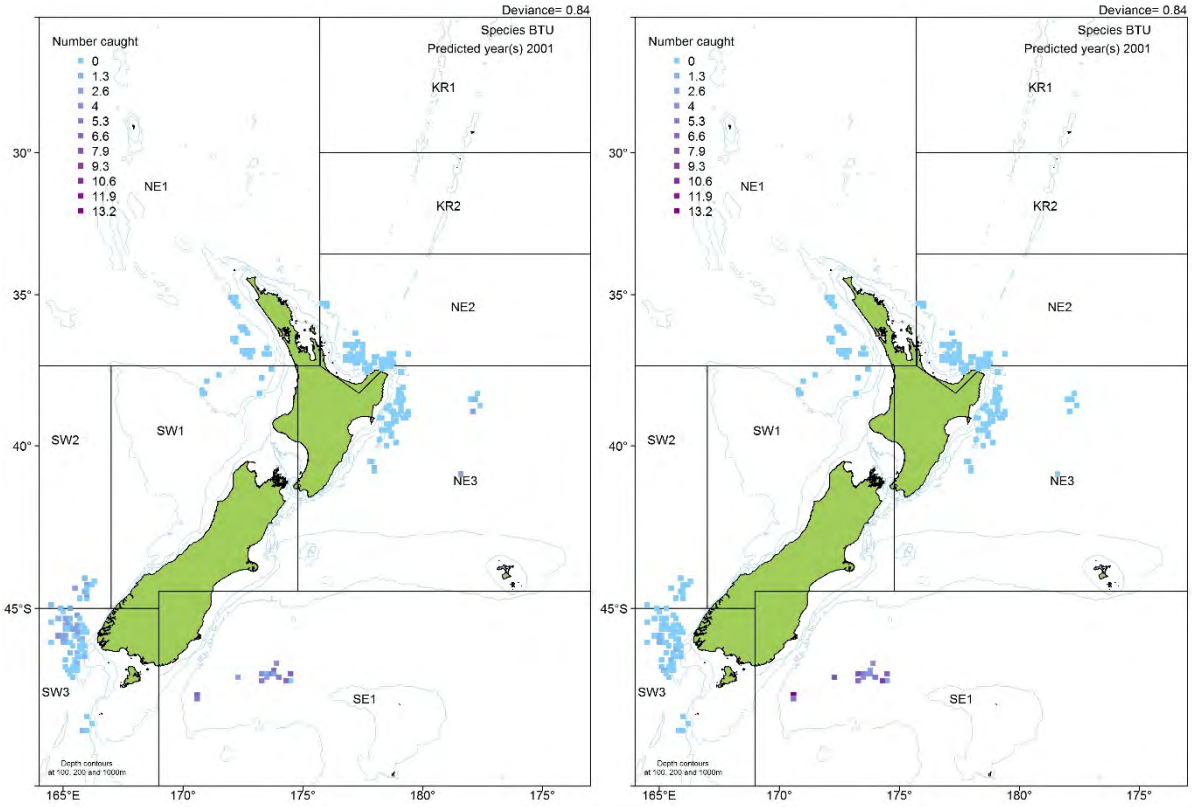


Figure 47: 2001 Poisson model observed (left) and predicted (right) numbers of BTU caught.

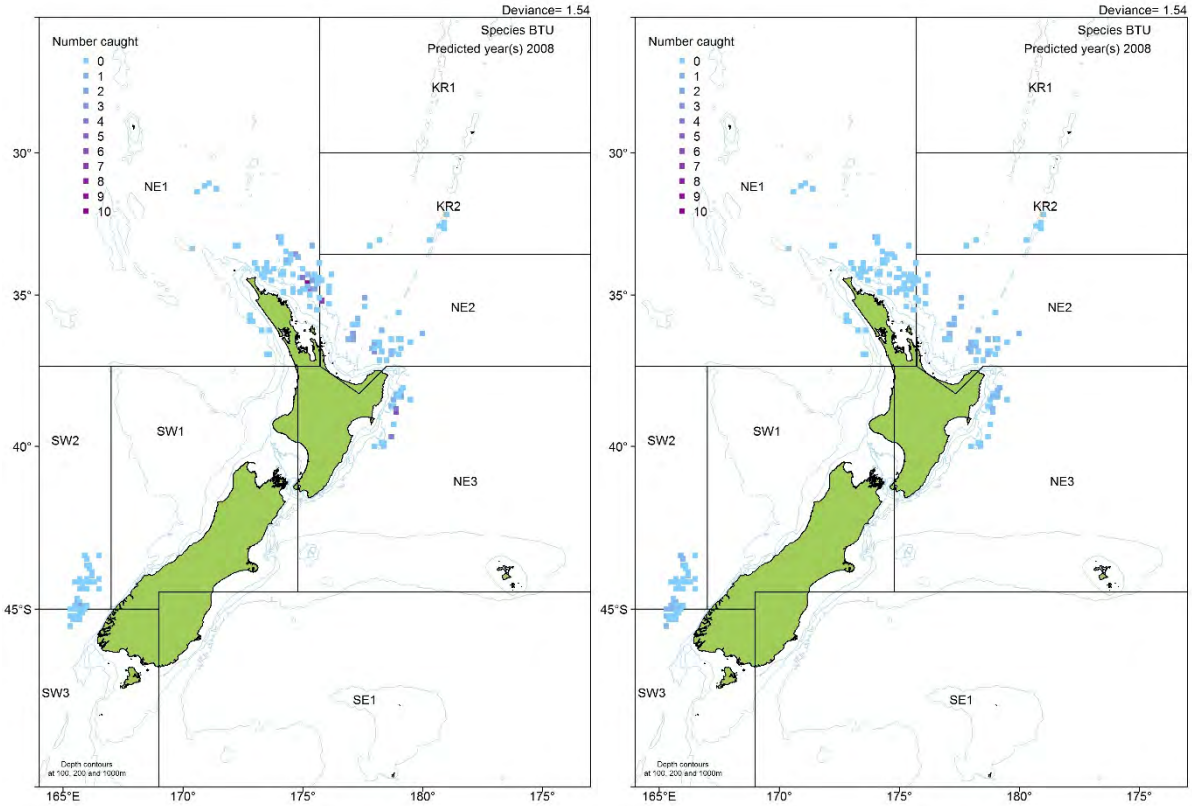


Figure 48: 2008 Poisson model observed (left) and predicted (right) numbers of BTU caught.

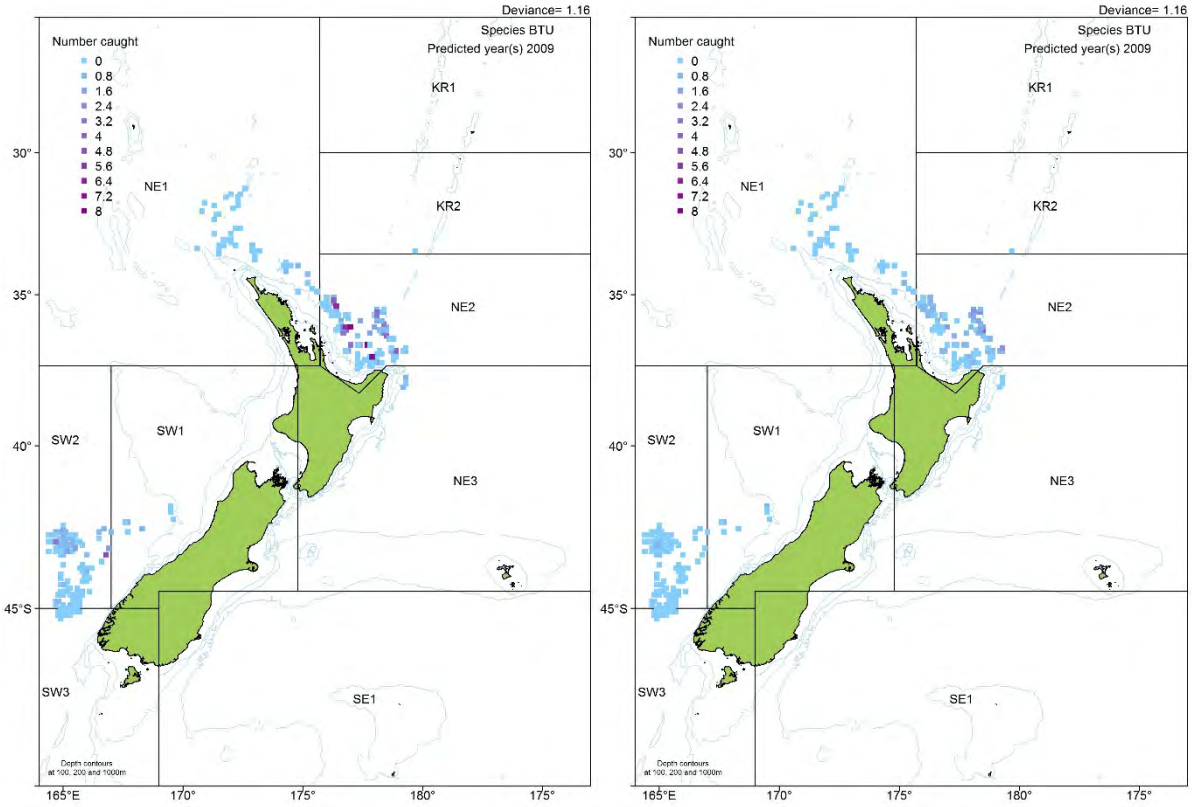


Figure 49: 2009 Poisson model observed (left) and predicted (right) numbers of BTU caught.

Binomial

Predictive ability was generally fair (Figure 50), although in several of the models, the predictions underestimated presences, especially in subareas NE2, SW1, SW2 and SW3. Two of the most extreme examples of this were the 2000 and 2009 models (Figures 51 and 52).

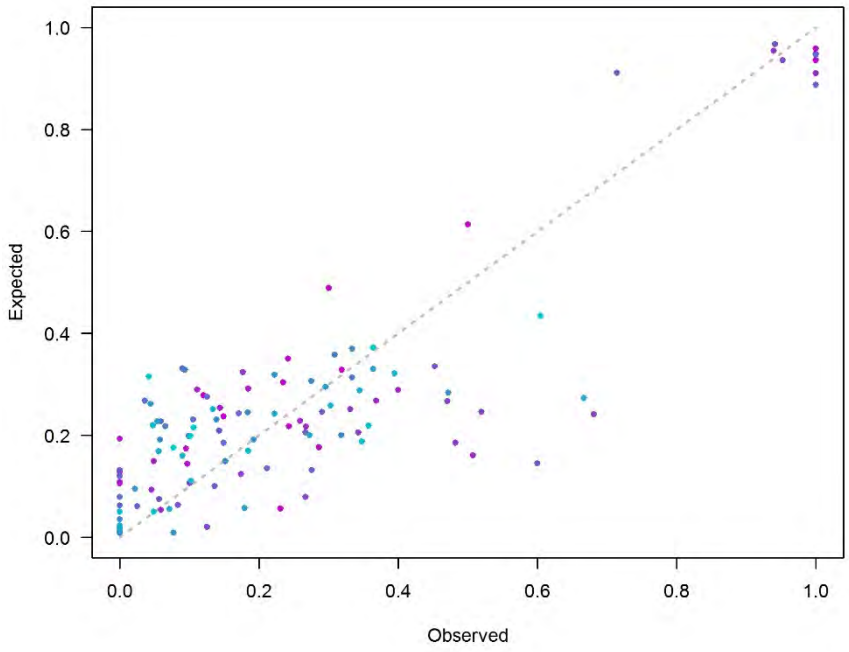


Figure 50: Observed and predicted probability of the presence of BTU for each year/subarea bin.

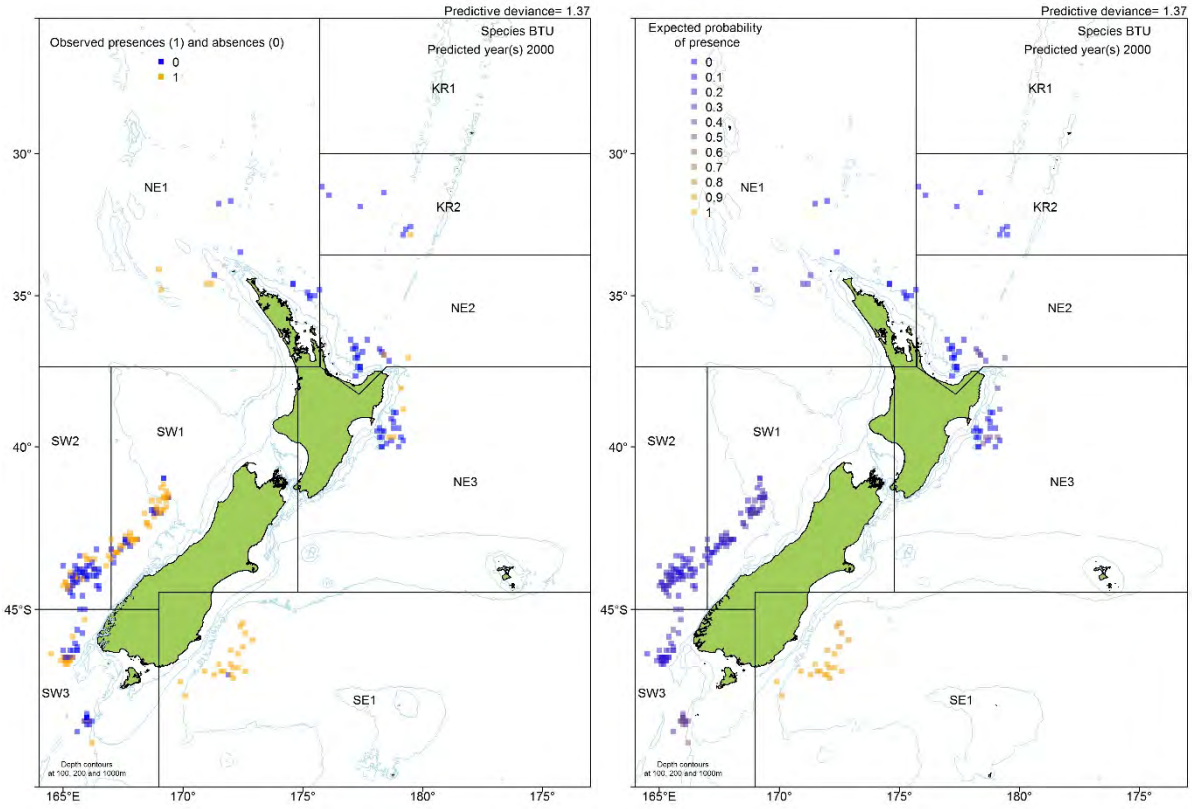


Figure 51: 2000 Binomial model observed (left) and predicted (right) presence/absence of BTU in the catch.

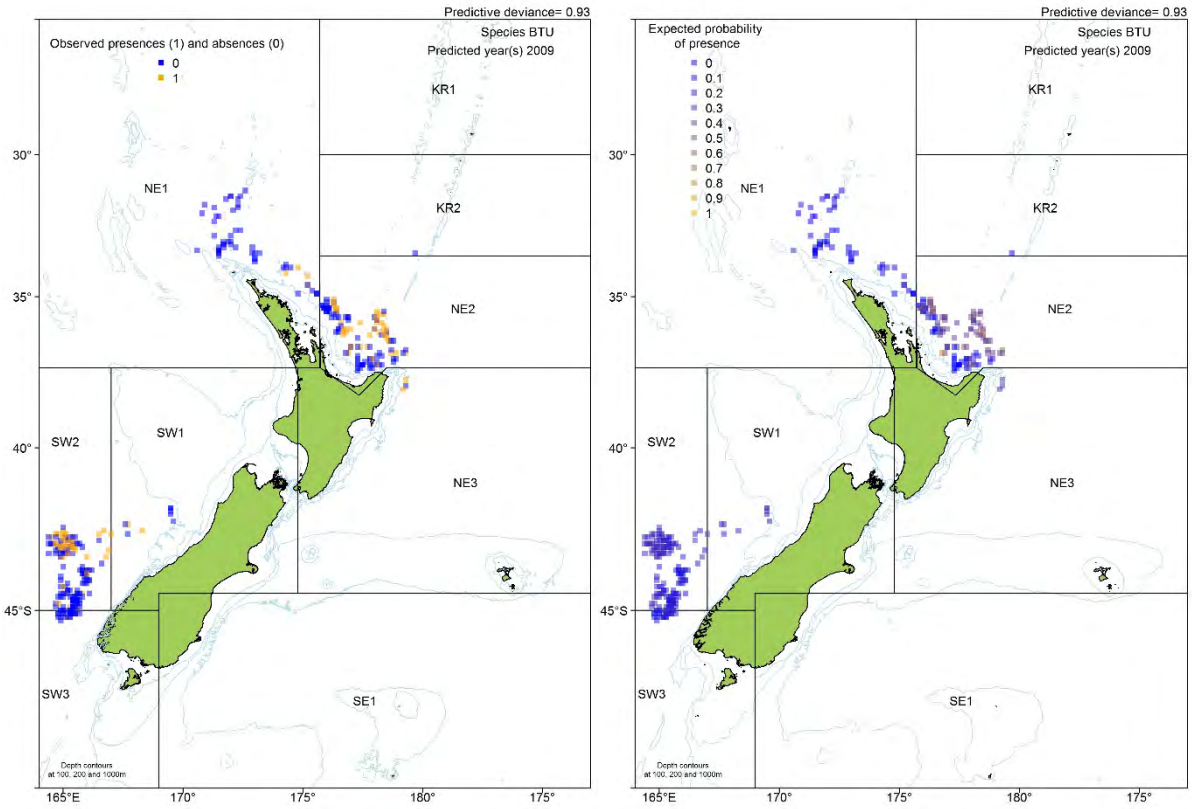


Figure 52: 2009 Binomial model observed (left) and predicted (right) presence/absence of BTU in the catch.

3.1.5 BWS

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most models, with slight increases or decreases in some (Figure 53). It was not likely that increasing the *tc* would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for BWS Poisson models.

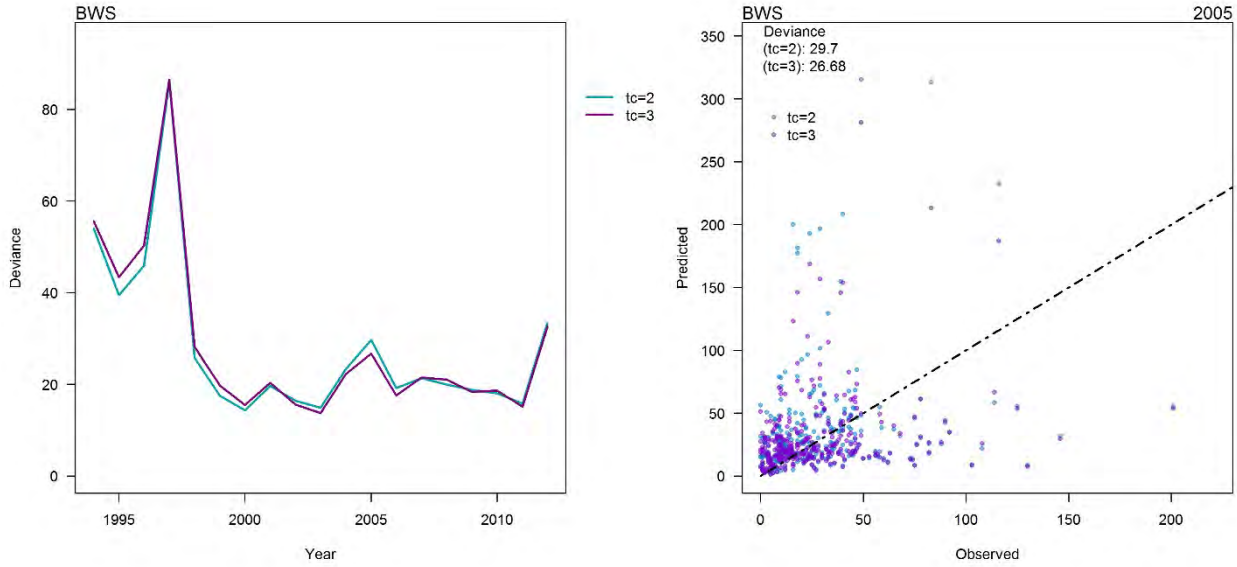


Figure 53: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2005 Poisson model (right) for species BWS.

Binomial

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years, with slight decreases in the 1998 and 2008 models (Figure 54). It was not likely that increasing the *tc* would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all BWS Binomial models.

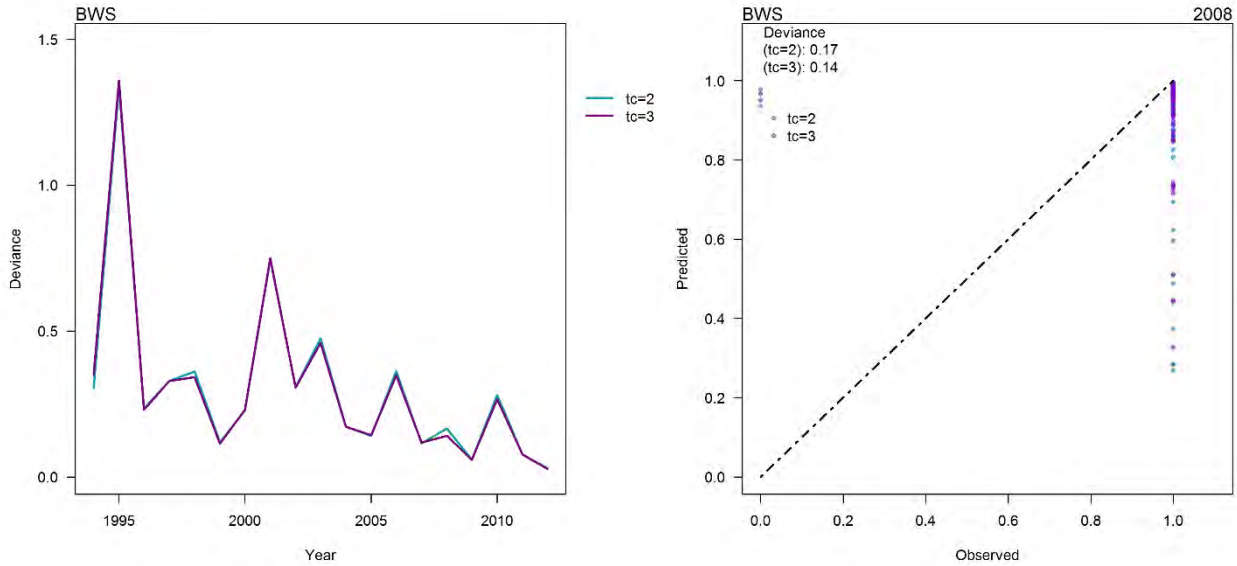


Figure 54: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2008 Binomial model (right) for species BWS.

Predictive ability

Poisson

The predictive ability was fair in most models (Figure 55) but poor in the 1995, 1996 and 1997 models. In all these years, the models underestimated the numbers caught (Figures 56, 57 and 58). The 1999, 2001 and 2006 models had quite good predictive power, with predicted numbers caught fairly well matched to those observed (Figures 59, 60 and 61).

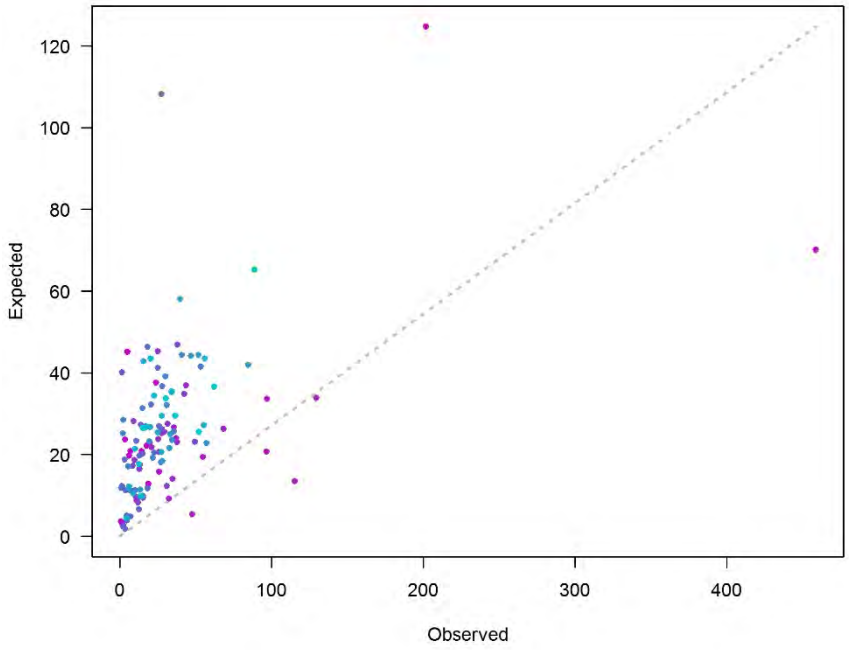


Figure 55: Observed and predicted counts of BWS for each year/subarea bin.

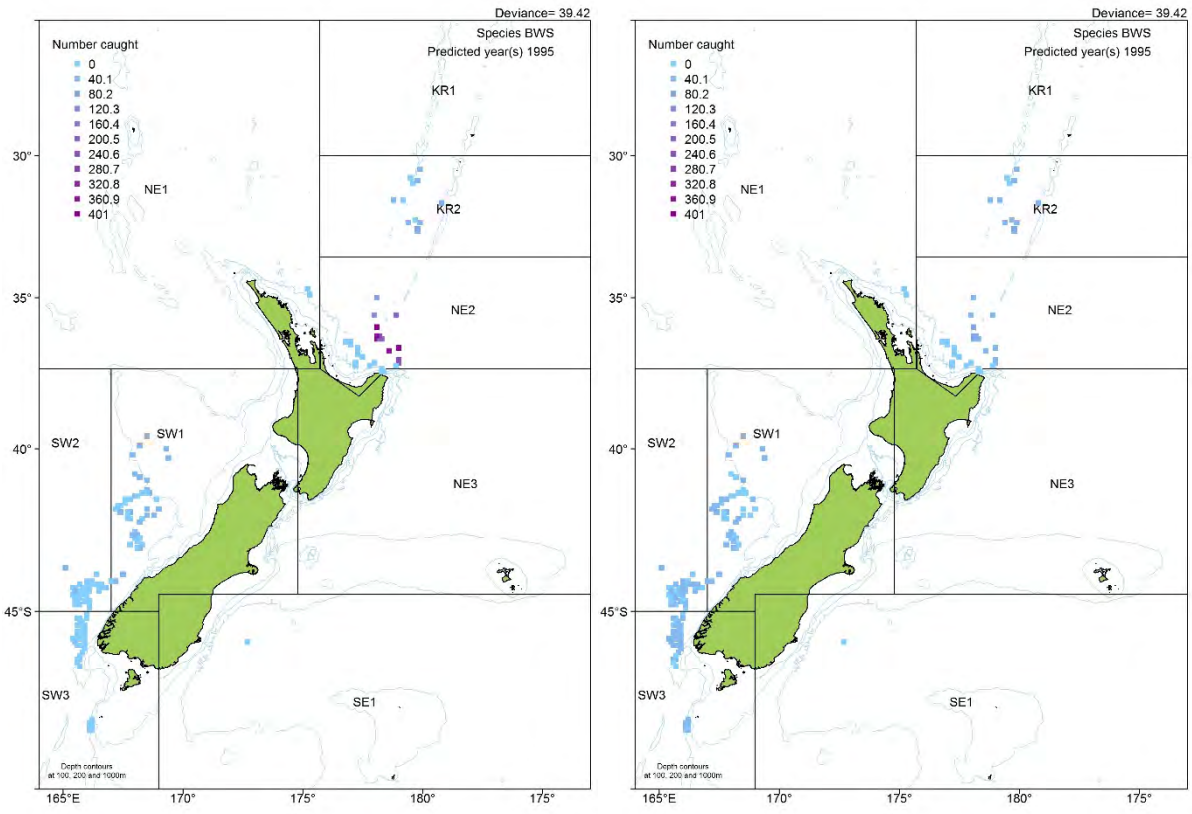


Figure 56: 1995 Poisson model observed (left) and predicted (right) numbers of BWS caught.

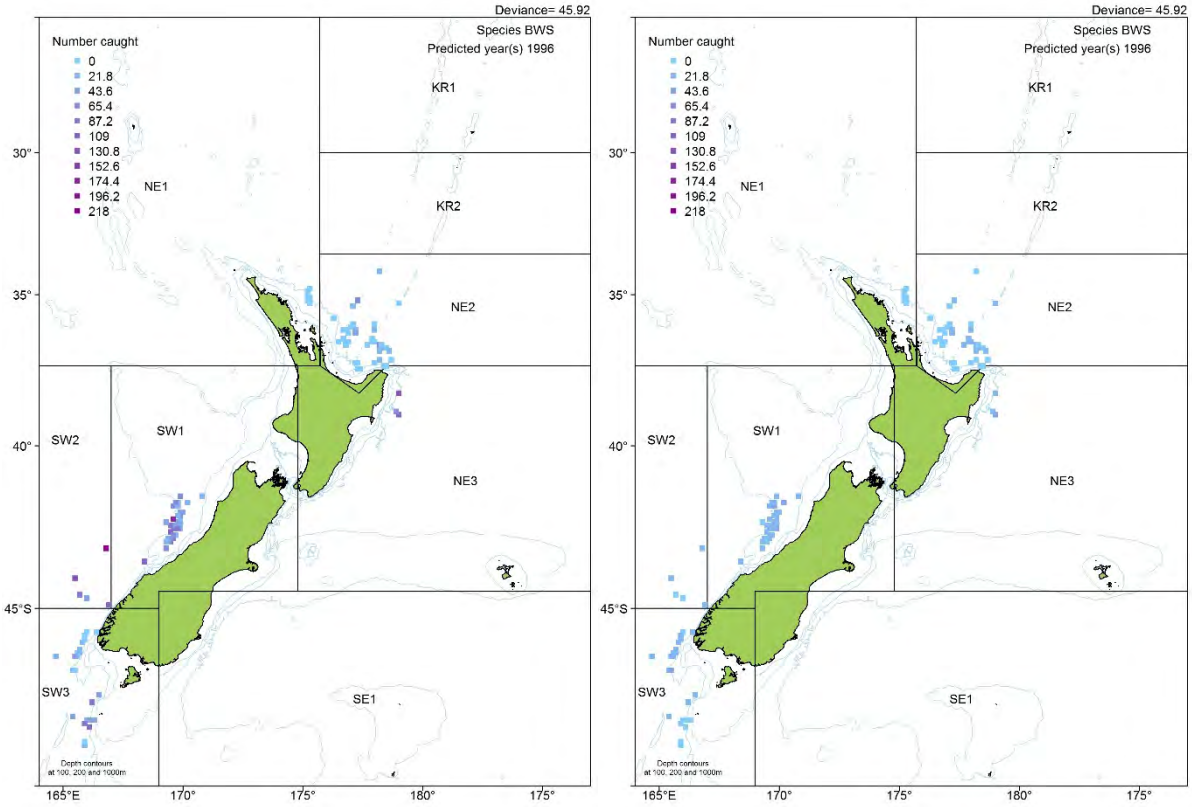


Figure 57: 1996 Poisson model observed (left) and predicted (right) numbers of BWS caught.

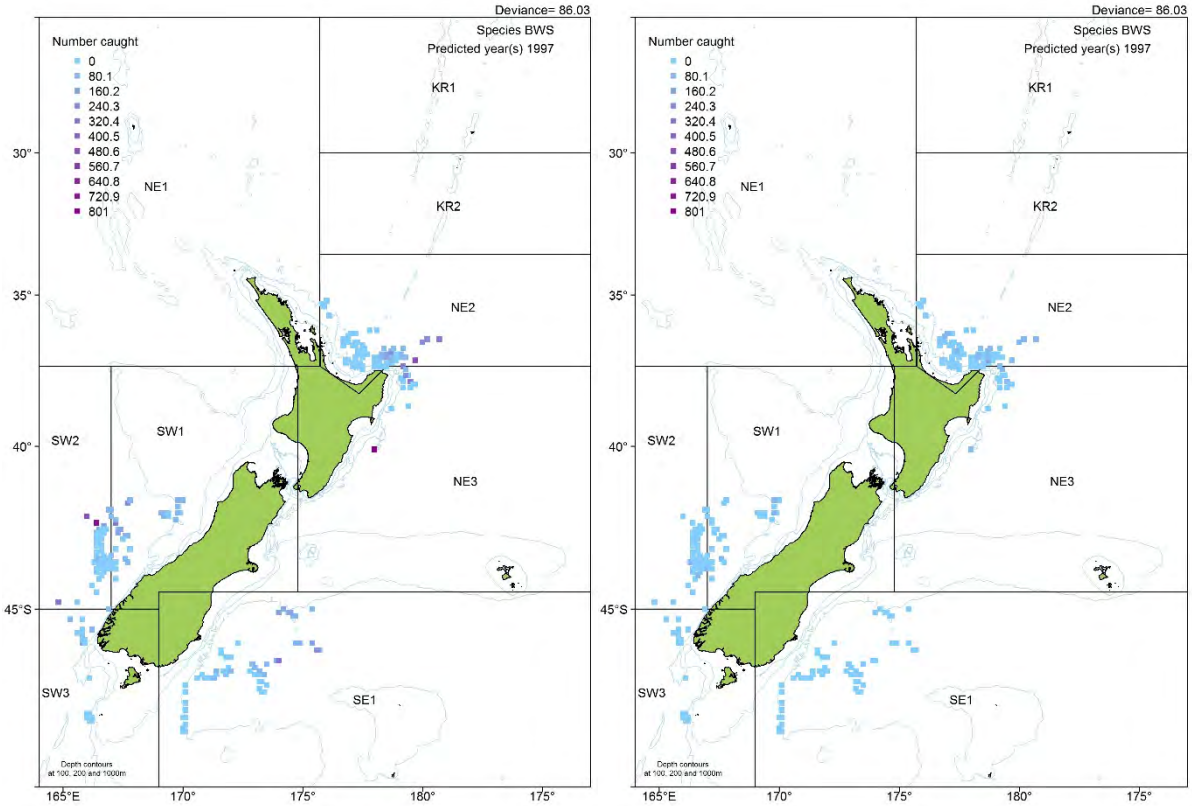


Figure 58: 1997 Poisson model observed (left) and predicted (right) numbers of BWS caught.

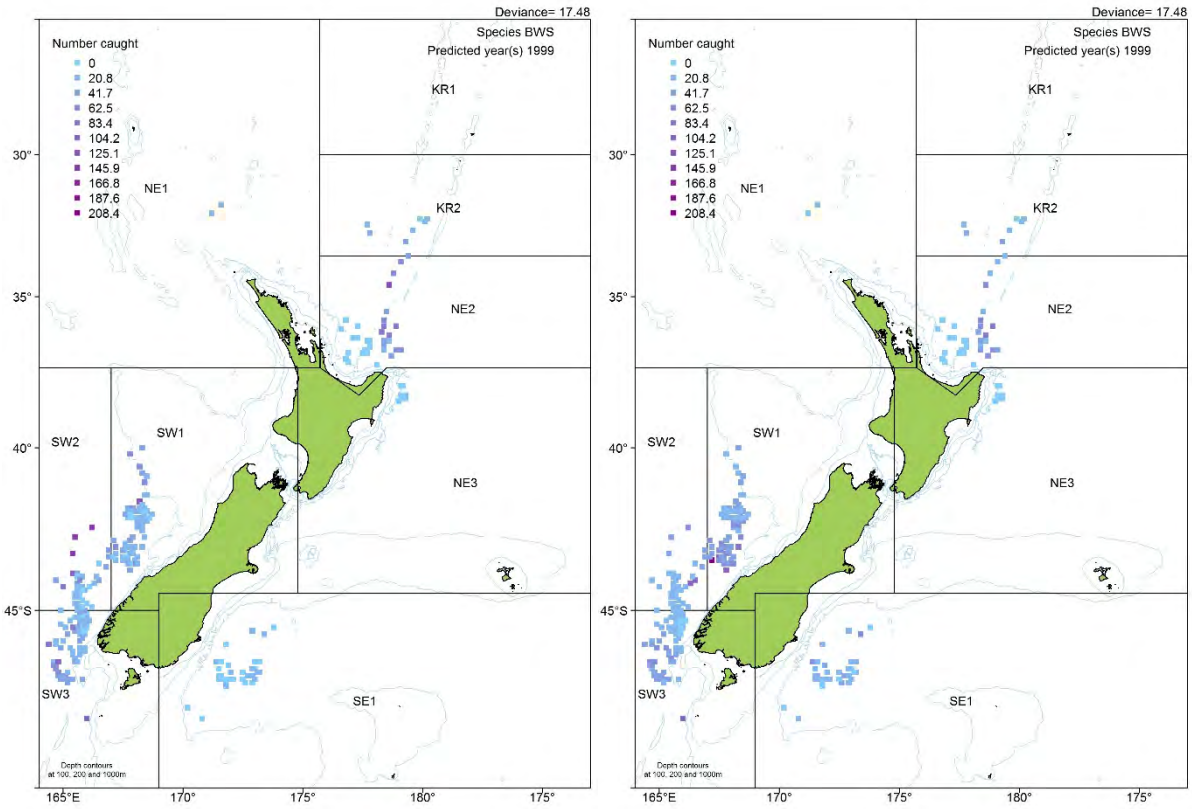


Figure 59: 1999 Poisson model observed (left) and predicted (right) numbers of BWS caught.

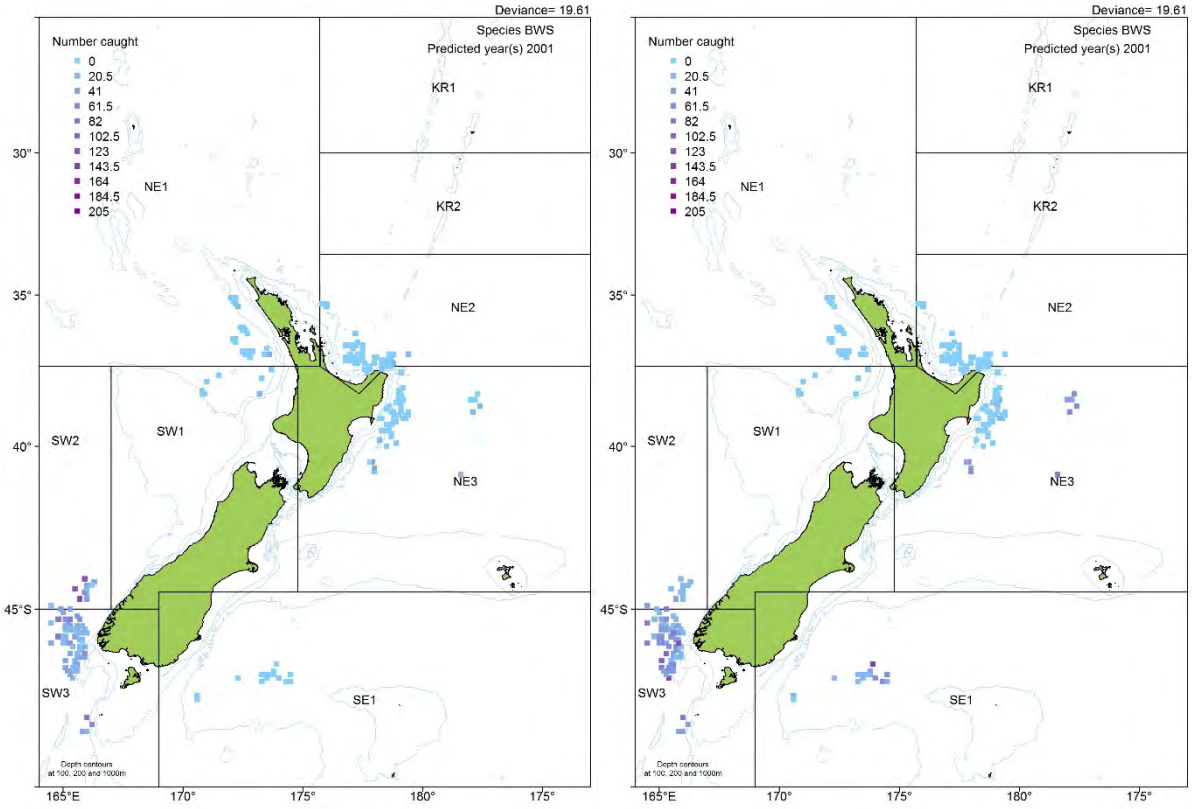


Figure 60: 2001 Poisson model observed (left) and predicted (right) numbers of BWS caught.

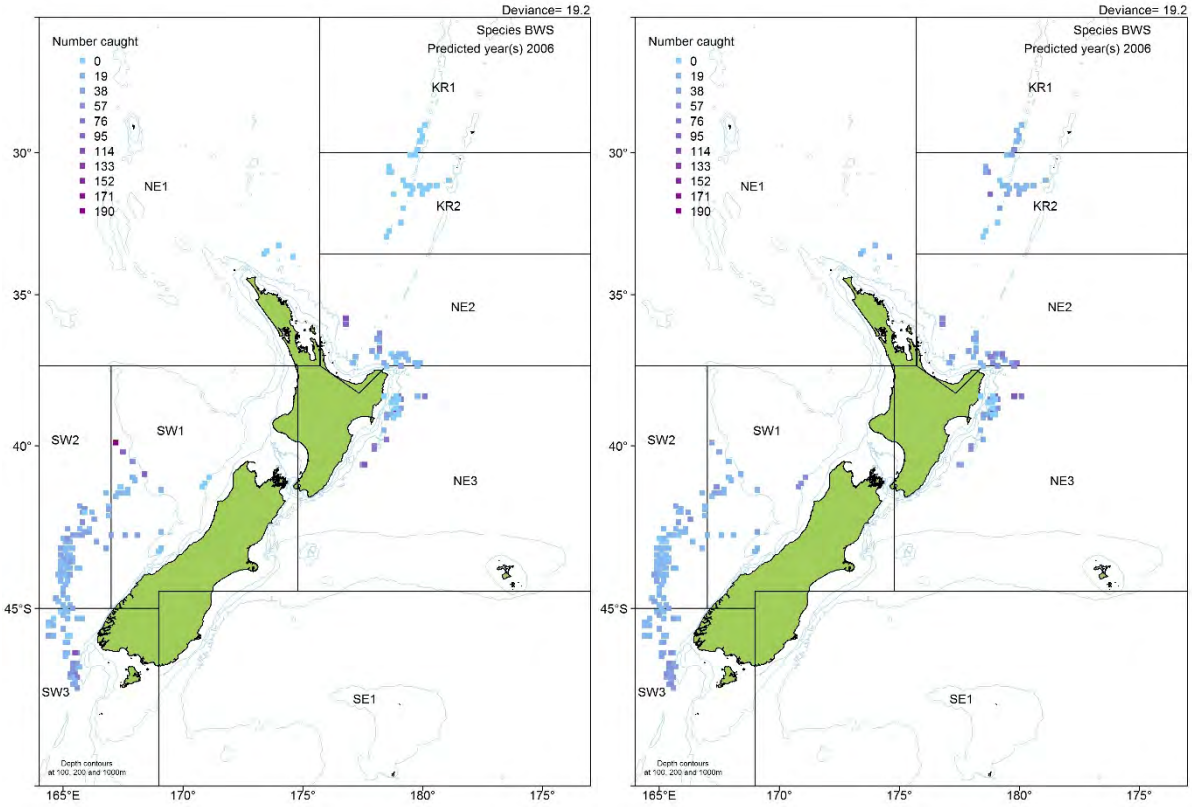


Figure 61: 2006 Poisson model observed (left) and predicted (right) numbers of BWS caught.

Binomial

Generally, the predictive ability was good (Figure 62), but this was partly because BWS were nearly always present. When they are absent, the predictions often get it wrong, such as in the 2001 and 2006 models (Figures 63 and 64).

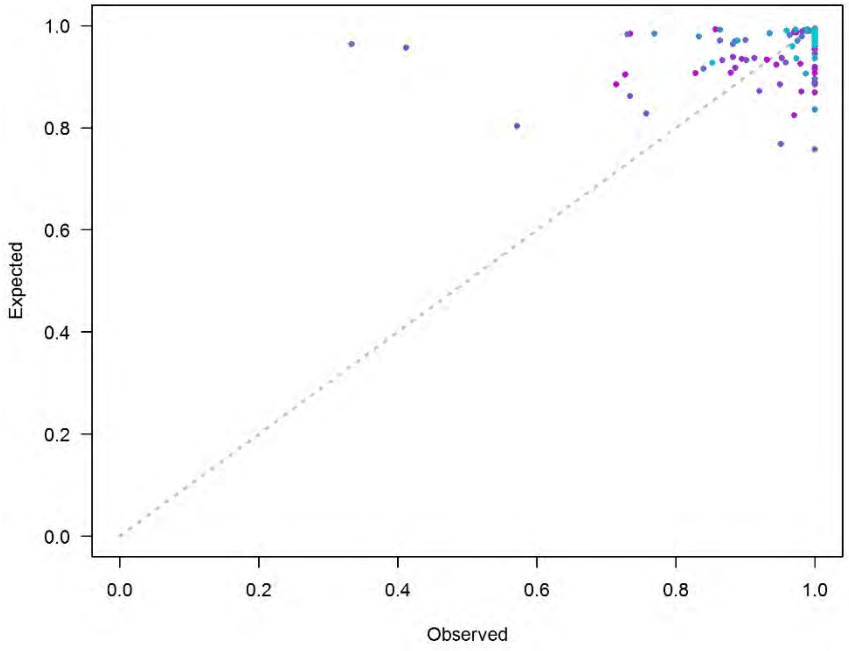


Figure 62: Observed and predicted probability of the presence of BWS for each year/subarea bin.

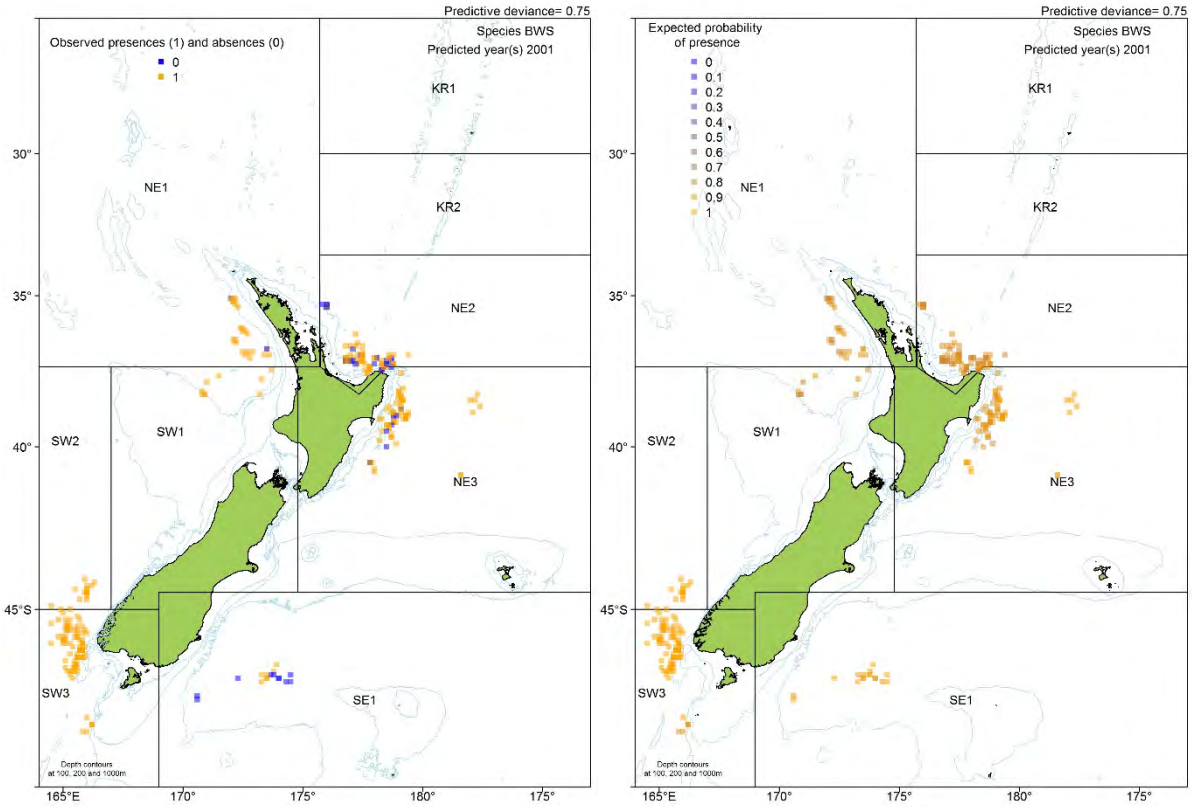


Figure 63: 2001 Binomial model observed (left) and predicted (right) presence/absence of BWS in the catch.

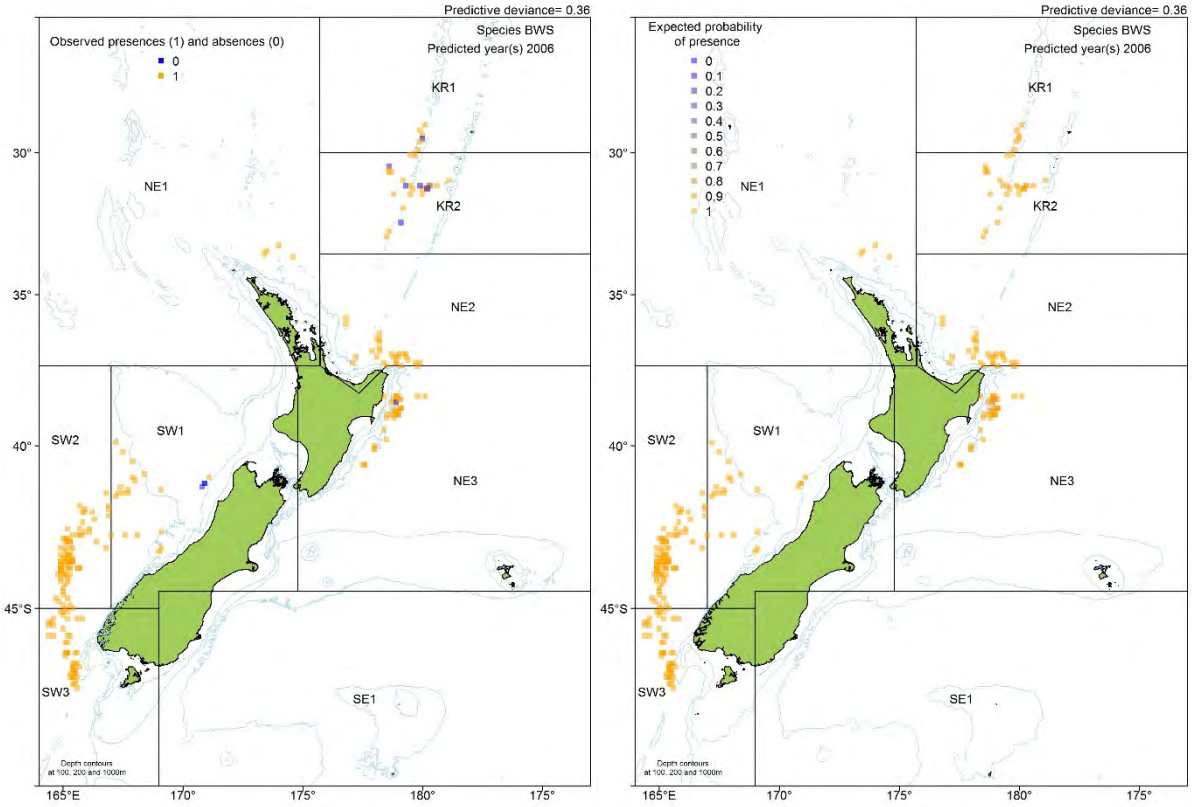


Figure 64: 2006 Binomial model observed (left) and predicted (right) presence/absence of BWS.

3.1.6 LAT

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years, except in 1997 where it made it higher (Figure 65). It was not likely that increasing the *tc* would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all LAT Poisson models.

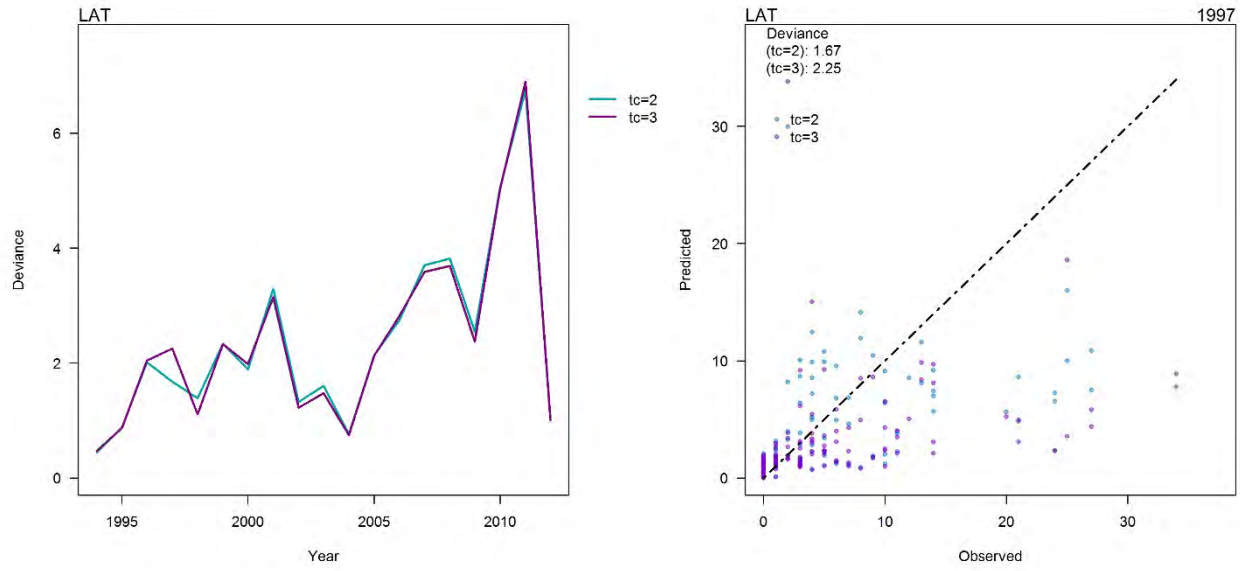


Figure 65: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2005 Poisson model (right) for species LAT.

Binomial

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance (Figure 66). There was a very slight decrease in some years such as 2001. It was not likely that further increasing the *tc* would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all LAT Binomial models.

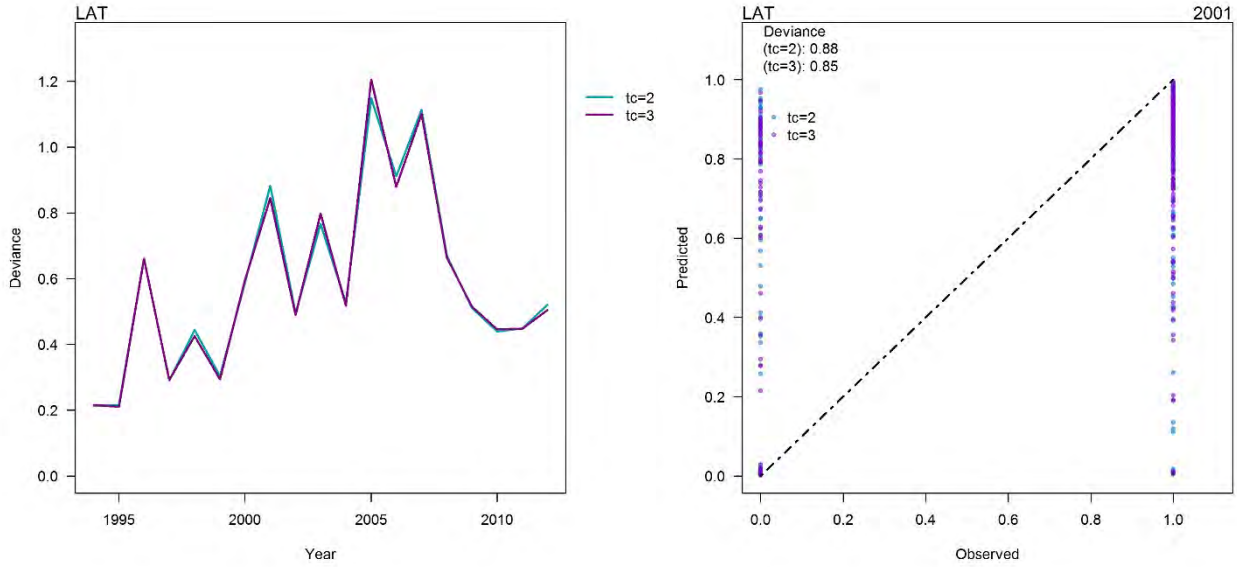


Figure 66: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2001 Binomial model (right) for species LAT.

Predictive ability

Poisson

The predictive ability was fair in most models (Figure 67). The 2011 model had the highest predictive deviance, and the numbers caught were underestimated (Figure 70). The 2006 and 2009 models had good predictive power, with predicted numbers caught well matched to those observed (Figures 68 and 69).

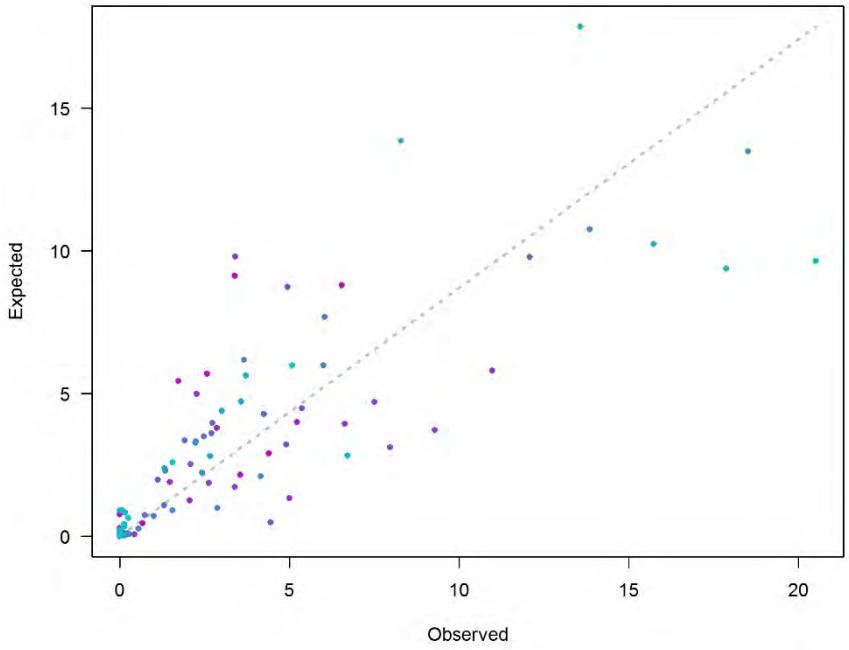


Figure 67: Observed and predicted counts of LAT for each year/subarea bin.

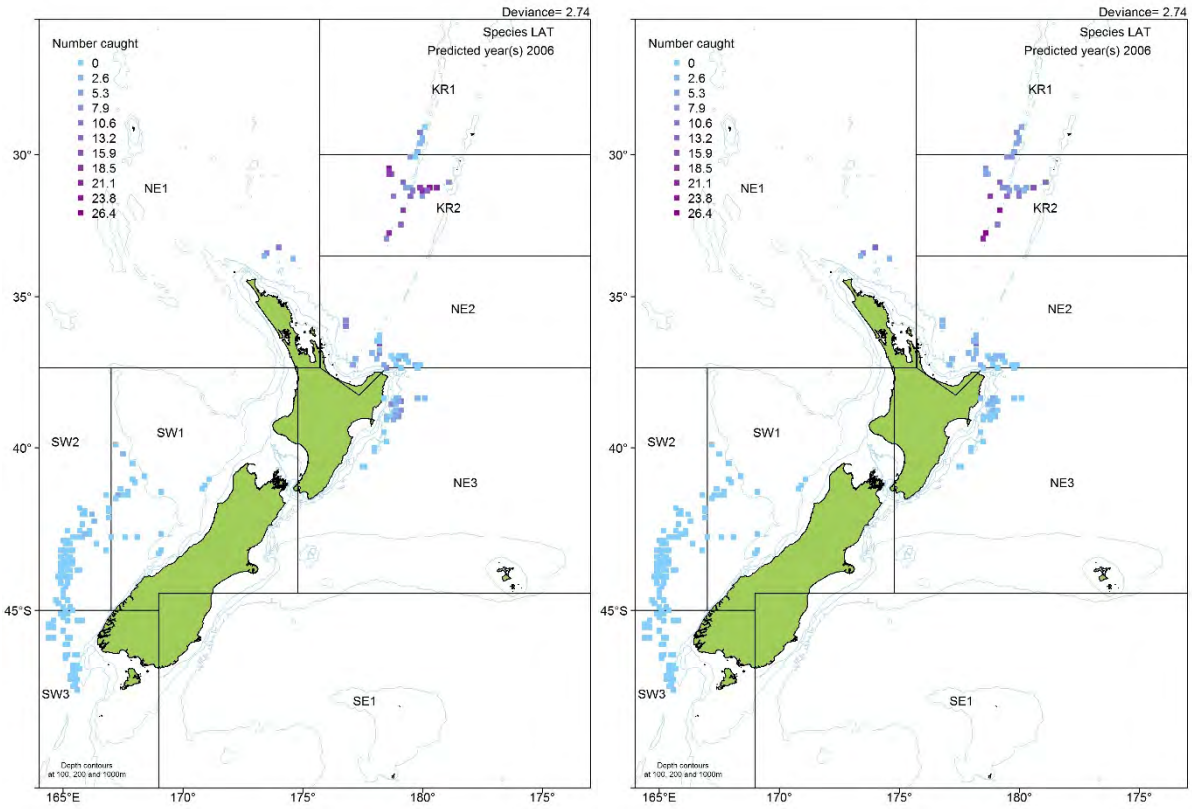


Figure 68: 2006 Poisson model observed (left) and predicted (right) numbers of LAT caught.

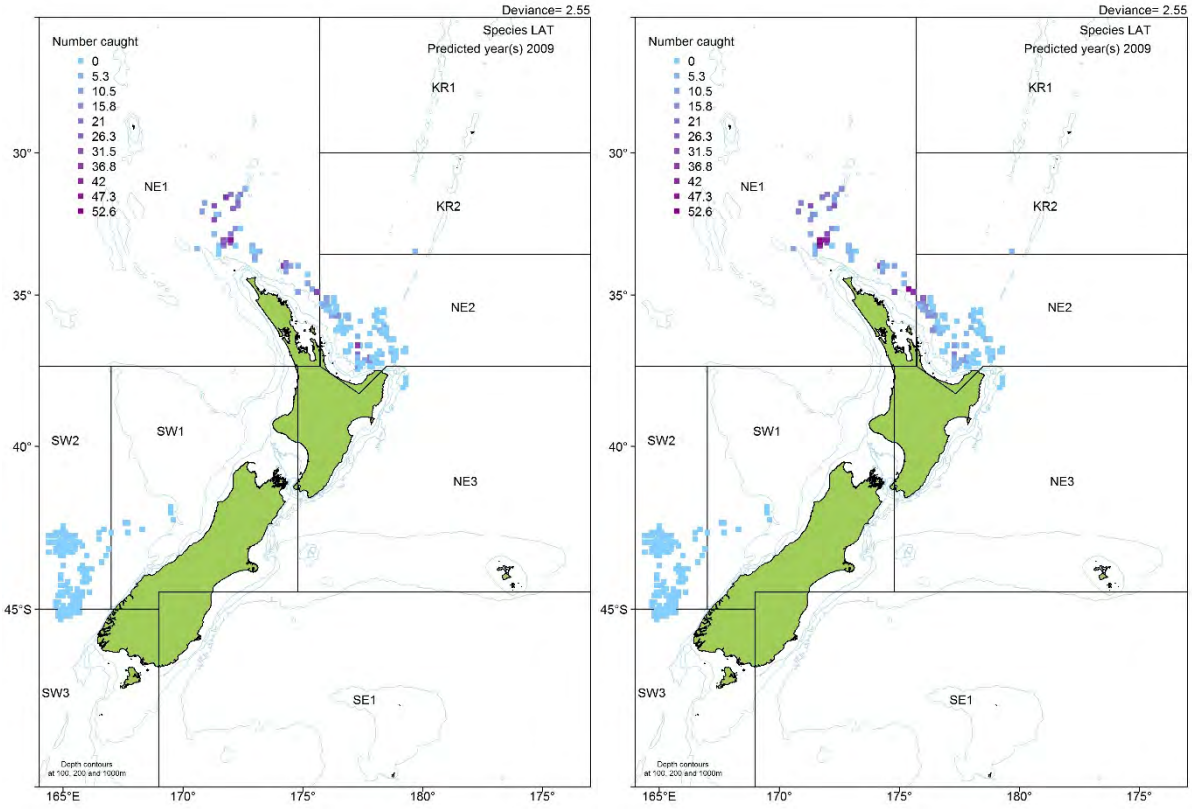


Figure 69: 2009 Poisson model observed (left) and predicted (right) numbers of LAT caught.

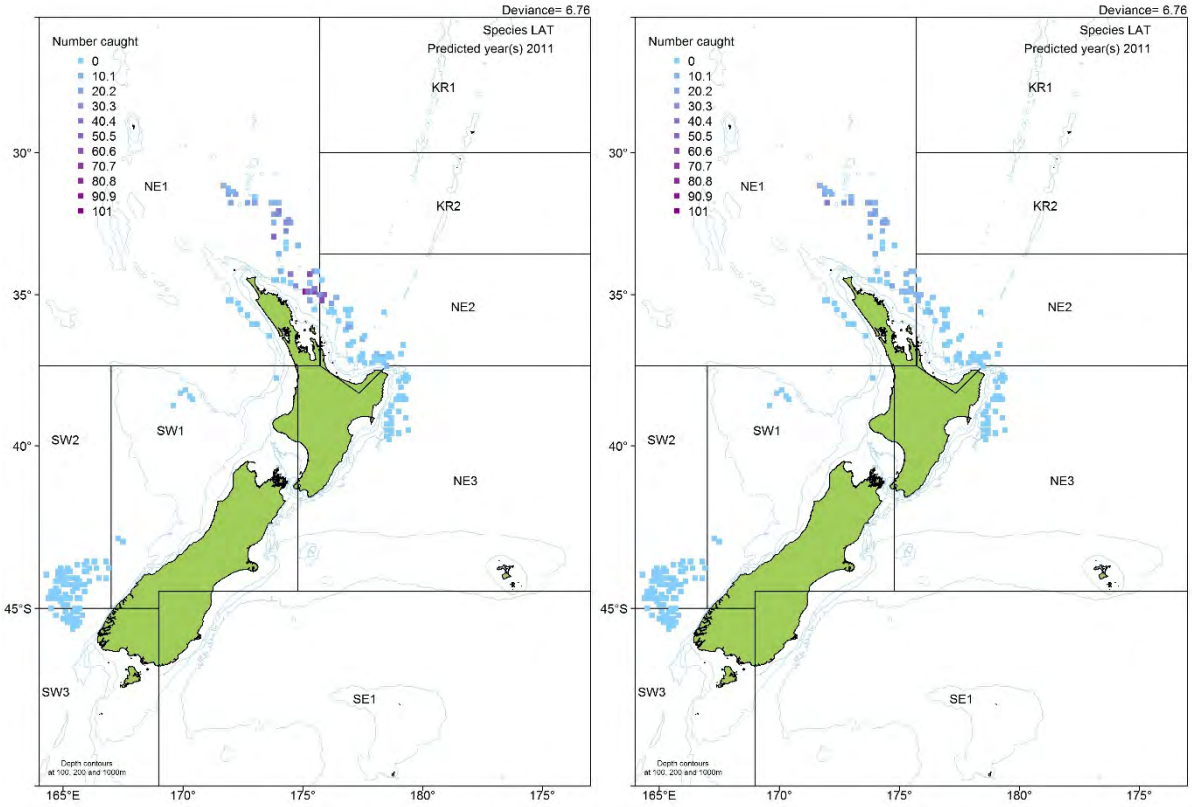


Figure 70: 2010 Poisson model observed (left) and predicted (right) numbers of LAT caught.

Binomial

Predictive ability was generally very good (Figure 71), although only fair in some models, the worst of which were 2001 and 2006 (Figures 73 and 74). There were quite strong subarea and latitude effects, which were likely to be the cause of more false misses in subareas SW1, SW2 and SW3 and more false hits in KR1, KR2, NE1 and NE2 (Figure 72).

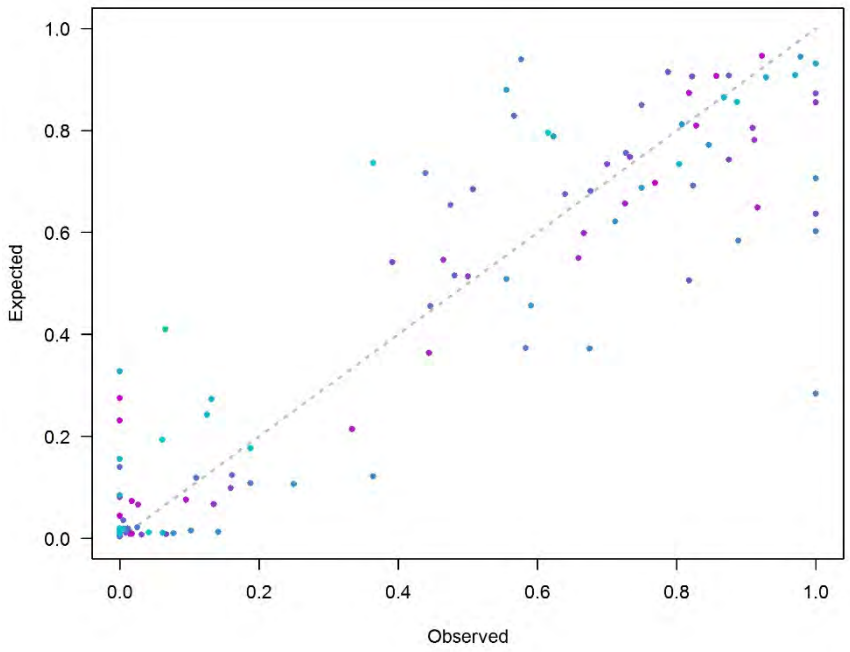


Figure 71: Observed and predicted probability of the presence of LAT for each year/subarea bin.

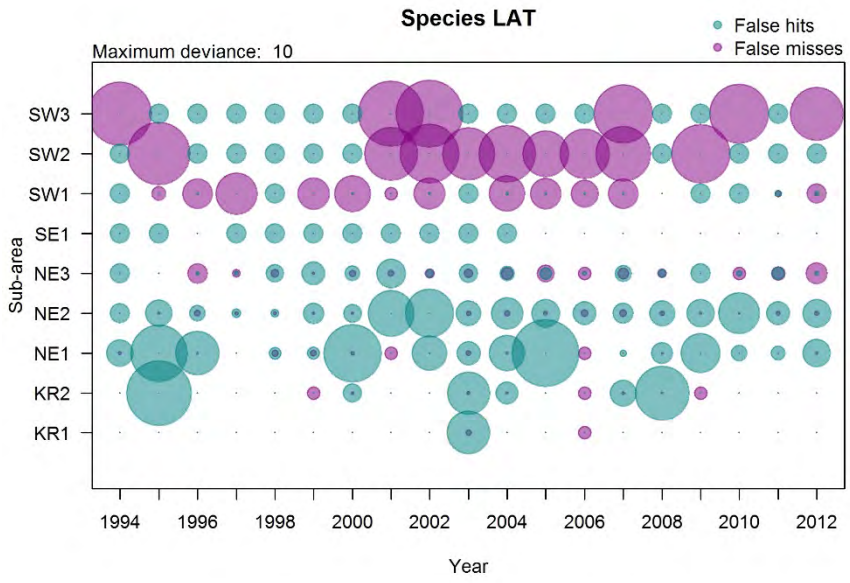


Figure 72: False misses (absences) and false hits (presences) by subarea for LAT Binomial models.

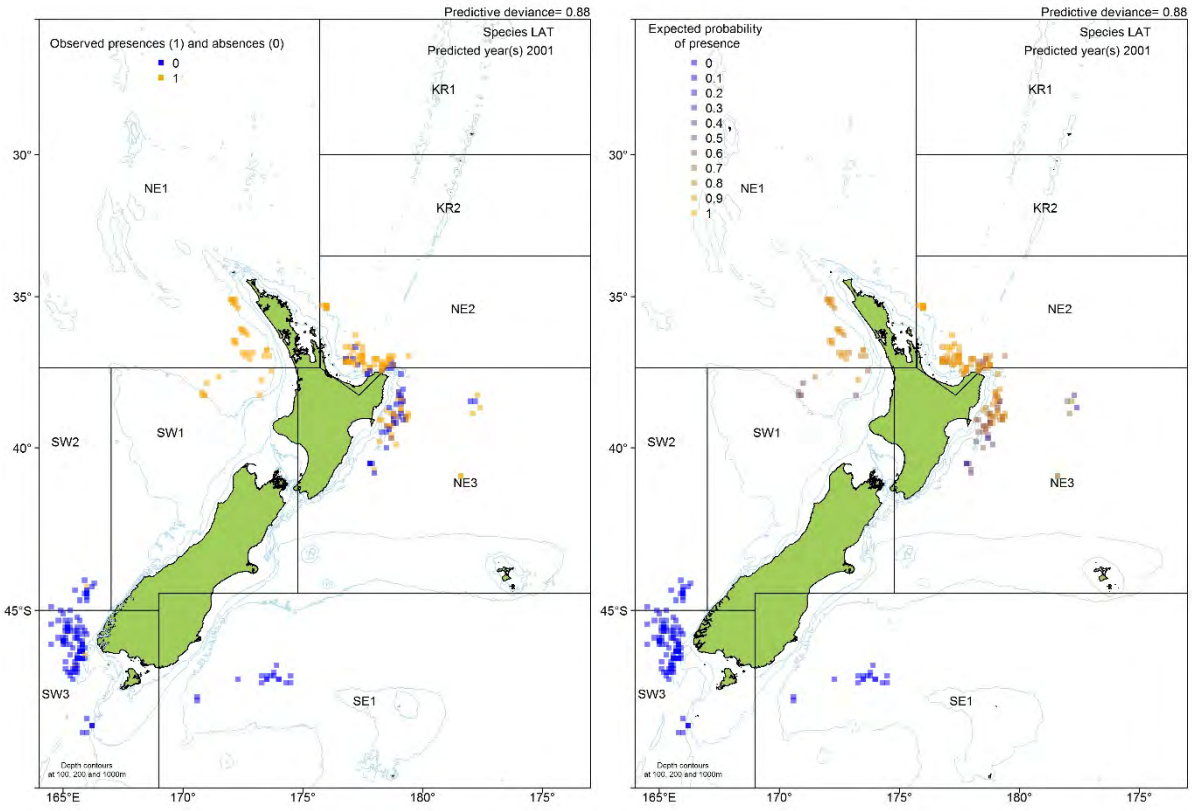


Figure 73: 2001 Binomial model observed (left) and predicted (right) presence/absence of LAT in the catch.

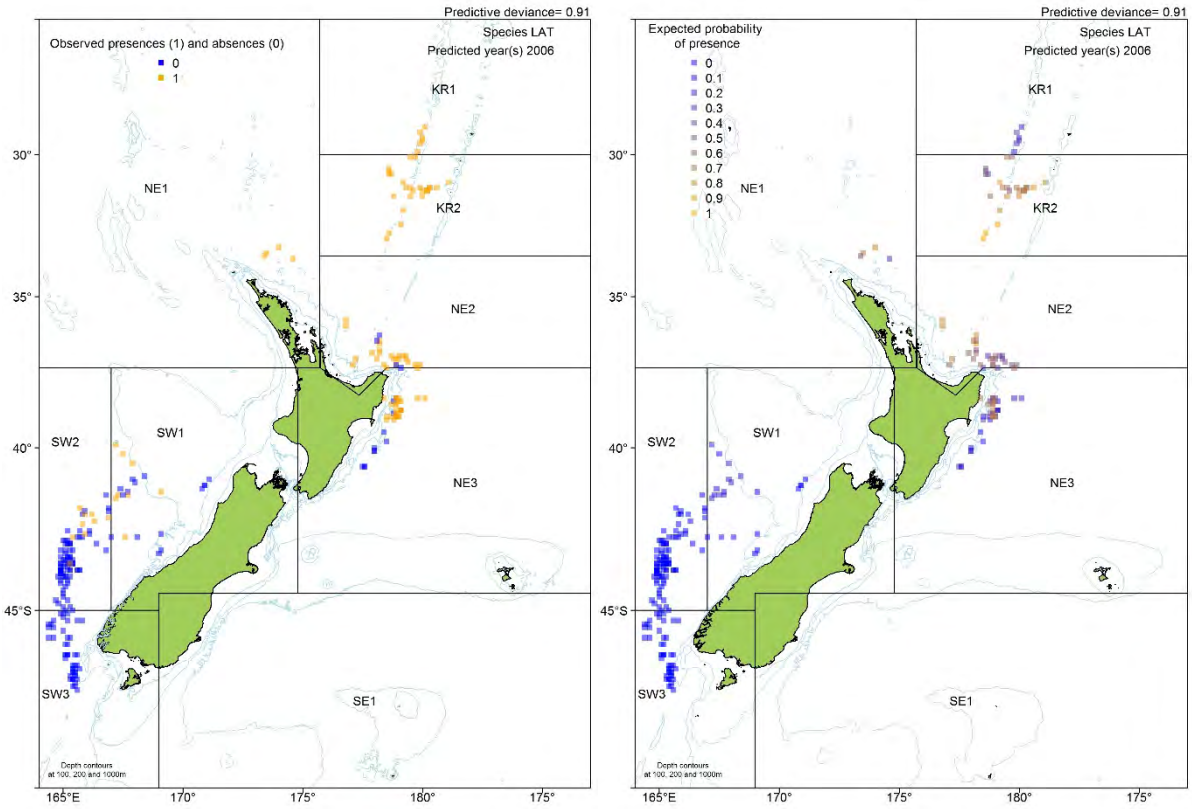


Figure 74: 2006 Binomial model observed (left) and predicted (right) presence/absence of LAT in the catch.

3.1.7 MAK

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years, with slight decreases in some models (Figure 75). It was not likely that increasing the *tc* further would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all MAK Poisson models.

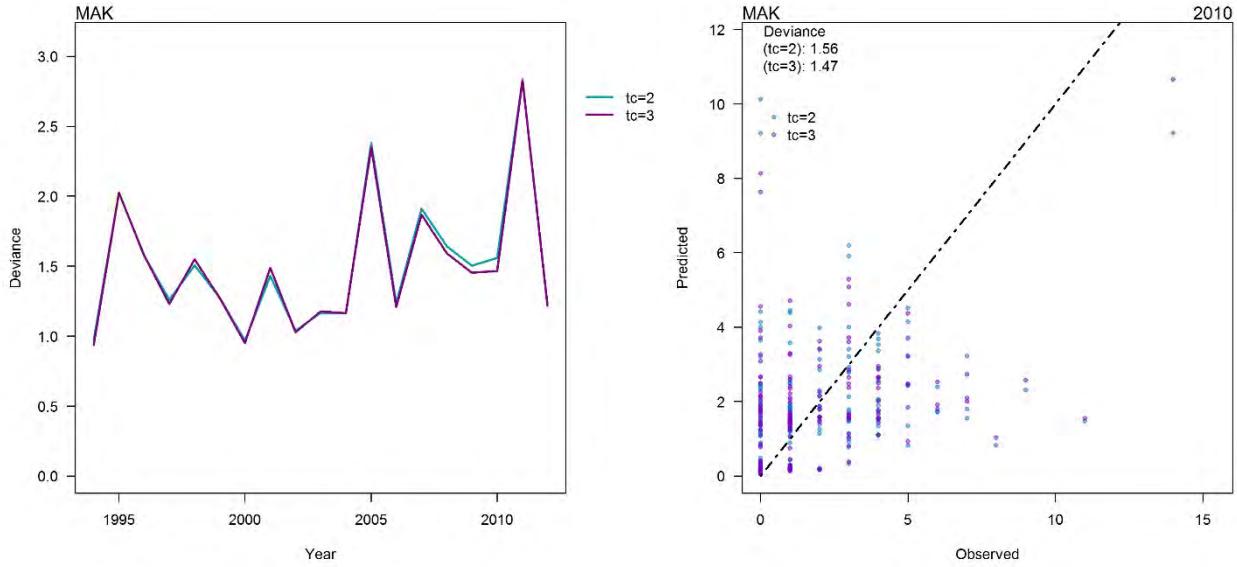


Figure 75: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2010 Poisson model (right) for species MAK.

Binomial

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years, with a very slight increase in the 2006 model (Figure 76). It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all MAK Binomial models.

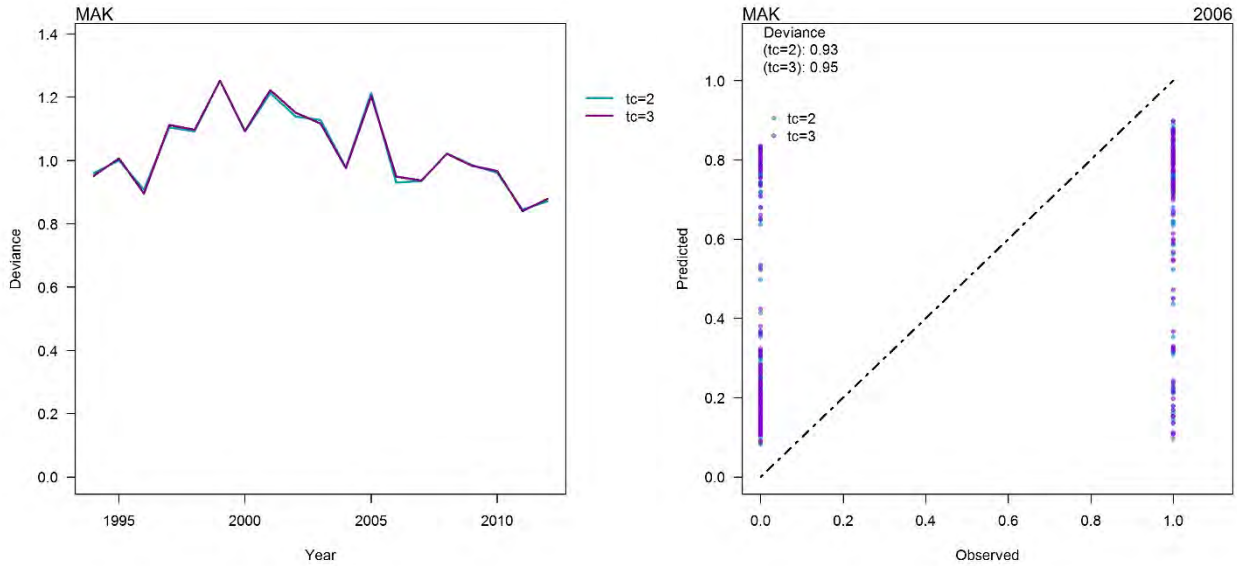


Figure 76: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2006 Binomial model (right) for species MAK.

Predictive ability

Poisson

The numbers caught were very small (usually less than 10 per year), but the predictive ability was generally fair and sometimes quite good (Figure 77) (e.g. the 1997 model, Figure 78). Generally the numbers were underestimated rather than overestimated, such as the 1999 model (Figure 79).

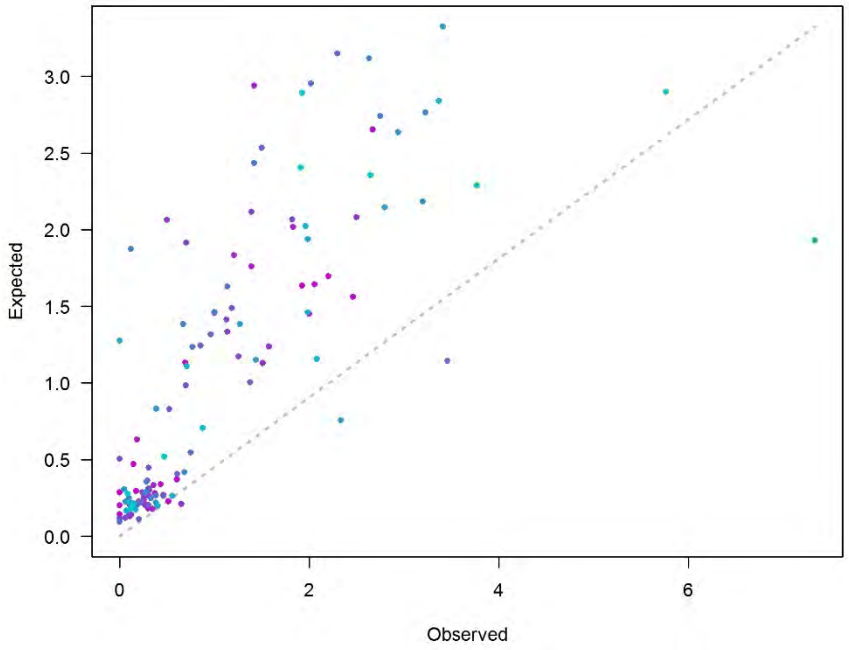


Figure 77: Observed and predicted counts of MAK for each year/subarea bin.

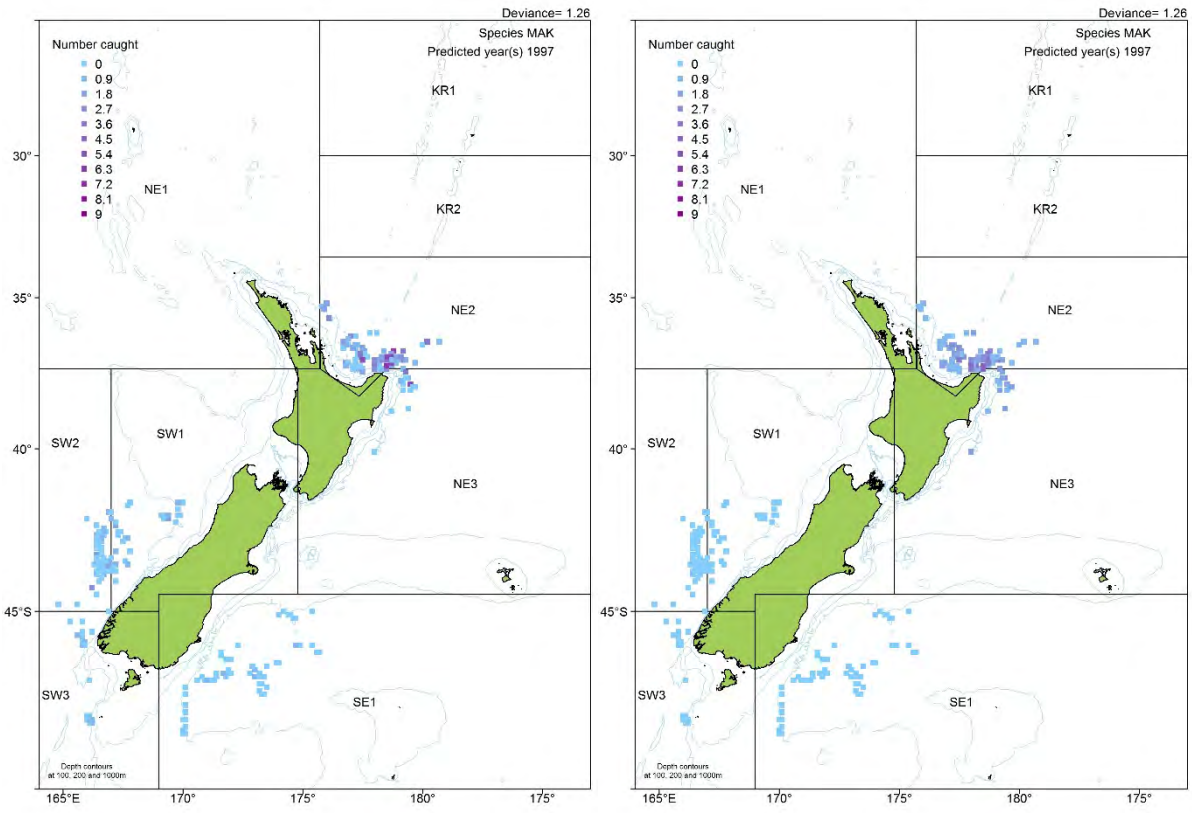


Figure 78: 1997 Poisson model observed (left) and predicted (right) numbers of MAK caught.

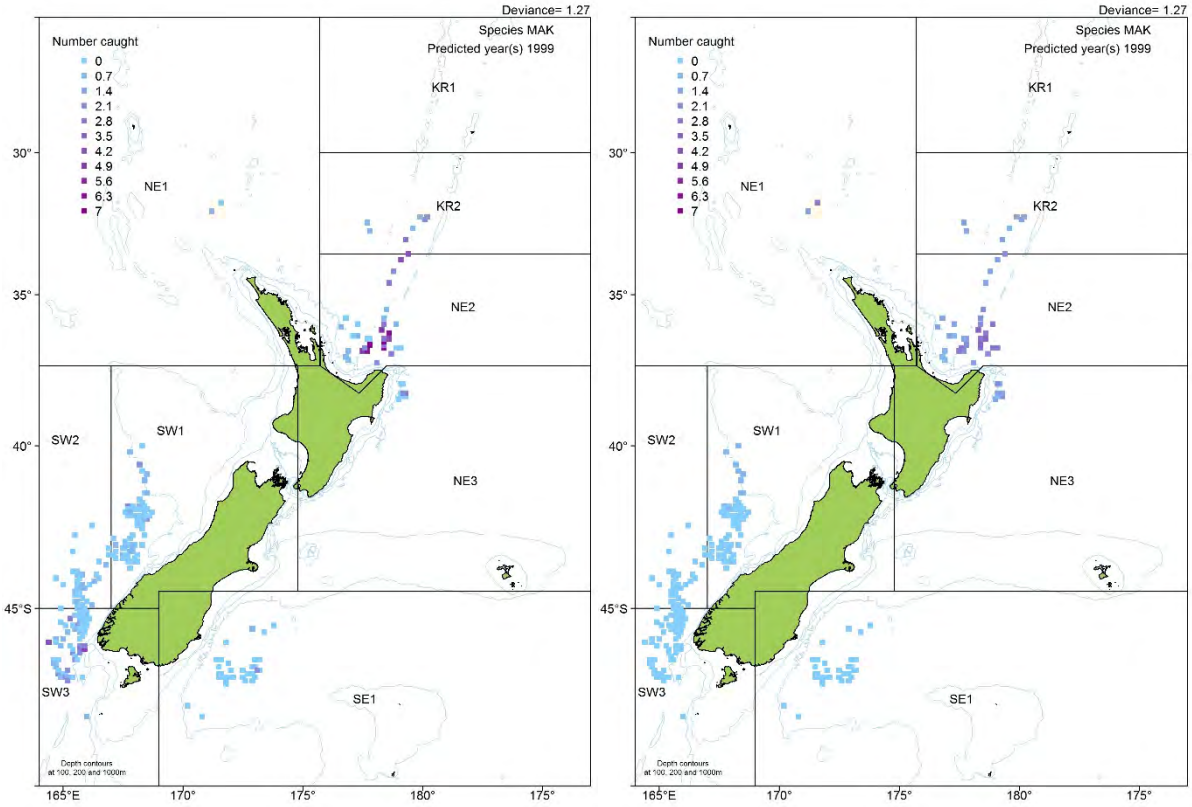


Figure 79: 1999 Poisson model observed (left) and predicted (right) numbers of MAK caught.

Binomial

Predictive ability was generally fair (Figure 80). Where there were often presences and absences quite close together in the observations, the model often predicted all points to be around 50% likely, rather than being able to specify to as fine a detail as the observations (e.g. 2007 model, Figure 82). Some of the models had difficulty predicting subareas KR1 and KR2, such as the 2006 model which underestimated the probability of presences in KR1 and KR2 (Figure 81), and the 2008 model which overestimated the probability of presences in KR2 (Figure 83). The 2007 model fairly correctly predicted the probability of presences in subarea KR2 (Figure 82).

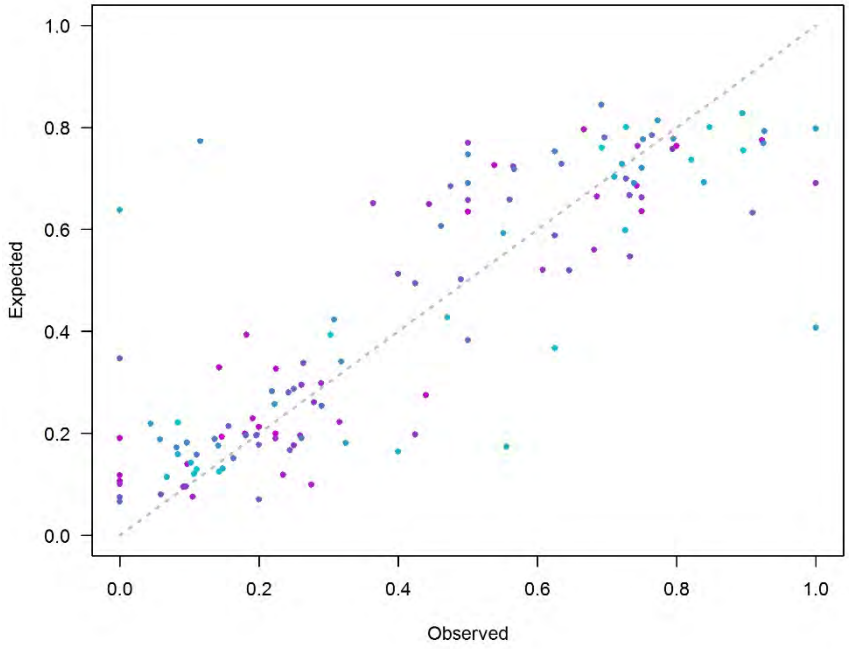


Figure 80: Observed and predicted probability of the presence of MAK for each year/subarea bin.

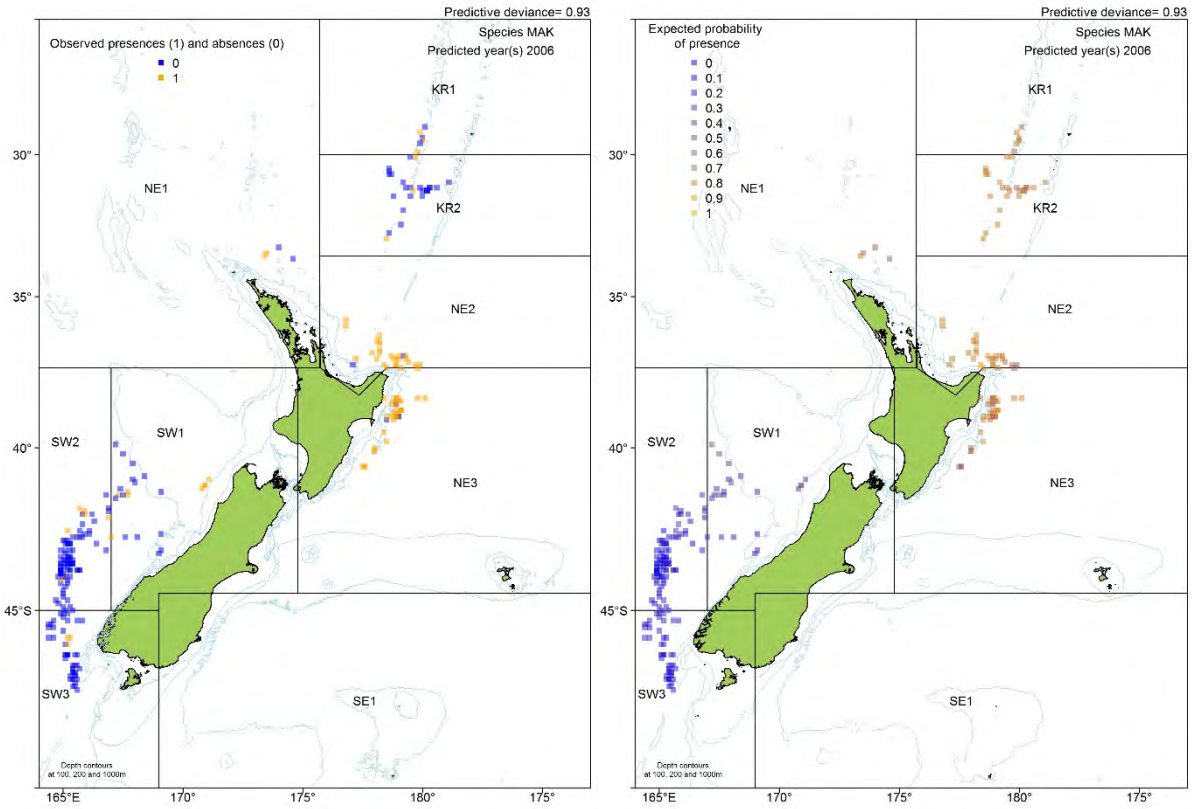


Figure 81: 2006 Binomial model observed (left) and predicted (right) presence/absence of MAK in the catch.

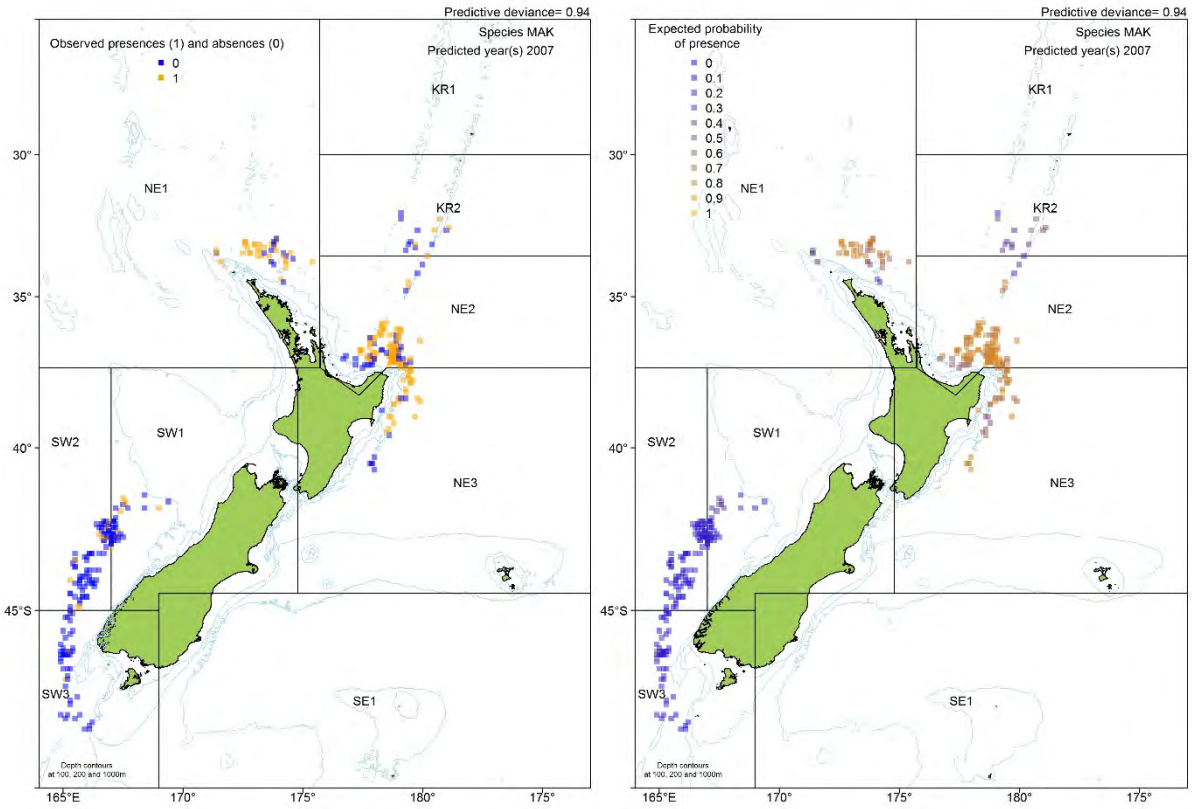


Figure 82: 2007 Binomial model observed (left) and predicted (right) presence/absence of MAK in the catch.

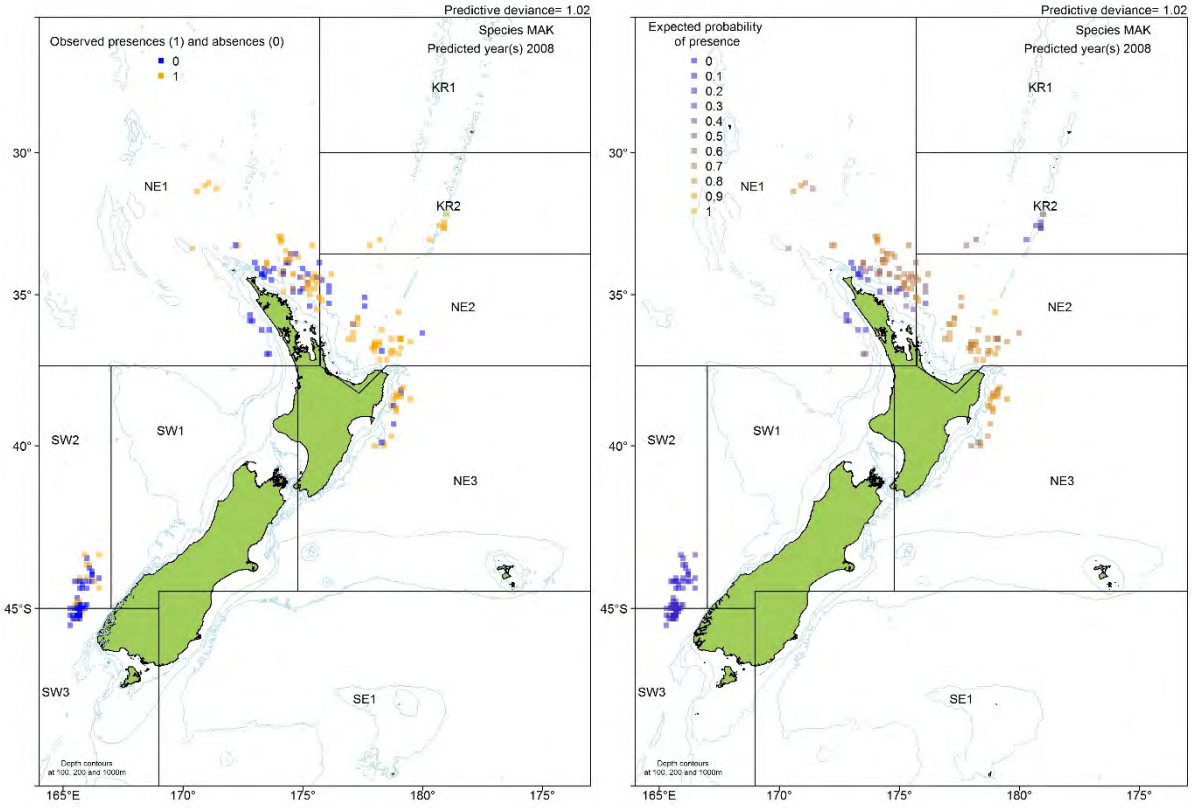


Figure 83: 2008 Binomial model observed (left) and predicted (right) presence/absence of MAK in the catch.

3.1.8 MOO

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years, with slight increases or decreases in some models (Figure 84). It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all MOO Poisson models.

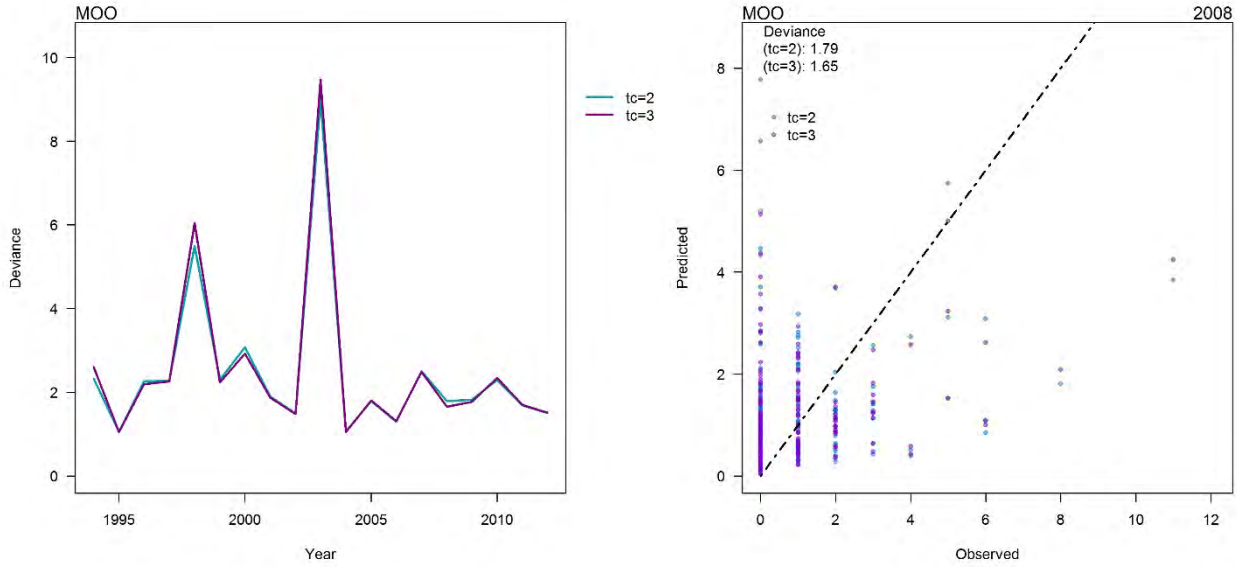


Figure 84: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2010 Poisson model (right) for species MOO.

Binomial

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years, with a very slight decrease in the 2005 model and a slight increase in the 2003 model (Figure 85). It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all MOO Binomial models.

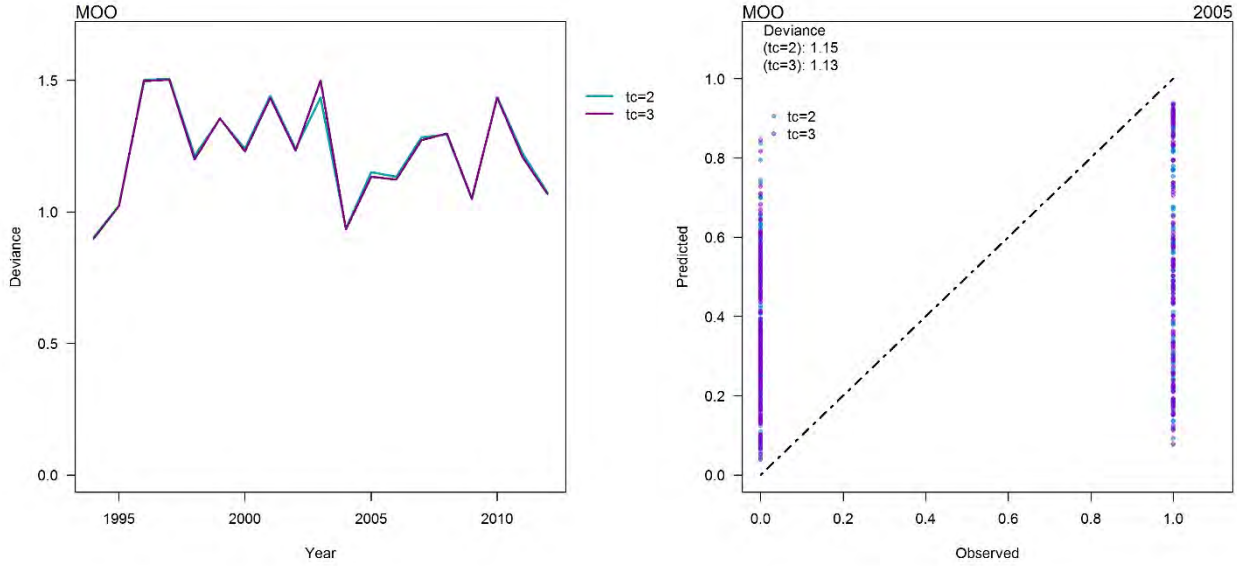


Figure 85: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2010 Poisson model (right) for species MOO.

Predictive ability

Poisson

Predictive ability was generally fair-good (Figure 86), but poor in some models. The 1998 model underestimated numbers caught in subareas NE1 and NE2 (Figure 88). In the 2001 and 1997 models, the numbers caught were underestimated in SW2 and SW3 (Figures 87 and 89). In the 2003 model, the numbers caught were overestimated in subarea NE3 (Figure 90).

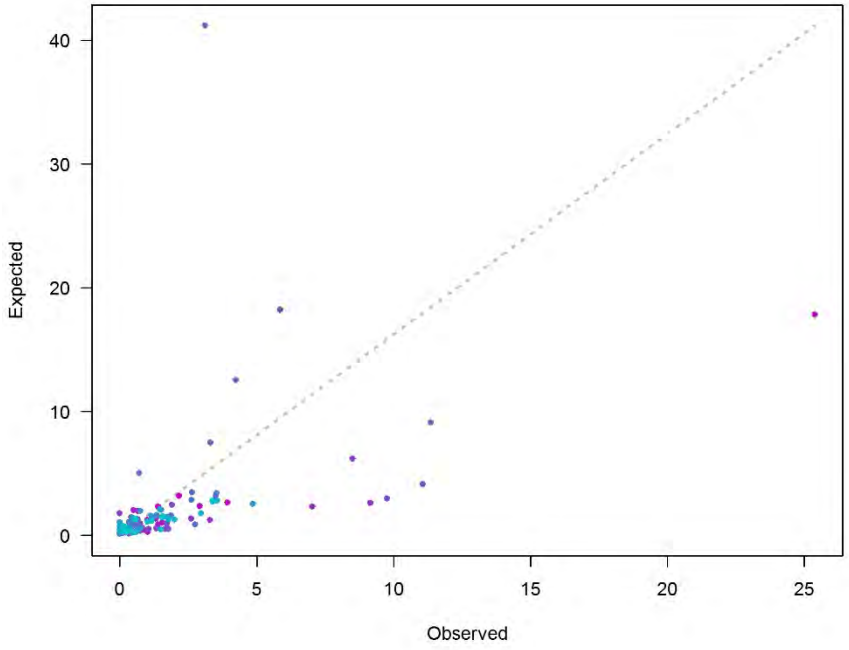


Figure 86: Observed and predicted counts of MOO for each year/subarea bin.

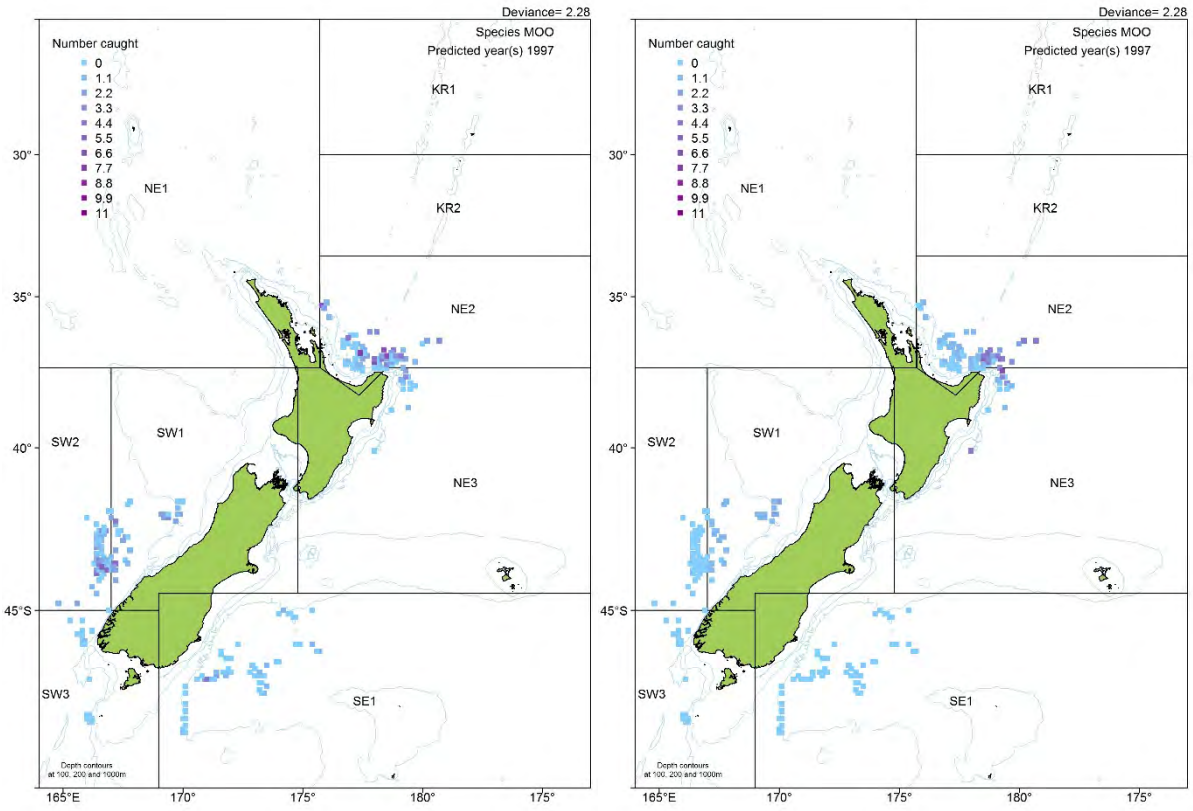


Figure 87: 1997 Poisson model observed (left) and predicted (right) numbers of MOO caught.

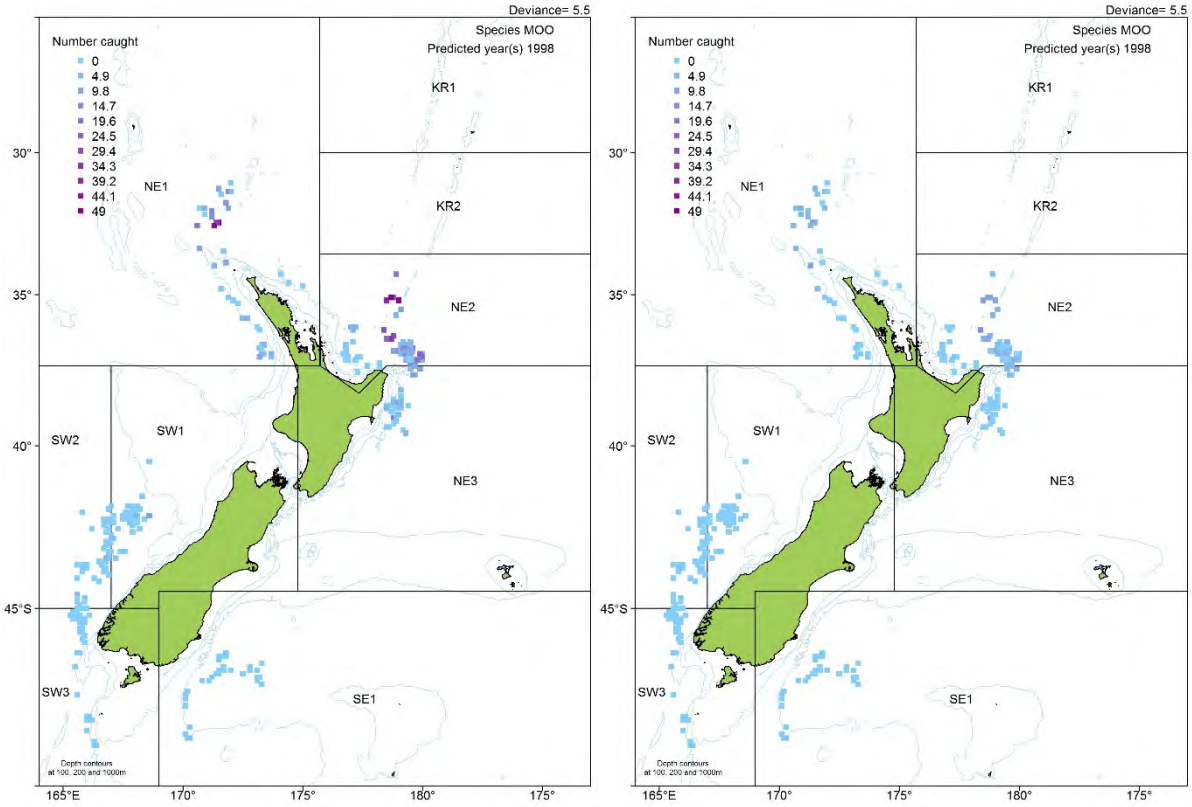


Figure 88: 1998 Poisson model observed (left) and predicted (right) numbers of MOO caught.

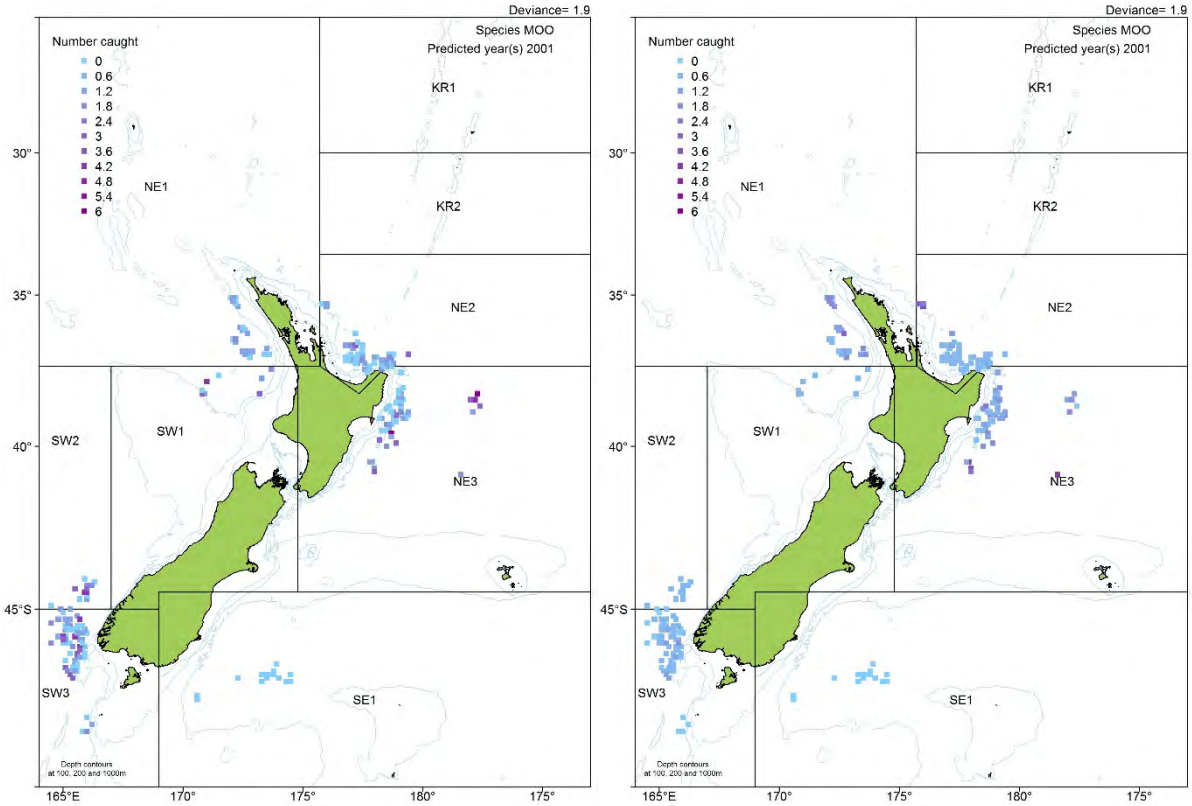


Figure 89: 2001 Poisson model observed (left) and predicted (right) numbers of MOO caught.

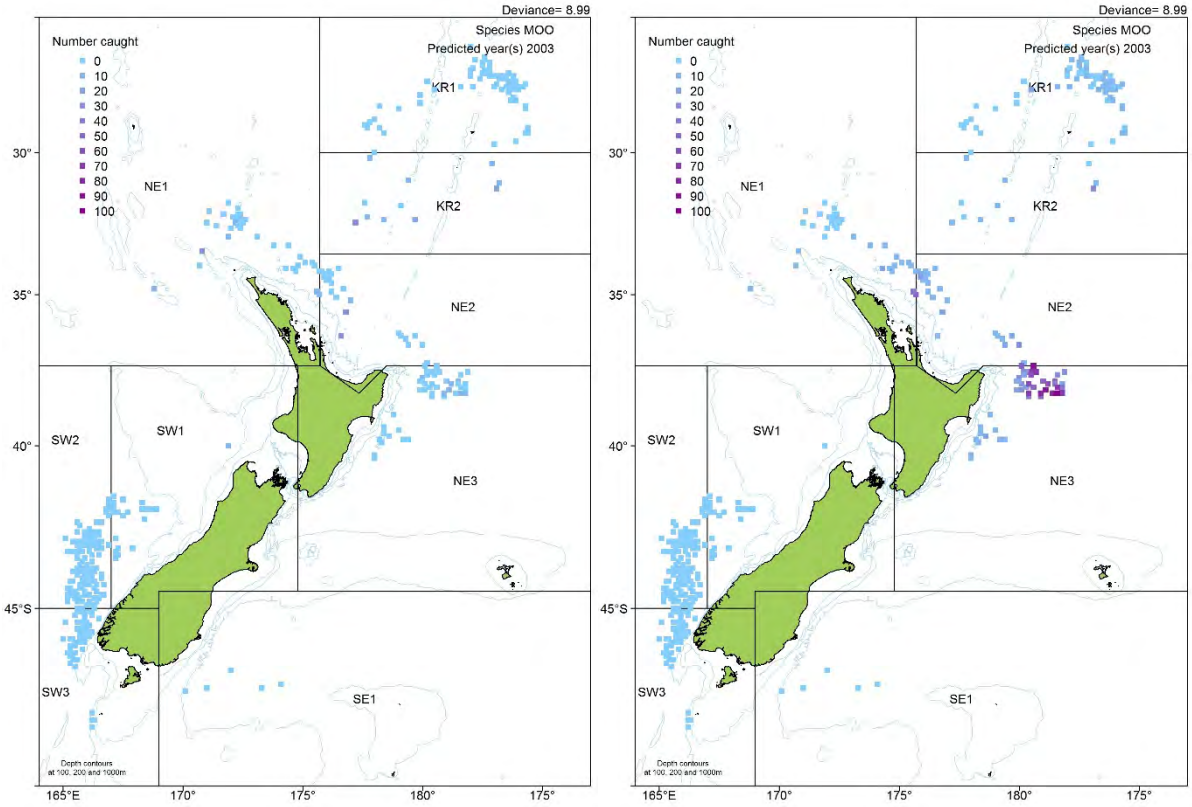


Figure 90: 2003 Poisson model observed (left) and predicted (right) numbers of MOO caught.

Binomial

Predictive ability was generally fair (Figure 91). The 2003 model was an exception, with some absences in the KR1 subarea falsely predicted as hits (Figure 92). The 2009 model was fairly typical in terms of predictive ability for these models (Figure 93).

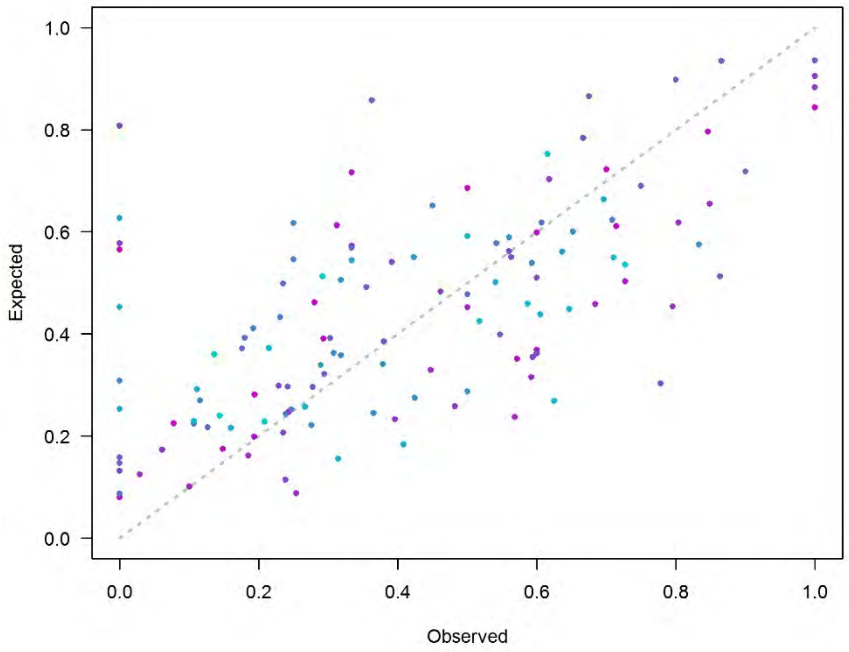


Figure 91: Observed and predicted probability of the presence of MOO for each year/subarea bin.

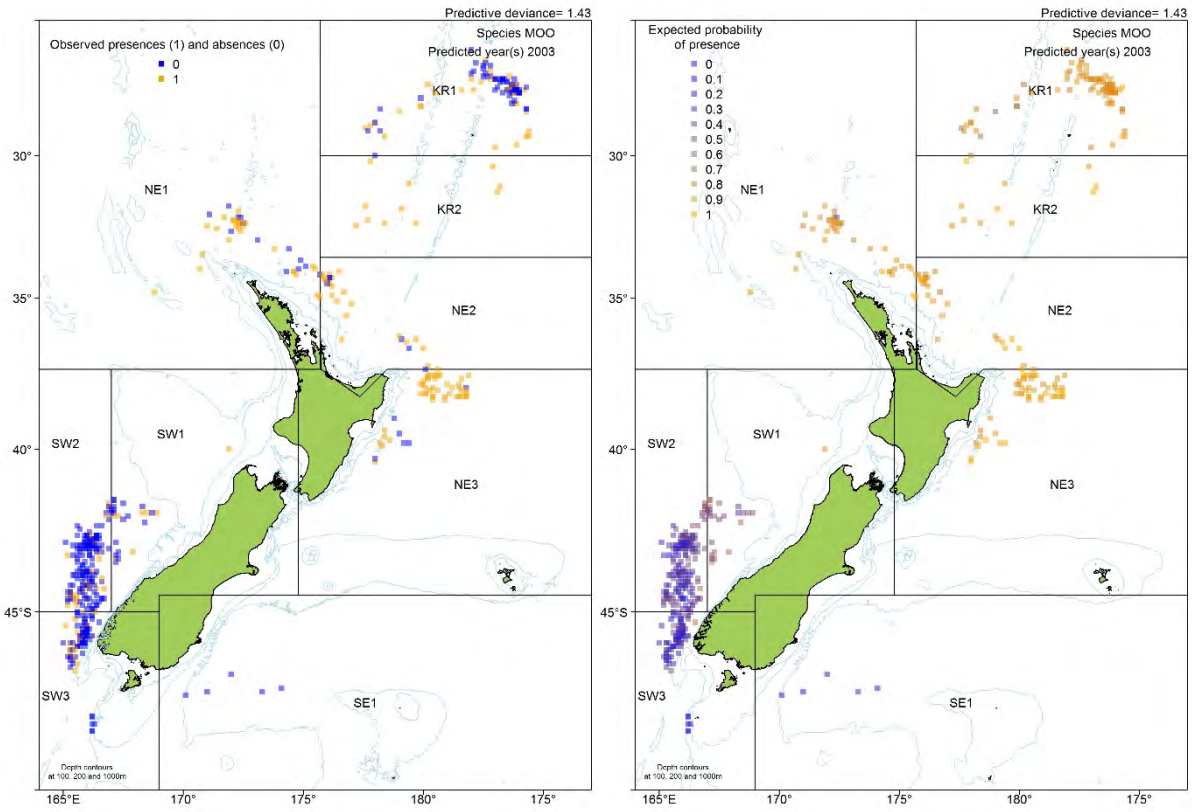


Figure 92: 2003 Poisson model observed (left) and predicted (right) presence/absence of MOO in the catch.

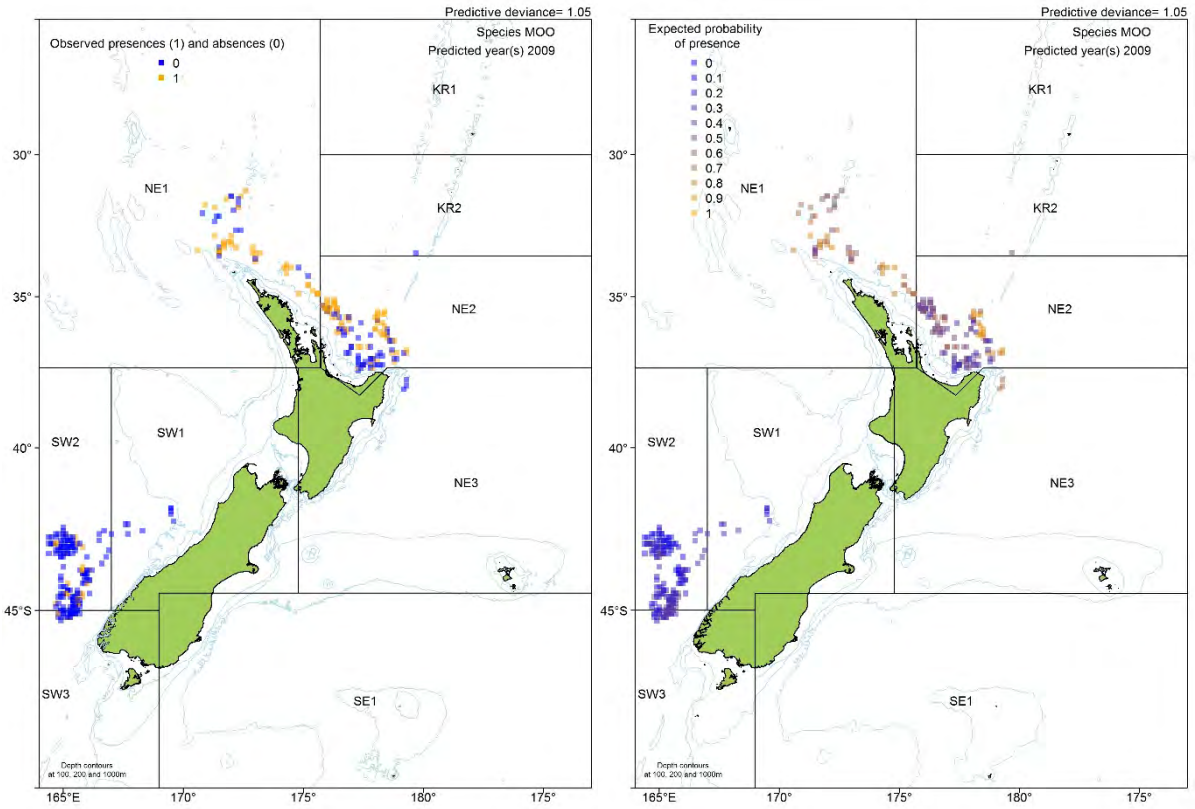


Figure 93: 2009 Poisson model observed (left) and predicted (right) presence/absence of MOO.

3.1.9 POS

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most models, with slight increases or decreases in some models (Figure 94). It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all POS Poisson models.

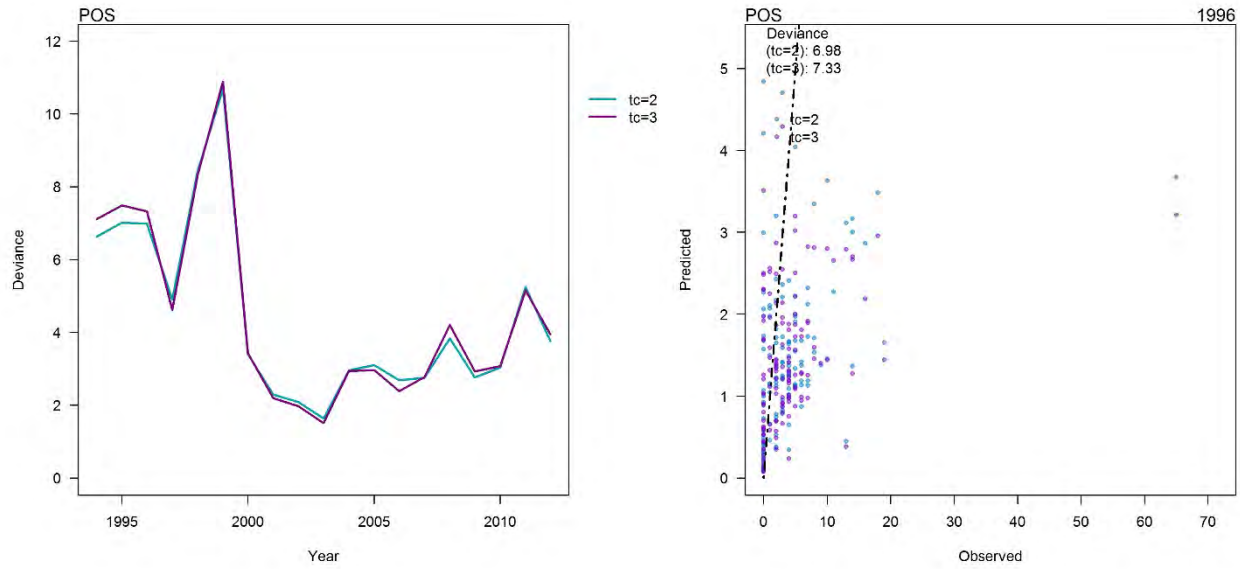


Figure 94: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 1996 Poisson model (right) for species POS.

Binomial

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years and slightly increased the predictive deviance in the 2003 model (Figure 95). It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all POS Binomial models.

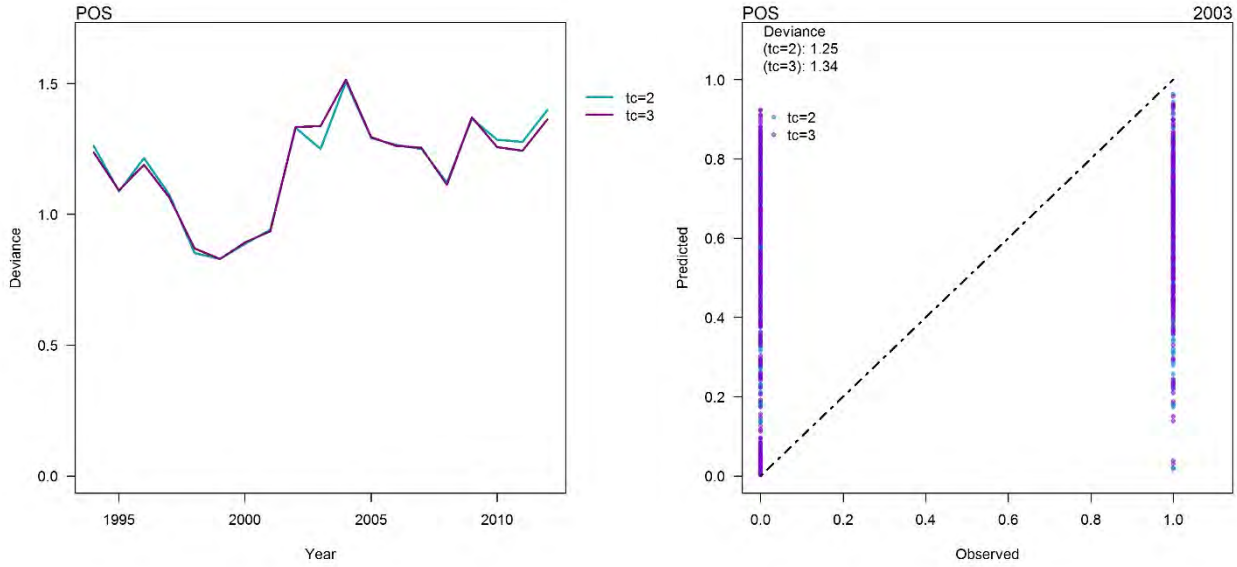


Figure 95: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2003 Poisson model (right) for species POS.

Predictive ability

Poisson

Predictive ability was generally fair (Figure 96), such as the 1997 and 2000 models (Figures 99 and 100). There were some models that were poorly predicted; the 1994 and 1995 models underestimated the numbers caught in subarea NE2 (Figures 97 and 98), and the 2002 model overestimated the numbers caught in subareas NE3 and SE1 (Figure 101).

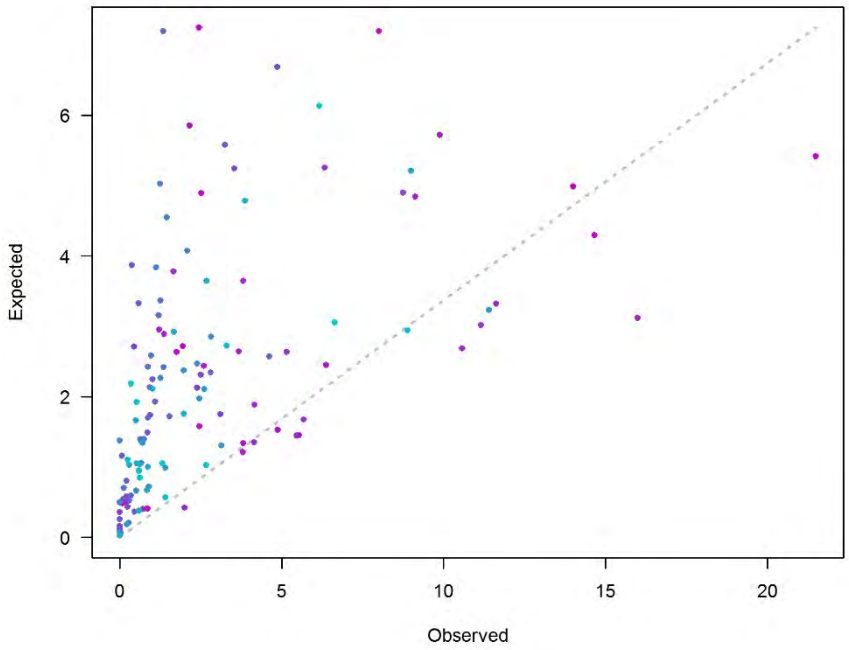


Figure 96: Observed and predicted counts of POS for each year/subarea bin.

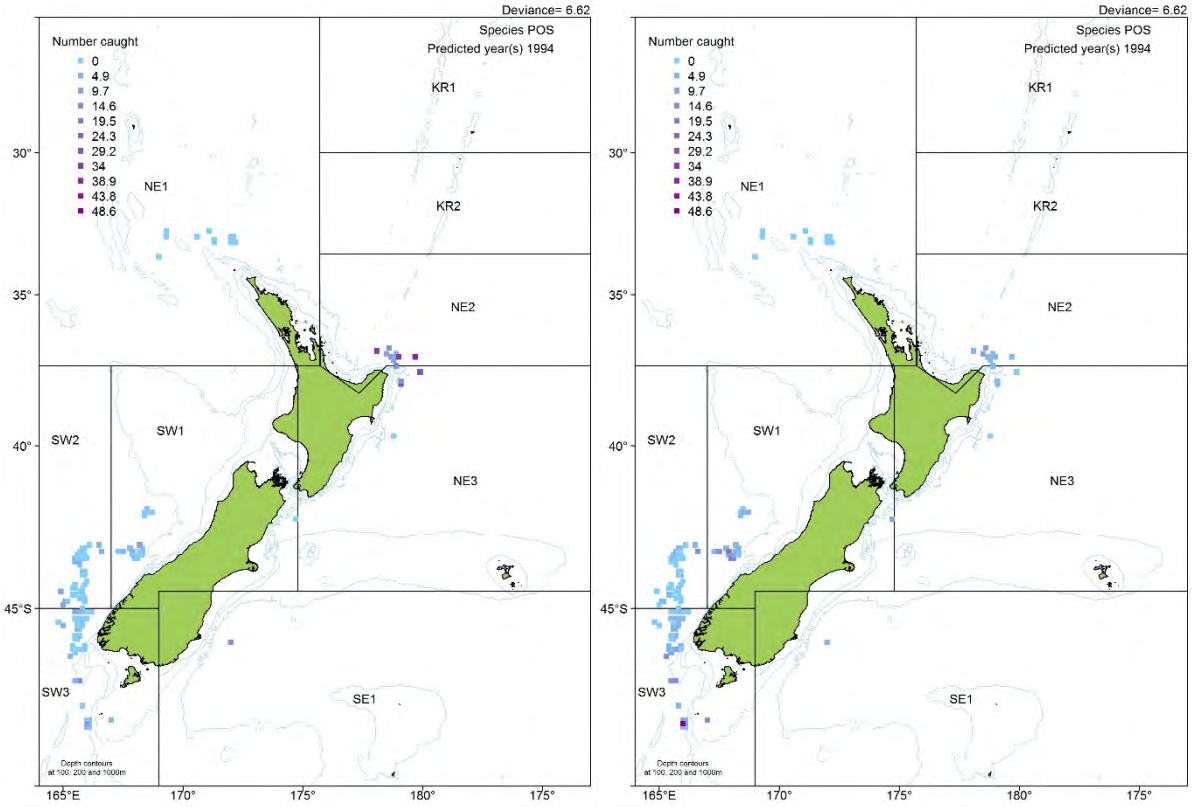


Figure 97: 1994 Poisson model observed (left) and predicted (right) numbers of POS caught.

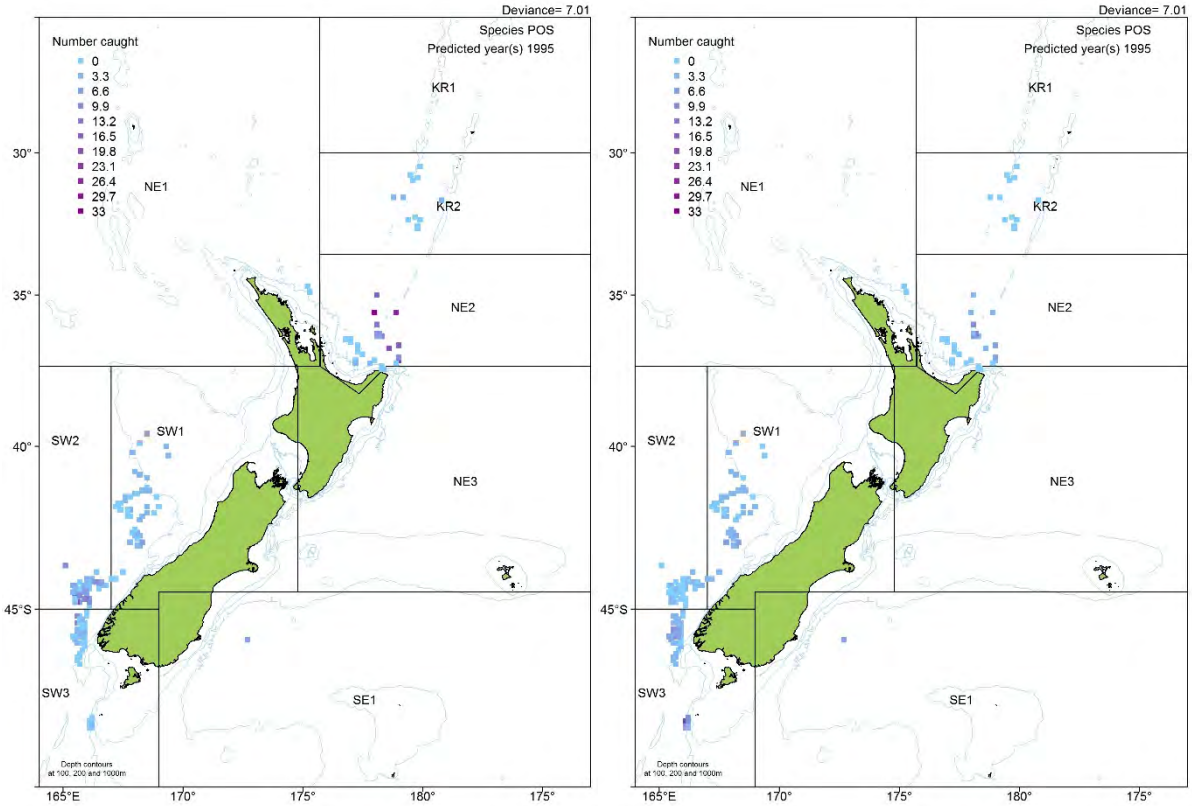


Figure 98: 1995 Poisson model observed (left) and predicted (right) numbers of POS caught.

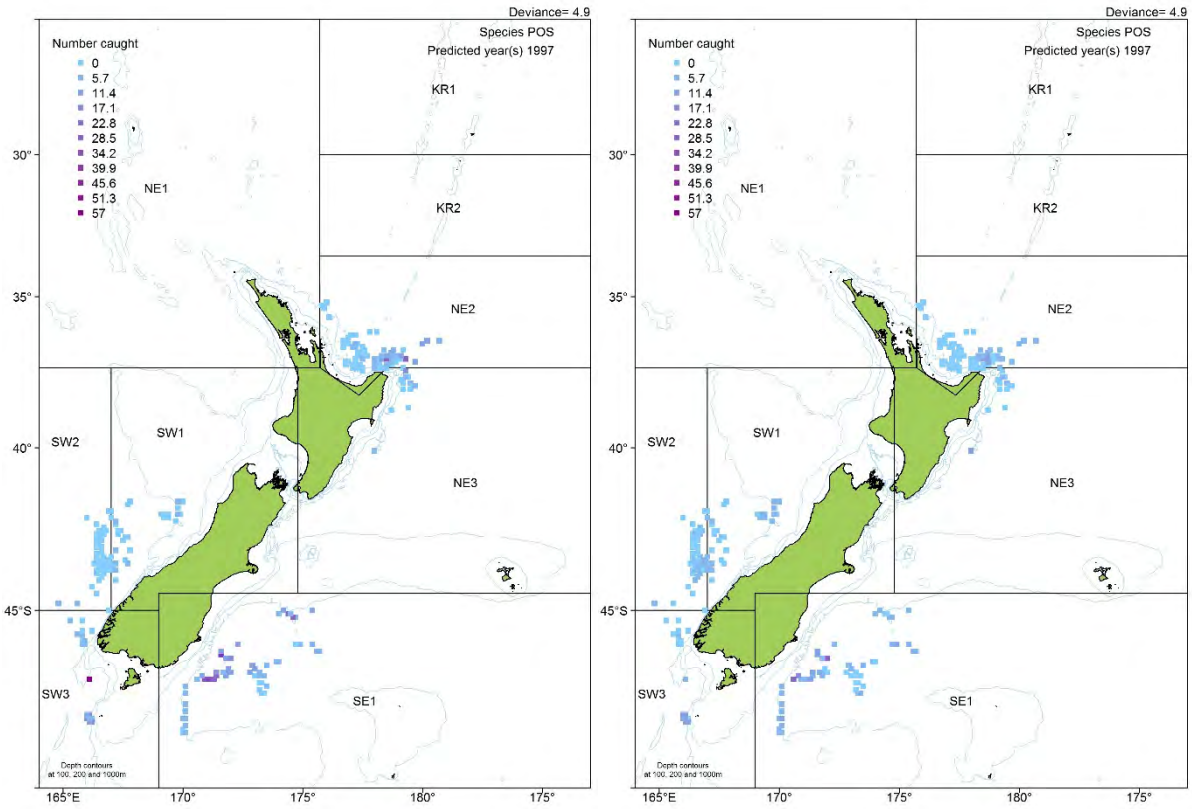


Figure 99: 1997 Poisson model observed (left) and predicted (right) numbers of POS caught.

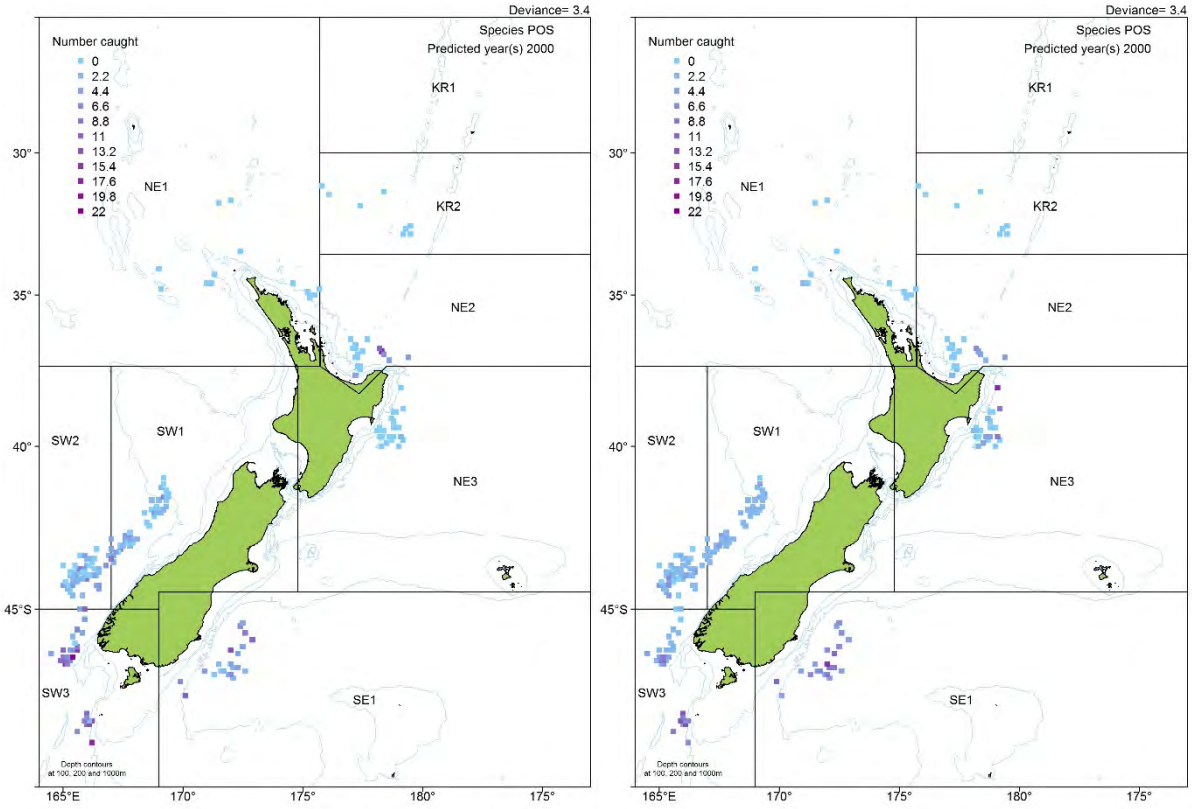


Figure 100: 2000 Poisson model observed (left) and predicted (right) numbers of POS caught.

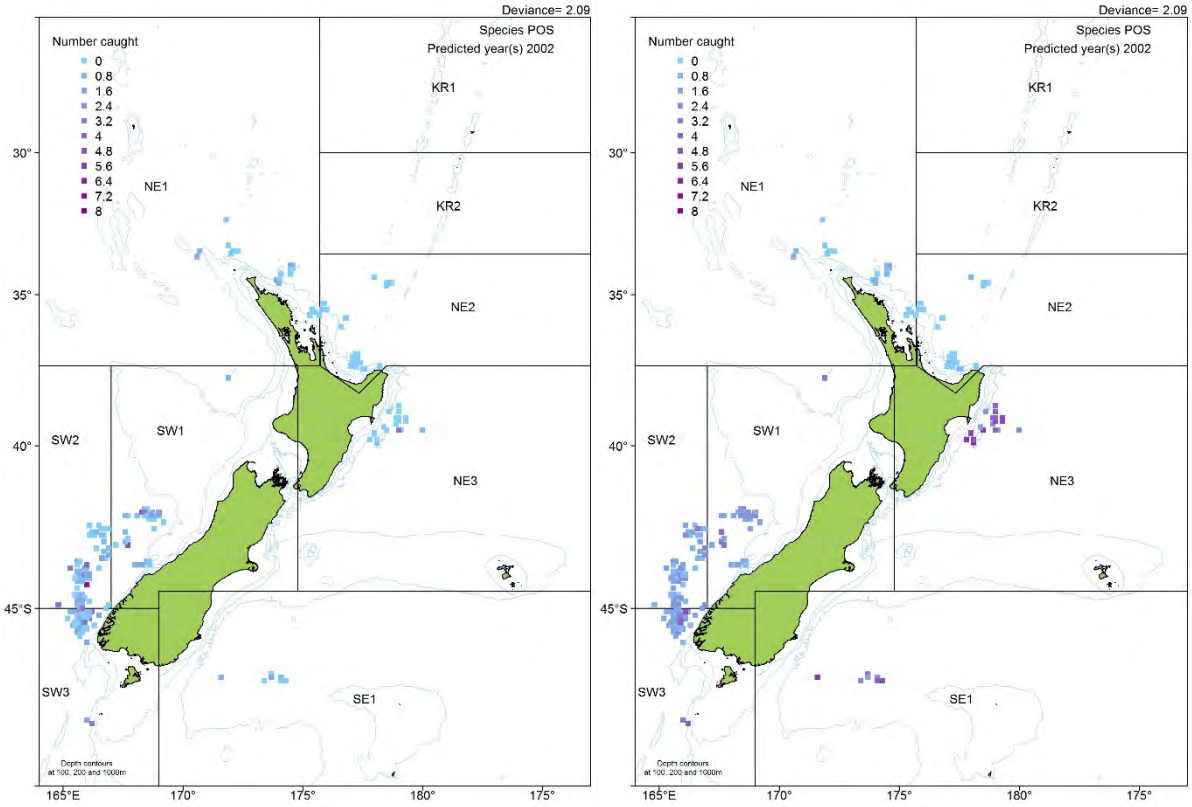


Figure 101: 2002 Poisson model observed (left) and predicted (right) numbers of POS caught.

Binomial

Predictive ability was generally fair (Figure 102), with some exceptions. The 1997, 1998 and 1999 models all wrongly predicted the south-western subareas. The 1997 model overestimated the presences in SW1 and SW, and the 1998 and 1999 models underestimated presences in SW1, SW2 and SW3 (Figures 103, 104 and 105).

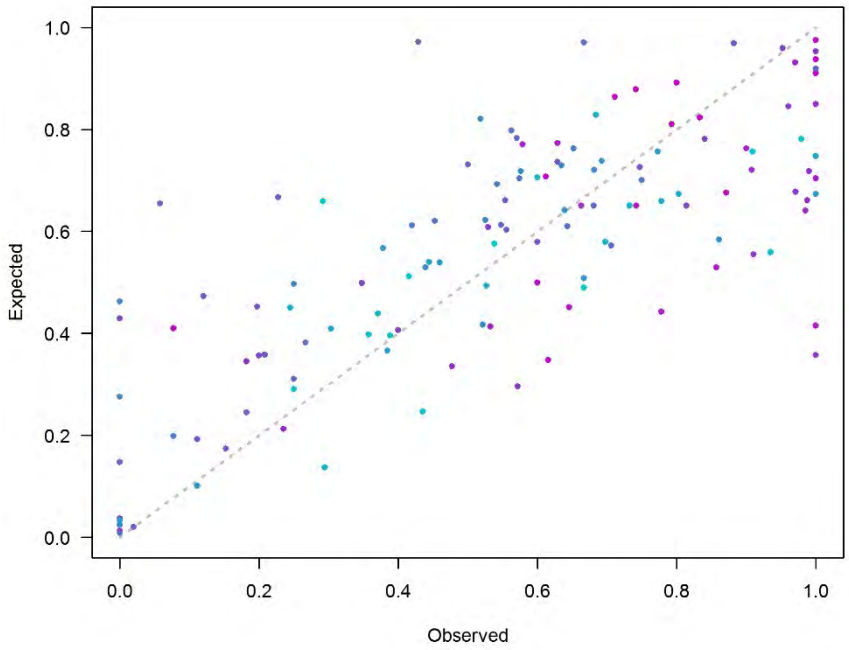


Figure 102: Observed and predicted probability of the presence of POS for each year/subarea bin.

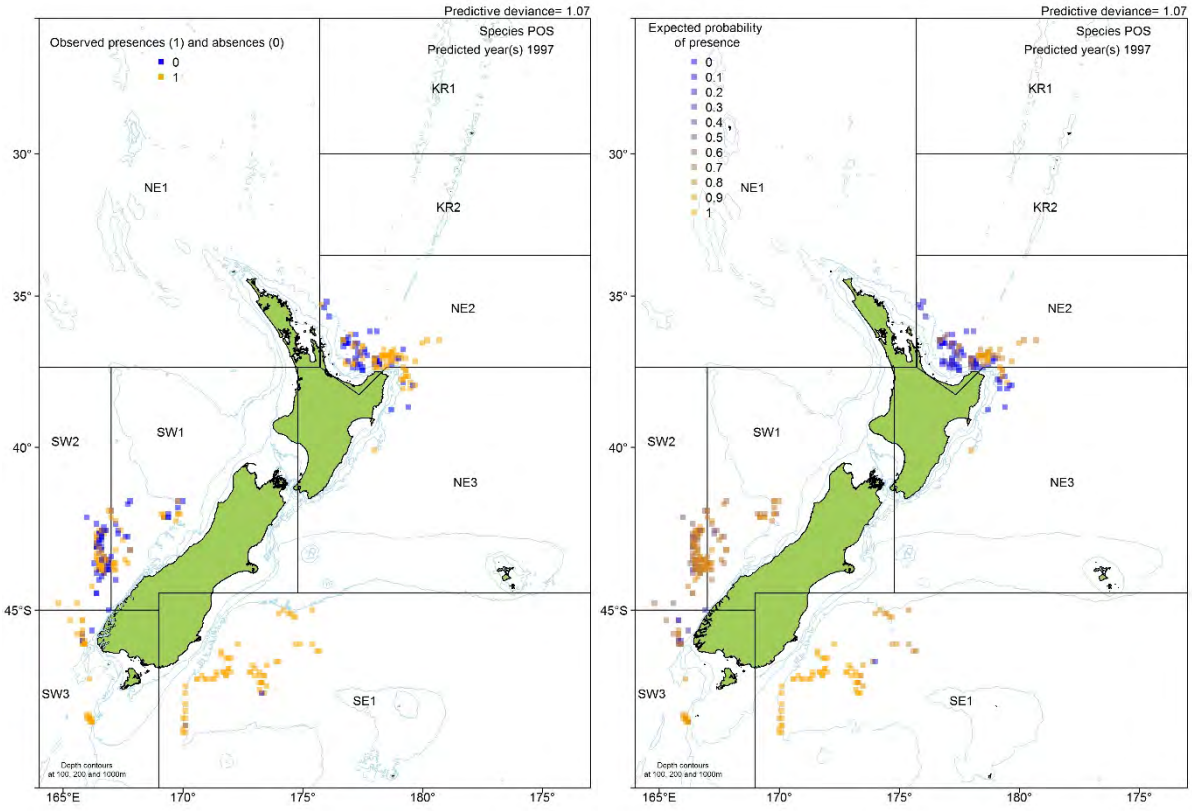


Figure 103: 1997 Binomial model observed (left) and predicted (right) presence/absence of POS.

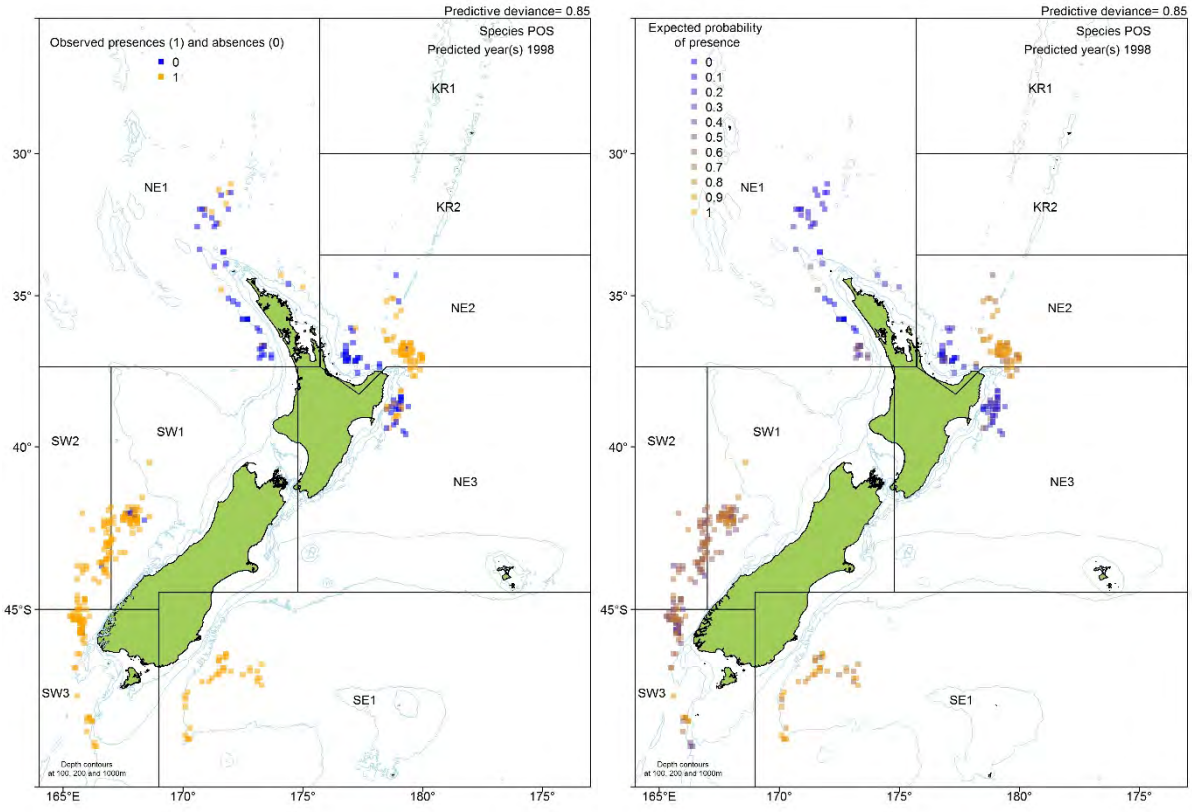


Figure 104: 1998 Binomial model observed (left) and predicted (right) presence/absence of POS in the catch.

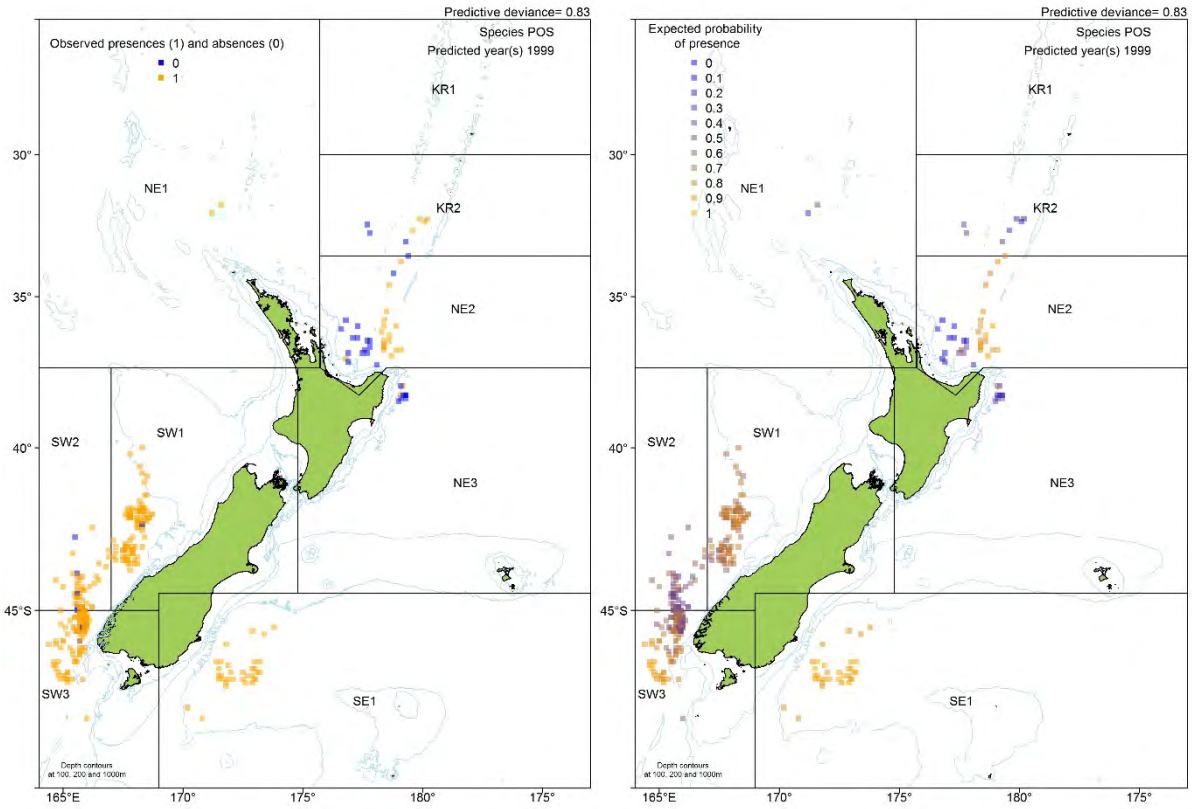


Figure 105: 1999 Binomial model observed (left) and predicted (right) presence/absence of POS in the catch.

3.1.10 RBM

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made a slight increase or decrease to the predictive deviance in some years (Figure 106). It was not likely that increasing the *tc* further would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all RBM Poisson models.

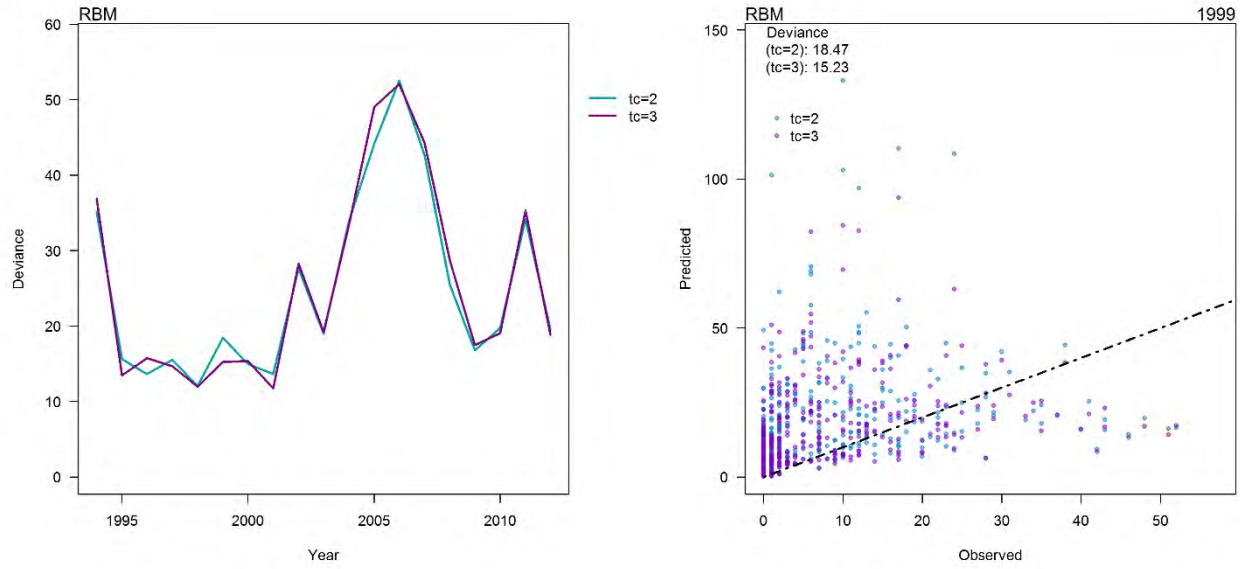


Figure 106: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 1999 Poisson model (right) for species RBM.

Binomial

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years (Figure 107). There was a slight decrease in the 2008 model. It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all RBM Binomial models.

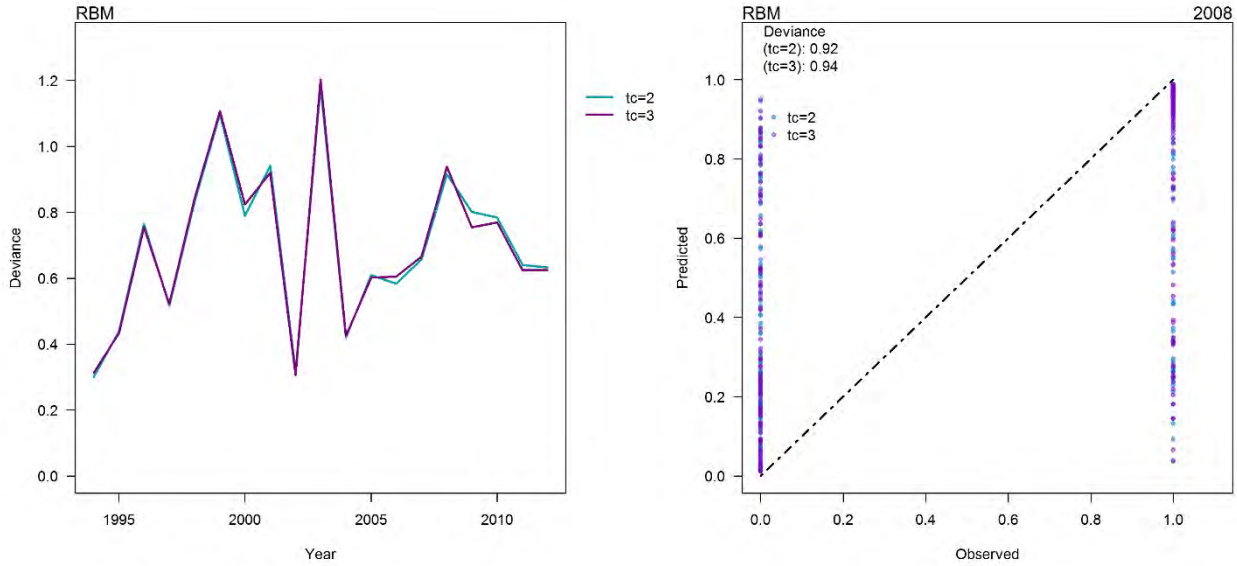


Figure 107: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2008 Binomial model (right) for species RBM.

Predictive ability

Poisson

Predictive ability was generally fair-poor (Figure 108). The poor fits were generally over or underestimated numbers caught in subareas SW2 and SW3. The 2007 model was an example of the numbers caught being underestimated (Figure 110) and the 2001 model was an example of the numbers caught being overestimated (Figure 109).

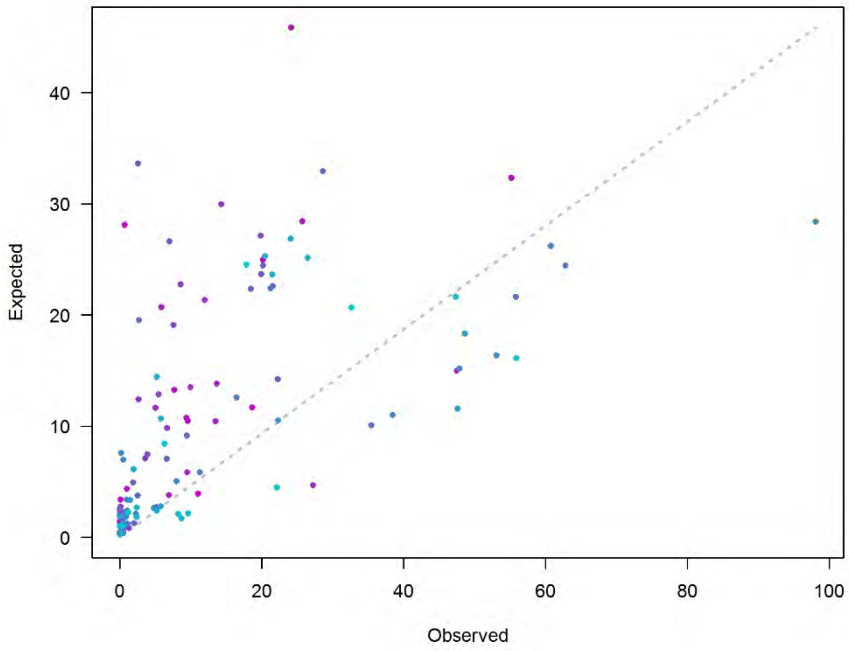


Figure 108: Observed and predicted counts of RBM for each year/subarea bin.

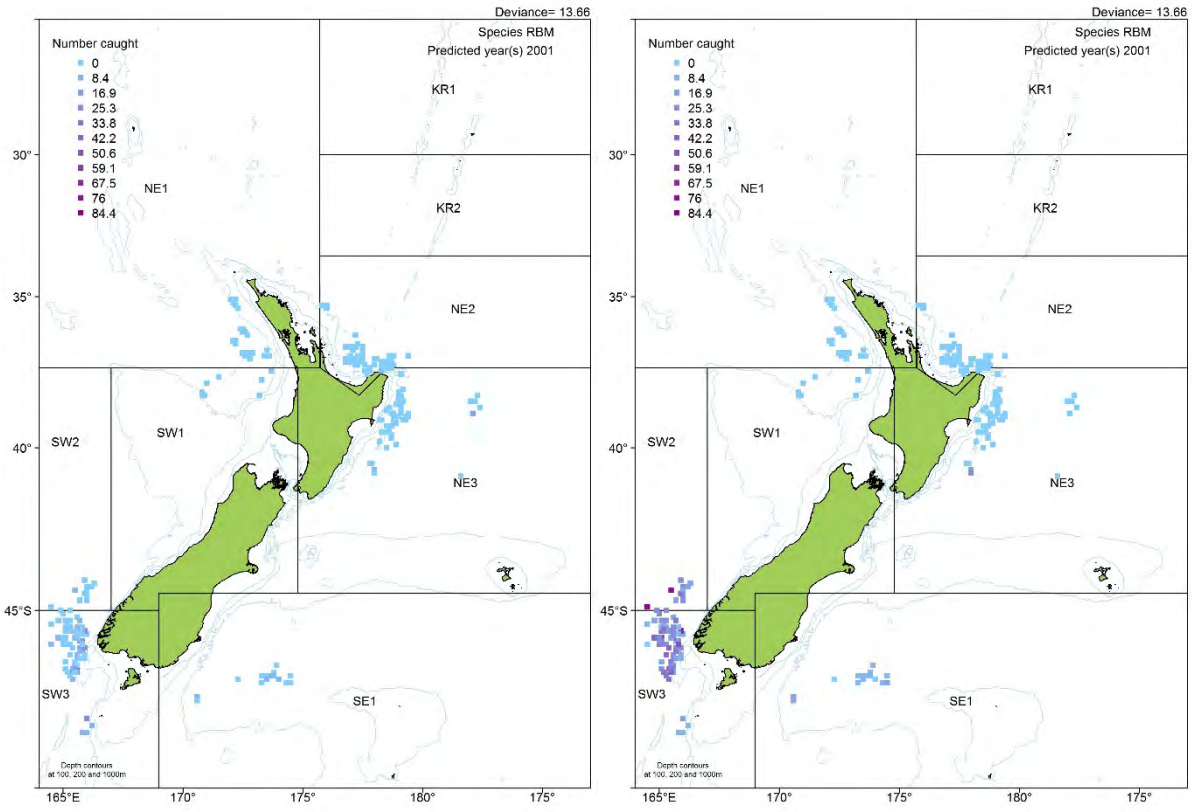


Figure 109: 2001 Poisson model observed (left) and predicted (right) numbers of RBM caught.

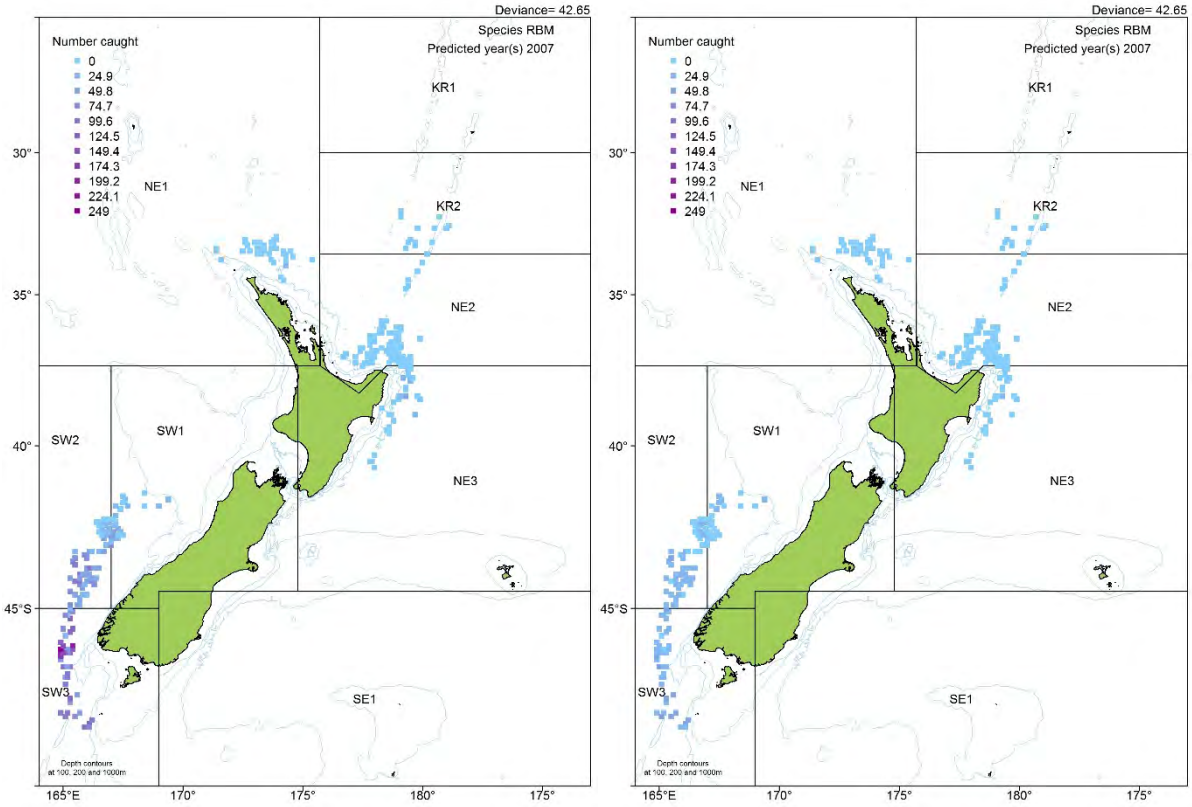


Figure 110: 2007 Poisson model observed (left) and predicted (right) numbers of RBM caught.

Binomial

Predictive ability was generally fair-good (Figure 111). There were a few models (1999, 2000 and 2003) where the probability of a presence is overestimated south of -40° latitude. The 1999 model is the most extreme case of this (Figure 112).

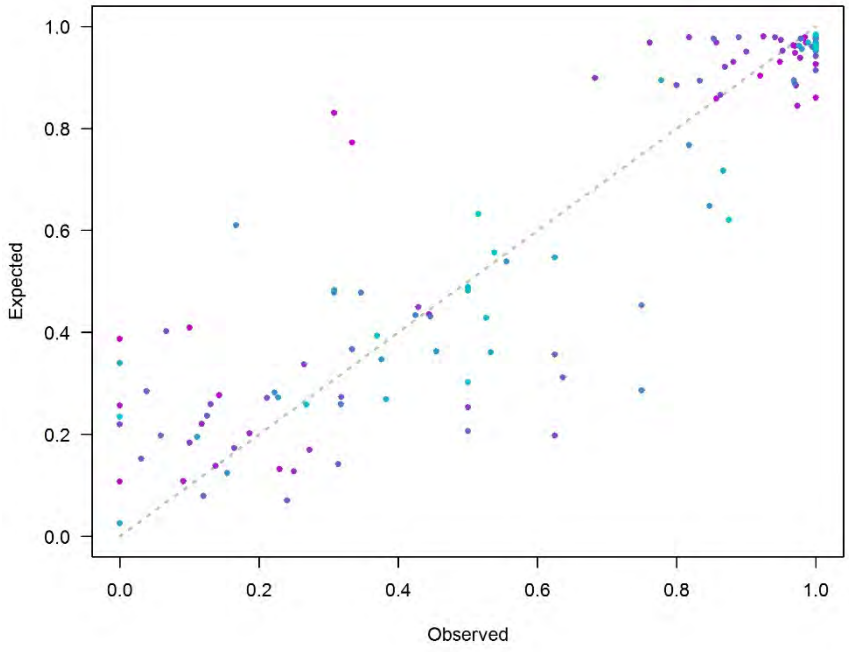


Figure 111: Observed and predicted probability of the presence of RBM for each year/subarea bin.

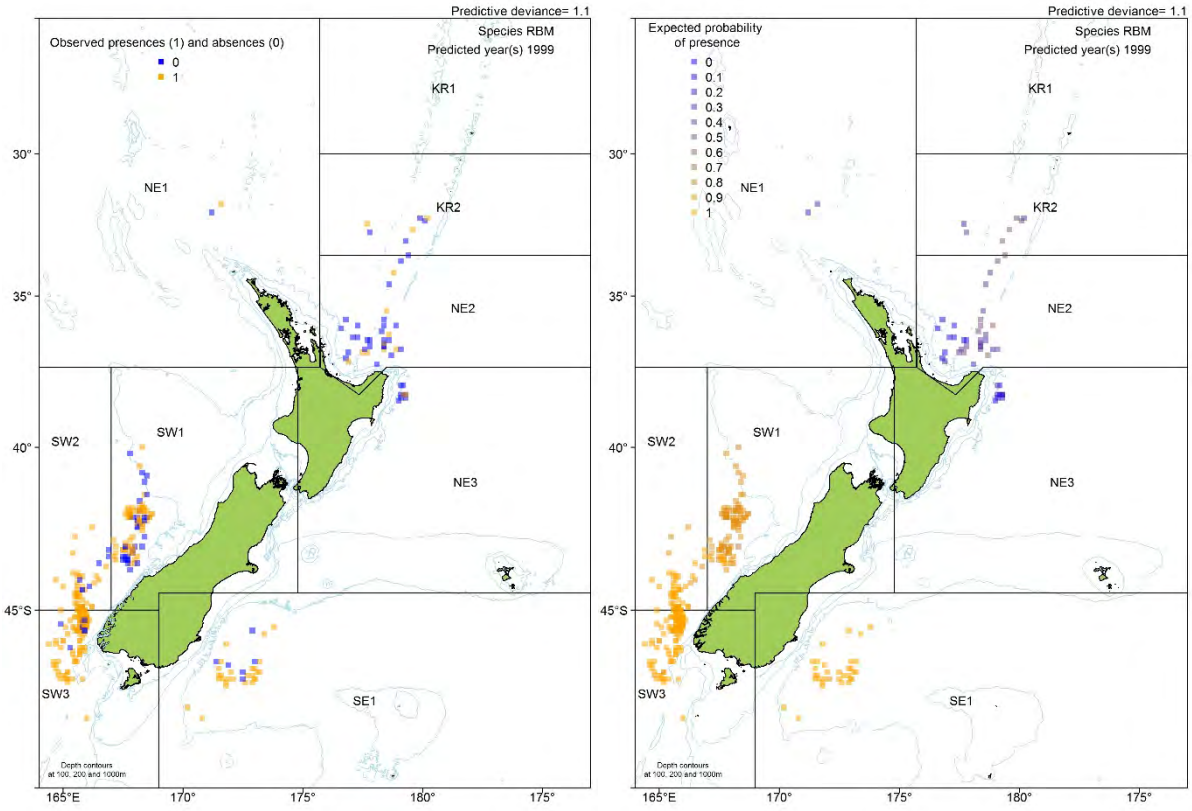


Figure 112: 1999 Binomial model observed (left) and predicted (right) presence/absence of RBM in the catch.

3.1.11 STN

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made very little difference to the predictive deviance (Figure 113). It was not likely that increasing the *tc* further would significantly improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all STN Poisson models.

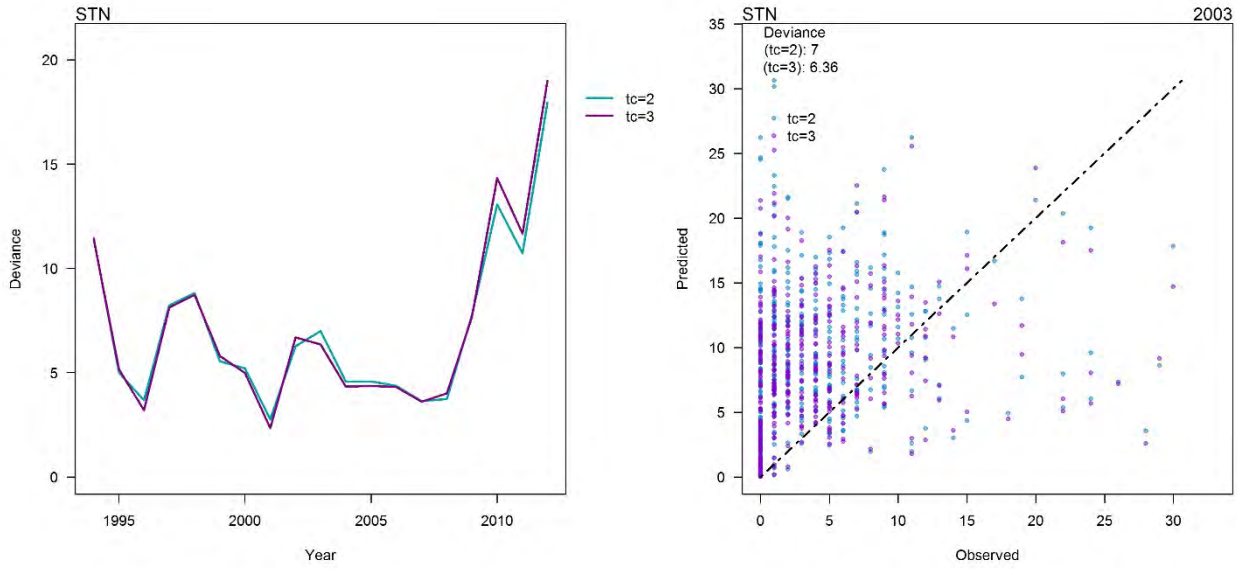


Figure 113: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 1999 Poisson model (right) for species STN.

Binomial

Increasing the *tc* from 2 to 3 made little difference to the predictive deviance in most years (Figure 114). There was a slight increase in the 2007 model. It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all STN Binomial models.

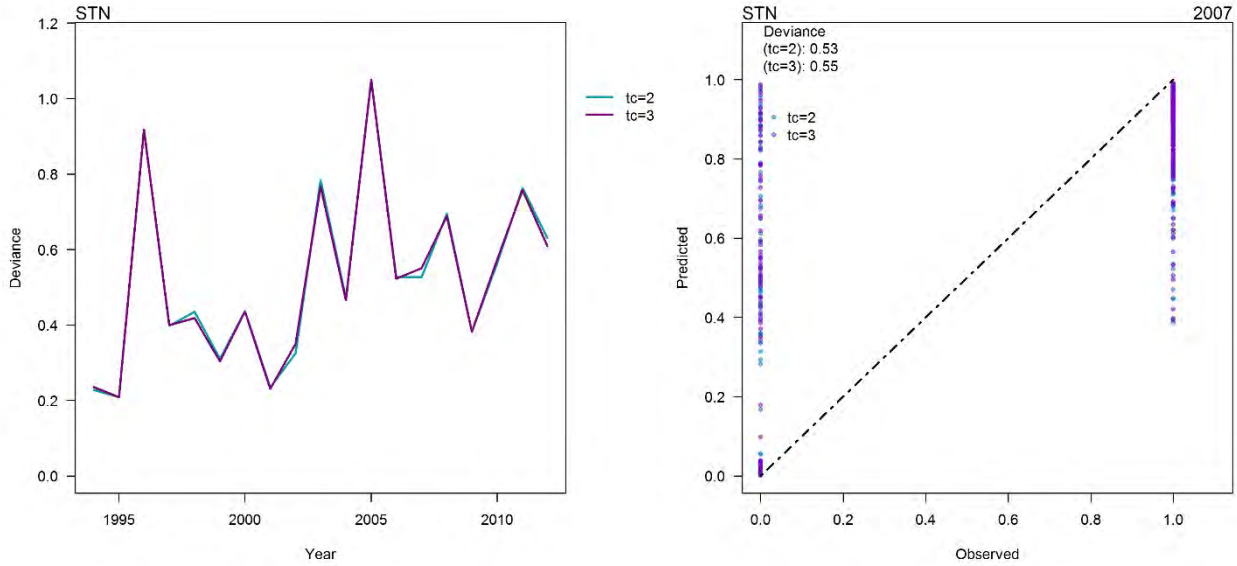


Figure 114: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2007 Binomial model (right) for species STN.

Predictive ability

Poisson

Predictive ability was fair-good in most models (Figure 115). There were several models where the numbers caught were either overestimated (2001, 2003, 2004 and 2005) or underestimated (2009, 2010, 2011 and 2012) in subareas SW1, SW2 or SW3. The 2003 model was the most extreme case of overestimated numbers caught in the SW1 and SW2 subareas (Figure 116) and the 2010 model was the most extreme case of underestimated numbers caught in the SW2 and SW3 subareas (Figure 117). The 2003 model also overestimated numbers caught in subarea NE3.

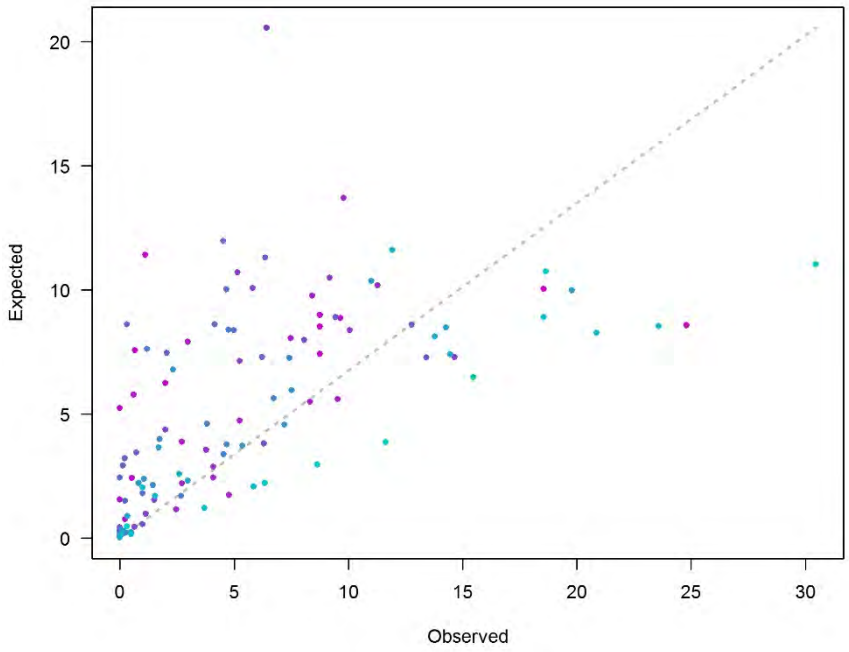


Figure 115: Observed and predicted counts of STN for each year/subarea bin.

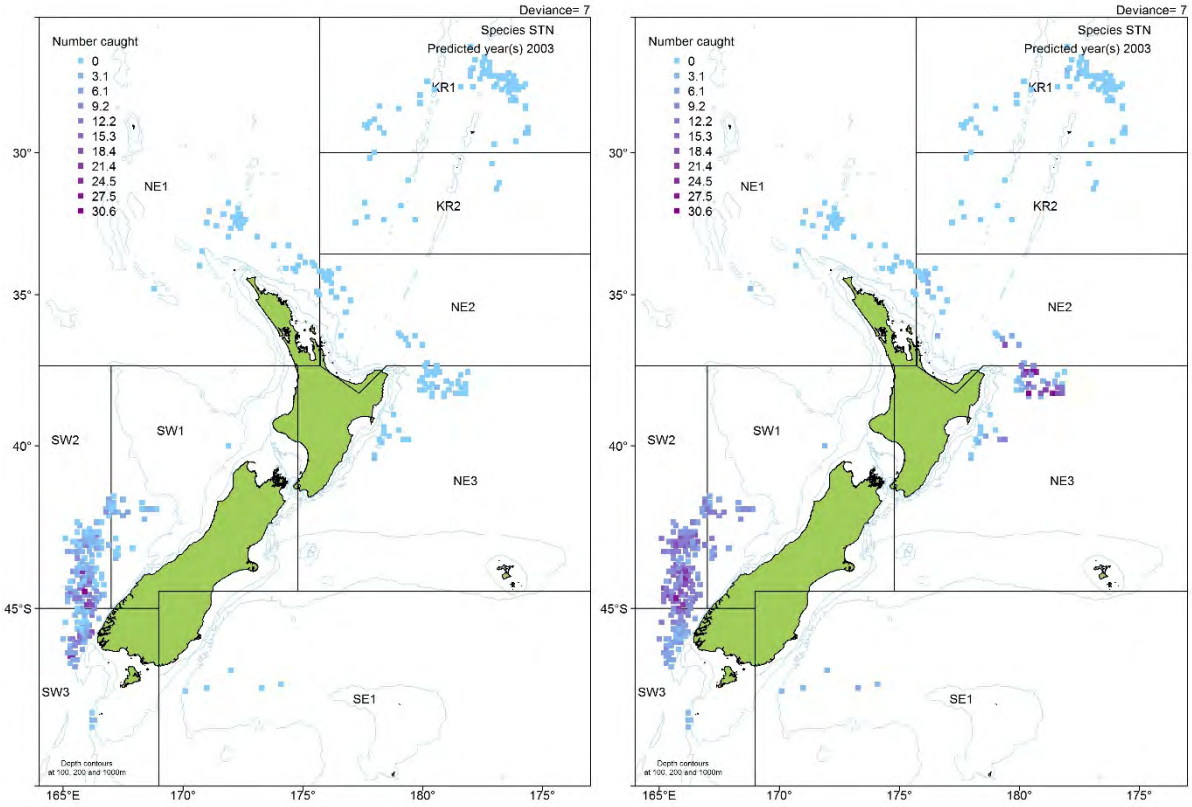


Figure 116: 2003 Poisson model observed (left) and predicted (right) numbers of STN caught.

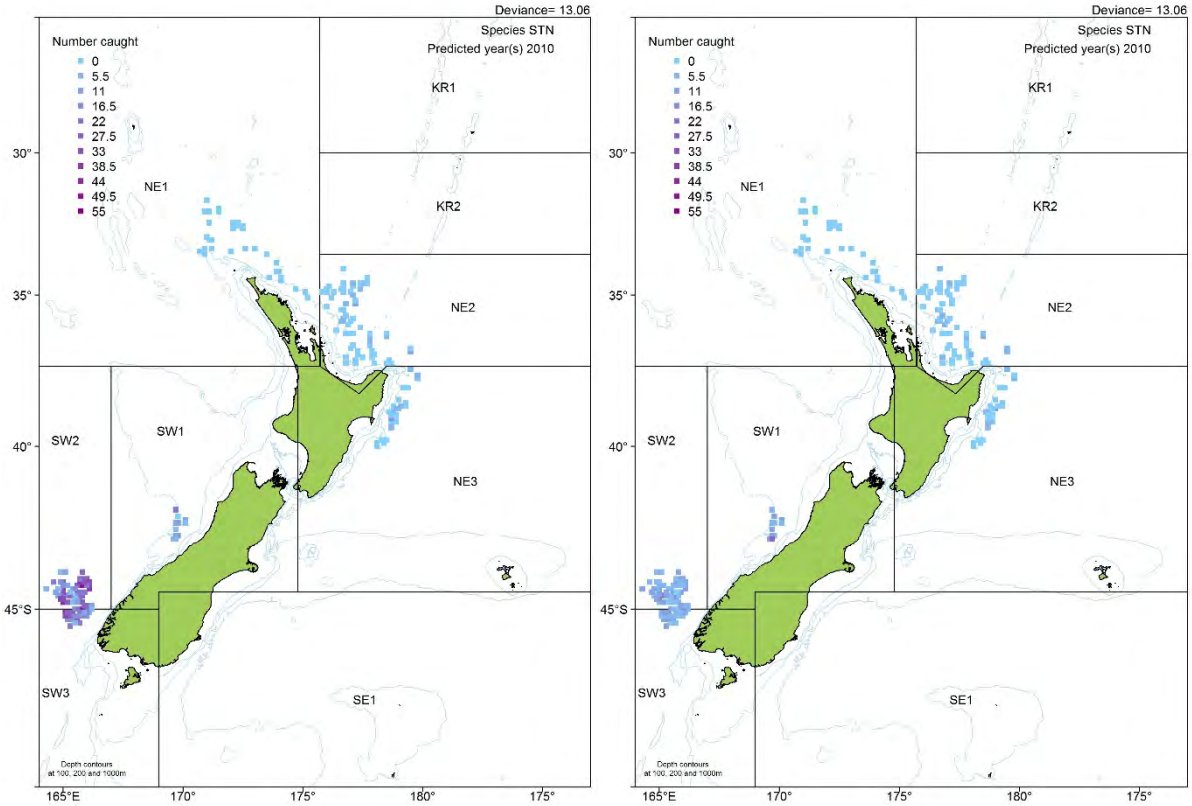


Figure 117: 2010 Poisson model observed (left) and predicted (right) numbers of STN caught.

Binomial

Predictive ability was generally fair-good (Figure 118). A few models failed to predict some observed absences in SW1, SW2, SW3 or SE1 (2003, 2004, 2005 and 2006). The 2003 model was the most extreme example of this (Figure 119).

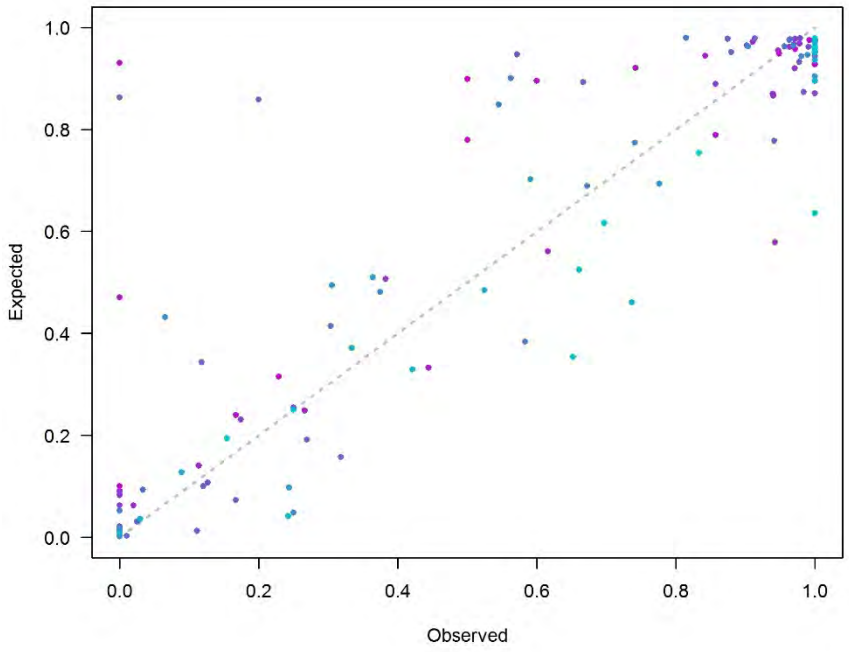


Figure 118: Observed and predicted probability of the presence of STN for each year/subarea bin.

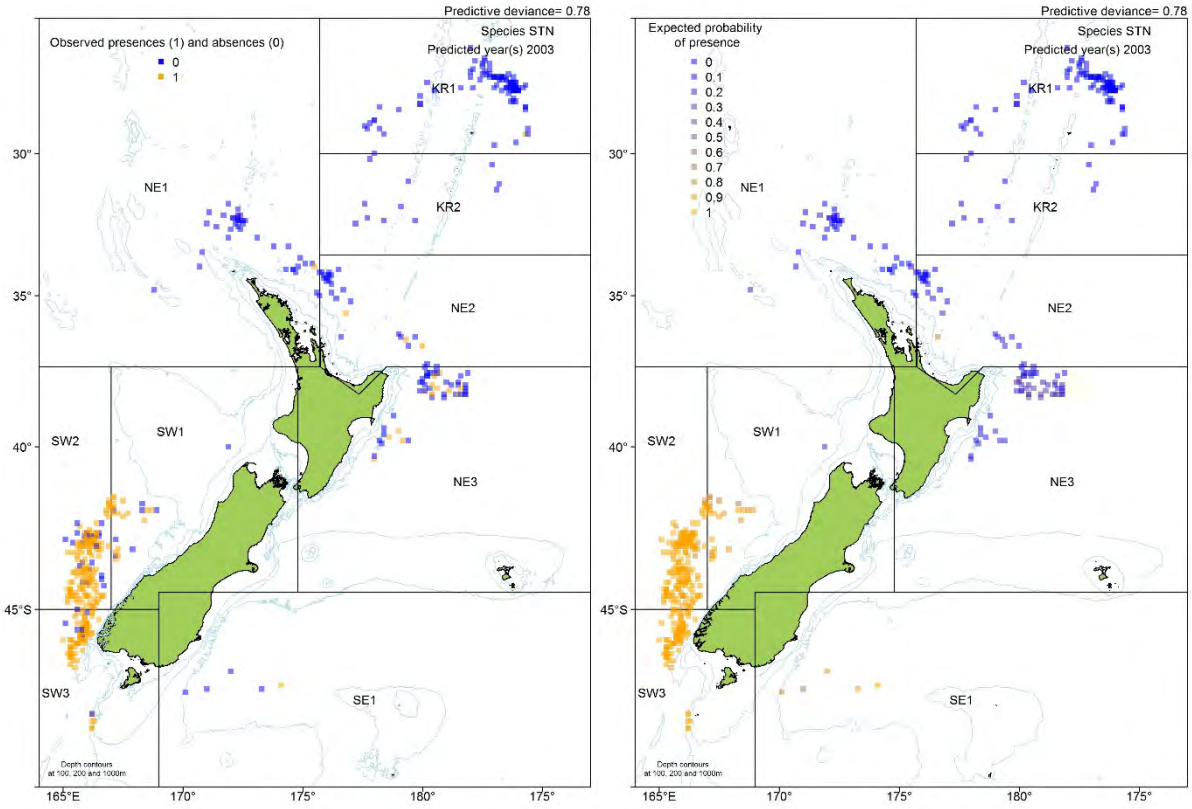


Figure 119: 2003 Binomial model observed (left) and predicted (right) presence/absence of STN in the catch.

3.1.12 SWO

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made very little difference to the predictive deviance in most models, but did increase it slightly in the 1998 and 2007 models and decrease it in the 2003 model (Figure 120). The decrease in predictive deviance in the 2003 model was sufficient such that it seemed appropriate to use *tc*=3 to fit these models (Figure 120). The increase in the 1998 and 2007 models was much less than the decrease in the 2003 model (Figure 121). It was not likely that increasing the *tc* further would significantly improve the predictive ability and *tc*=3 has been used for the remainder of the analyses for all SWO Poisson models.

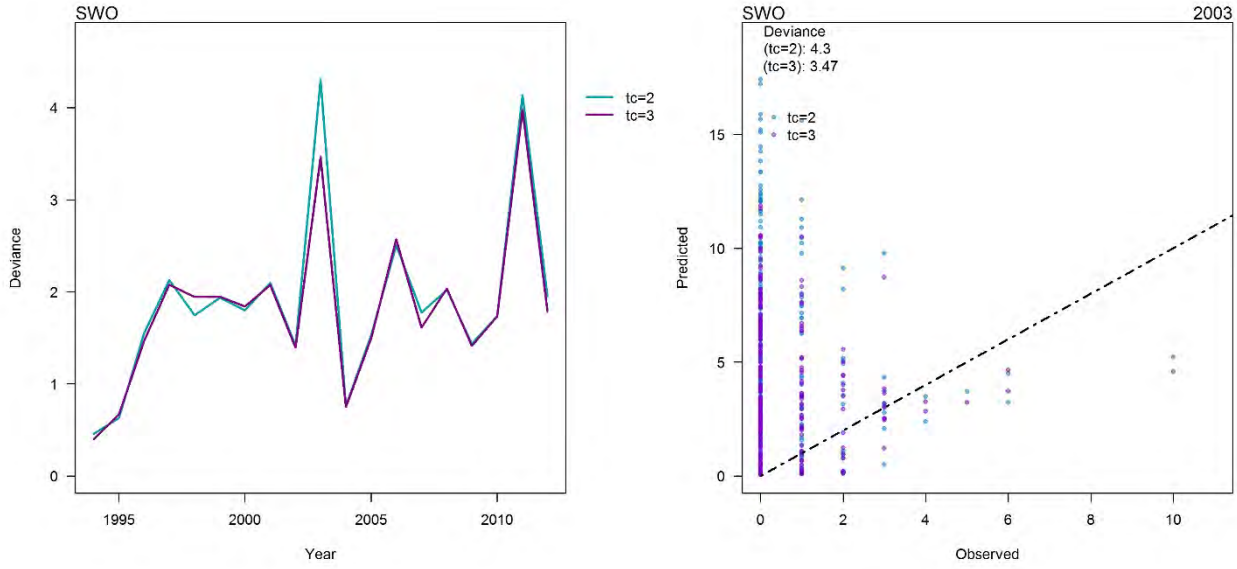


Figure 120: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2003 Poisson model (right) for species SWO.

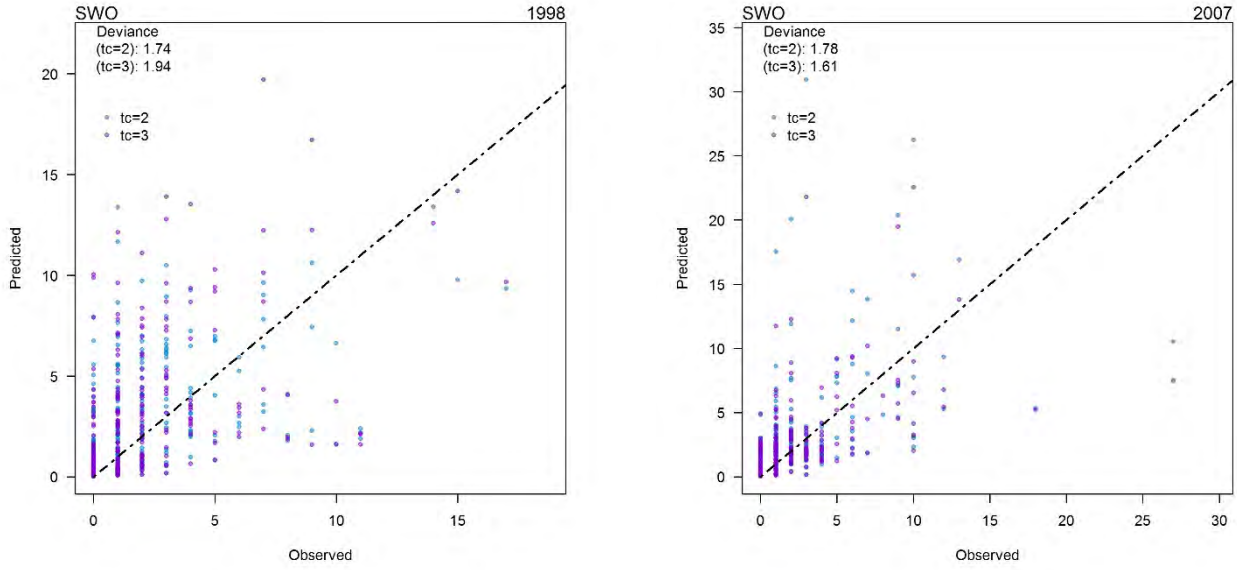


Figure 121: Predictive deviance using tree complexity of 2 and 3 for the 1998 (left) and 2007 (right) Poisson models for species SWO.

Binomial

Increasing the *tc* from 2 to 3 made very little difference to the predictive deviance in all models (Figure 122). It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all SWO Binomial models.

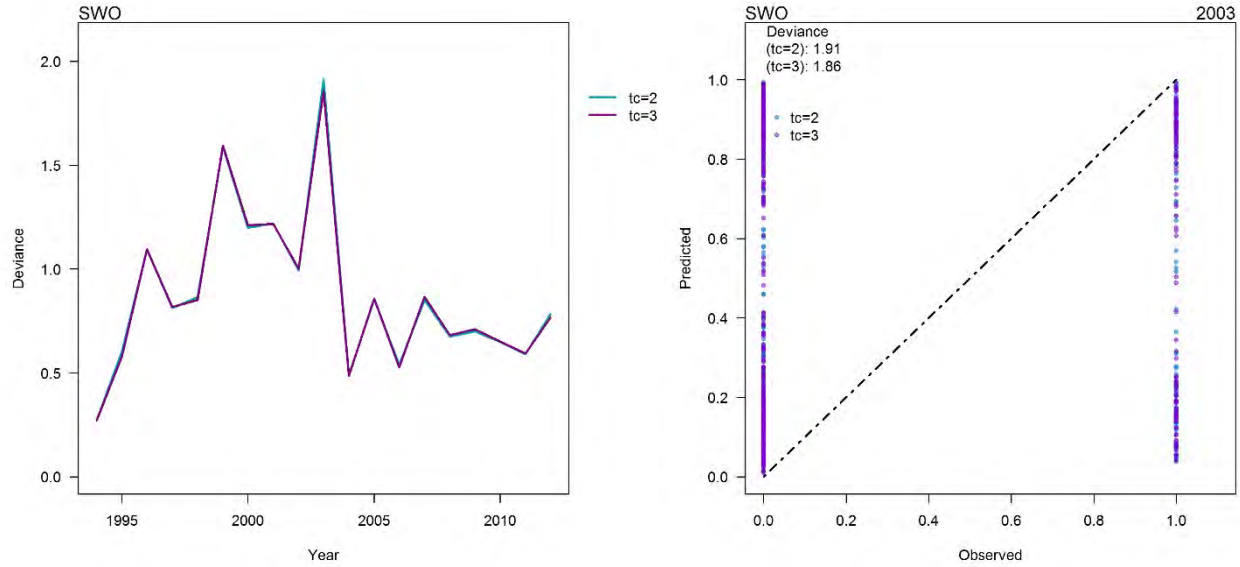


Figure 122: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2003 Poisson model (right) for species SWO.

Predictive ability

Poisson

Predictive ability was generally fair-good (Figure 123), except for a few of the models; the 2003 model overestimated the numbers caught in subareas KR1, KR2, NE2 and NE3 (Figure 126), the 2006 model underestimated numbers caught in subareas KR1 and KR2 (Figure 127), the 1995 model overestimated numbers caught in subarea KR2 (Figure 124), and the 1996 model overestimated numbers caught in subarea NE2 (Figure 125).

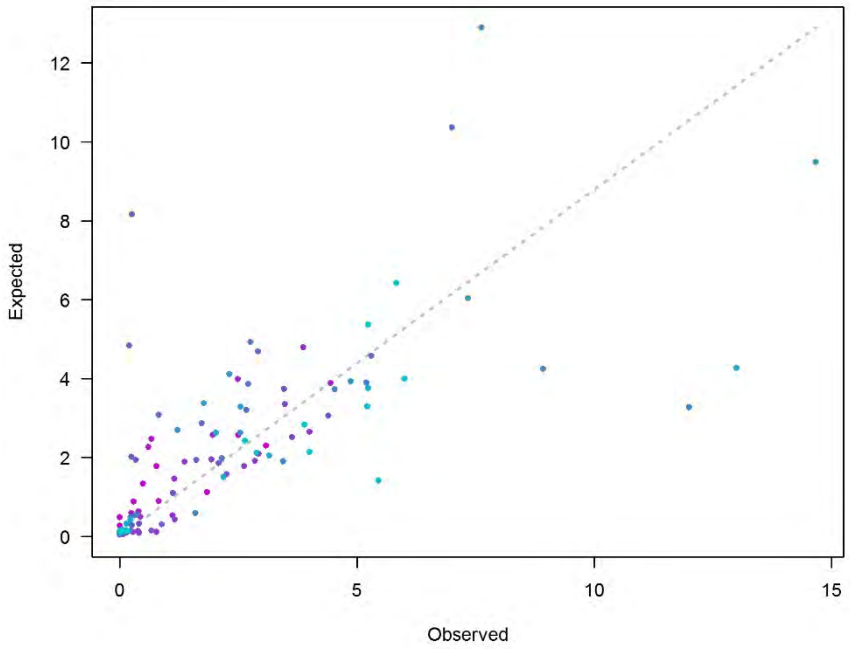


Figure 123: Observed and predicted counts of SWO for each year/subarea bin.

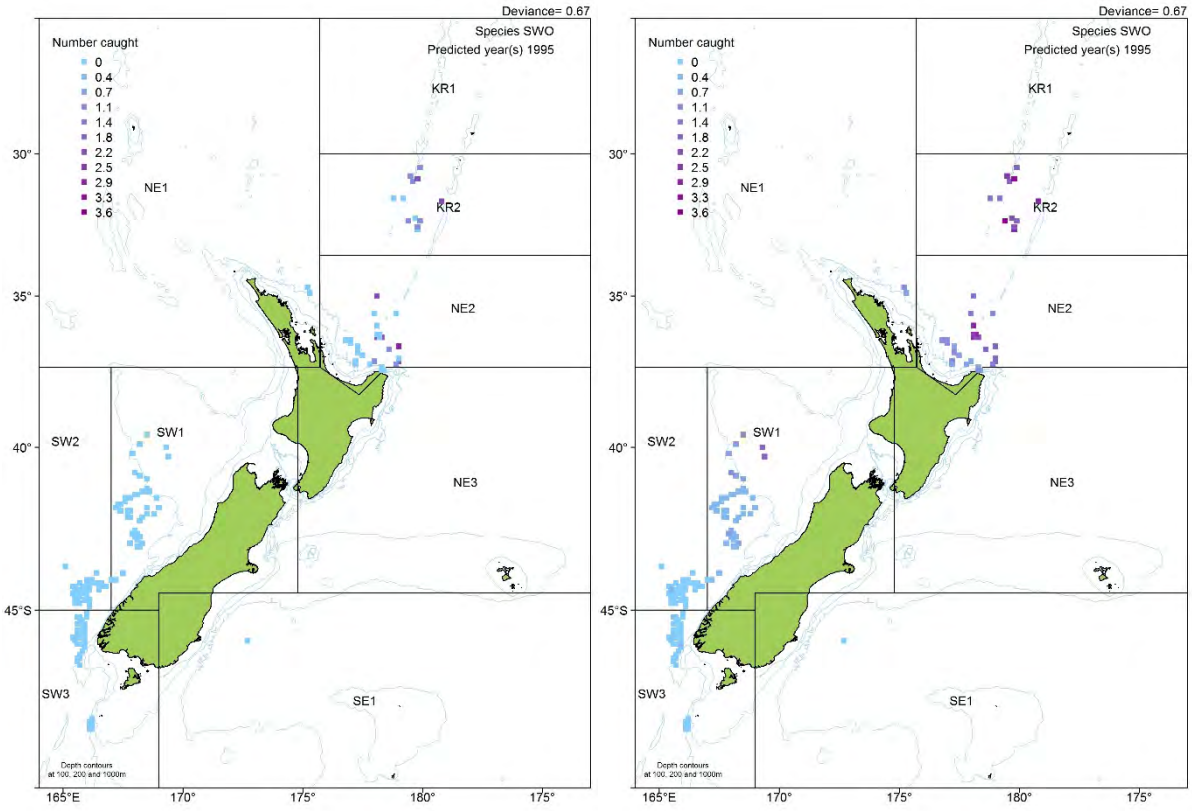


Figure 124: 1995 Poisson model observed (left) and predicted (right) numbers of SWO caught.

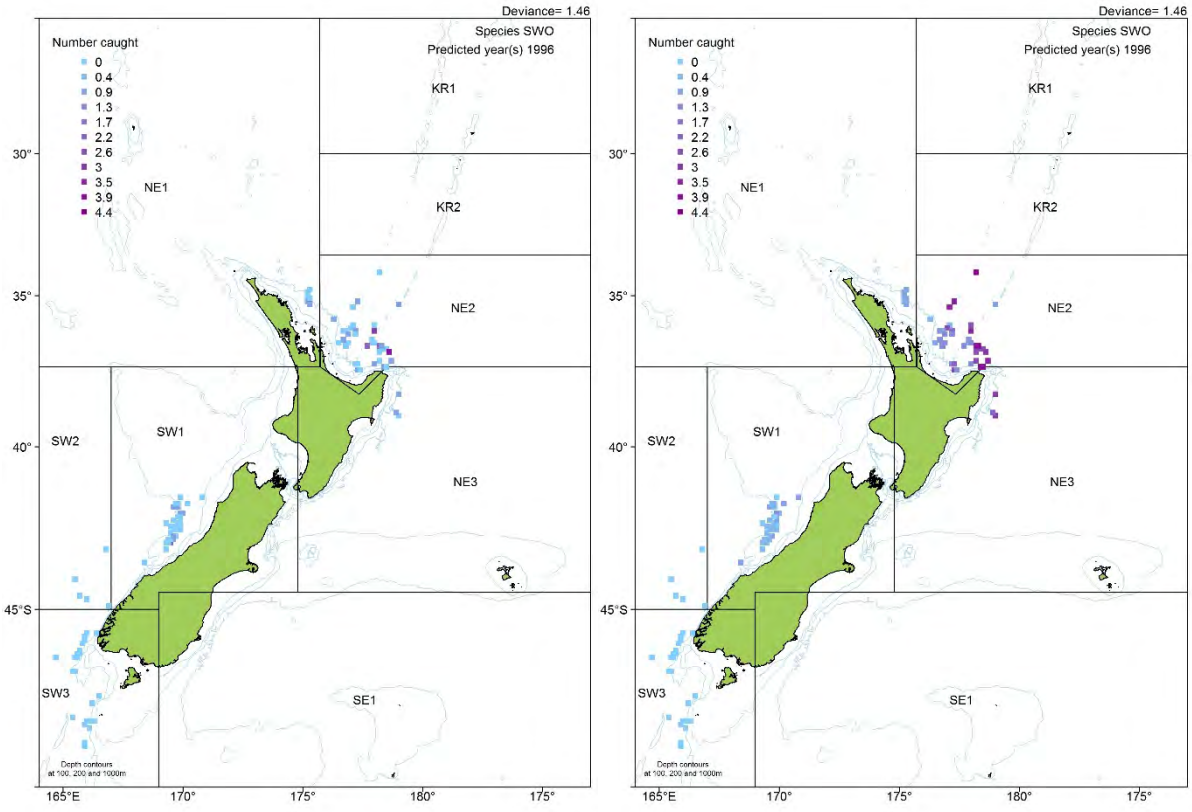


Figure 125: 1996 Poisson model observed (left) and predicted (right) numbers of SWO caught.

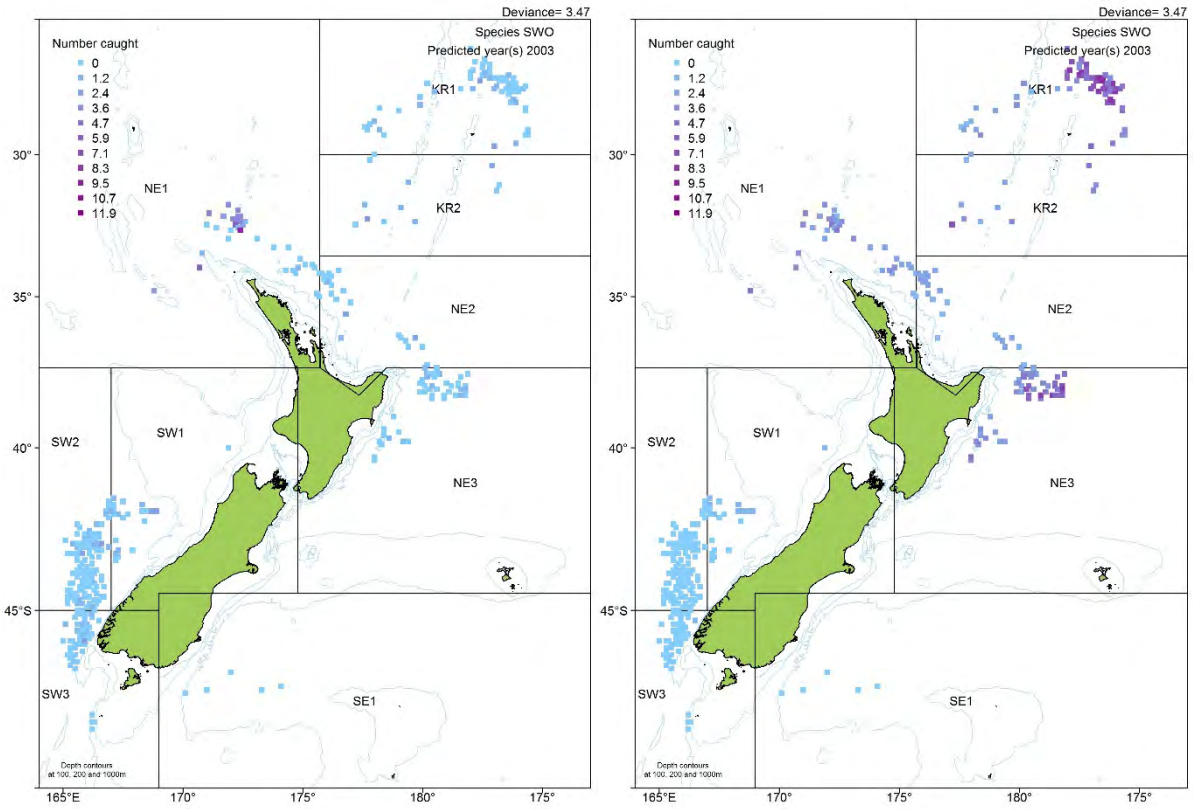


Figure 126: 2003 Poisson model observed (left) and predicted (right) numbers of SWO caught.

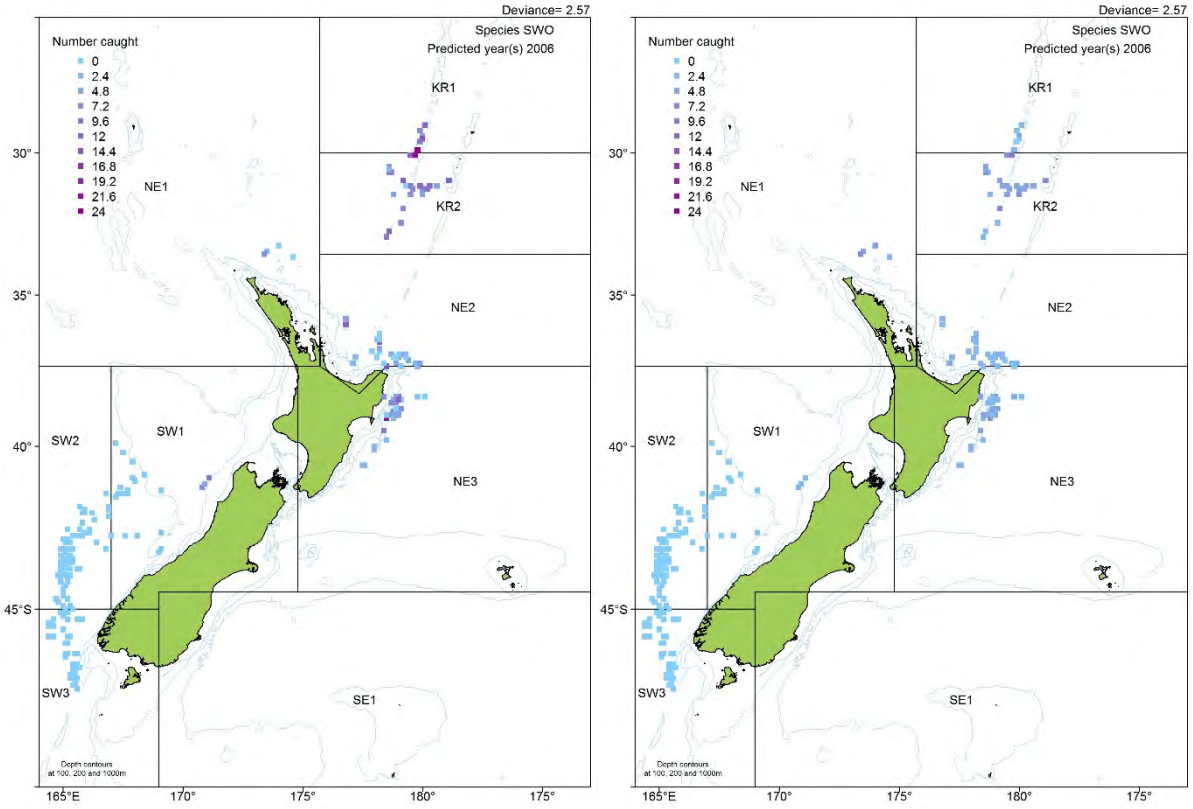


Figure 127: 2006 Poisson model observed (left) and predicted (right) numbers of SWO caught.

Binomial

Predictive ability was generally fair (Figure 128), except for the 2003 model which overestimated the probability of a presence north of -40° latitude (Figure 129).

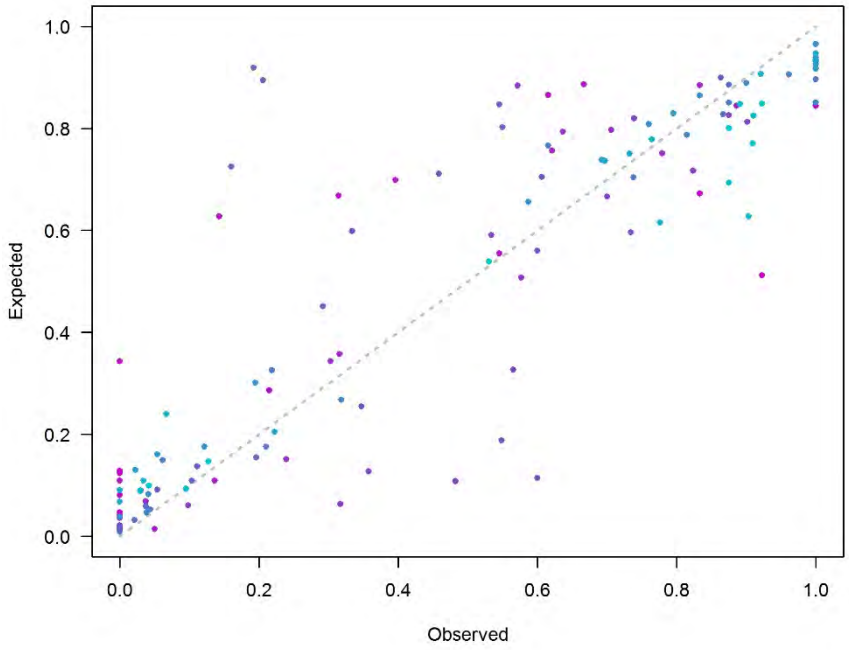


Figure 128: Observed and predicted probability of the presence of SWO for each year/subarea bin.

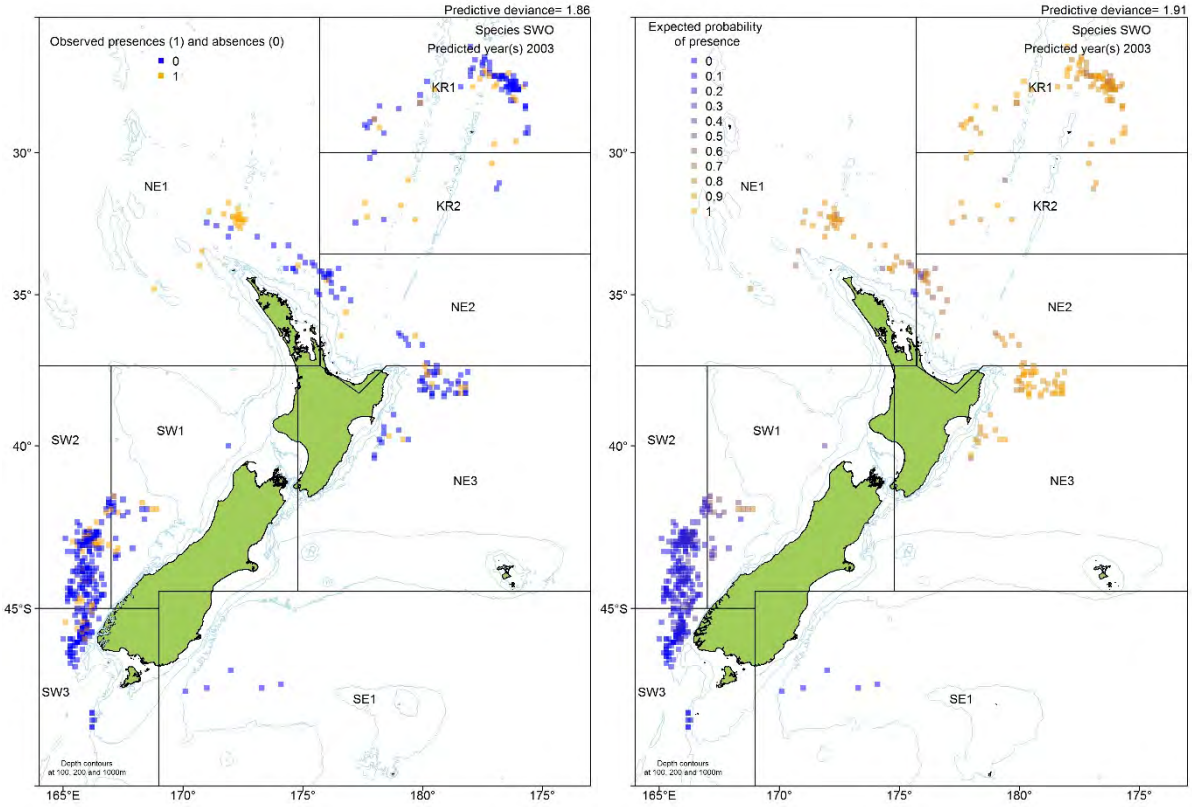


Figure 129: 2003 Binomial model observed (left) and predicted (right) presence/absence of SWO in the catch.

3.1.13 YFN

Selecting tree complexity (*tc*)

Poisson

Increasing the *tc* from 2 to 3 made very little difference to the predictive deviance in all models, with a very slight increase in the 2006 model (Figure 130). It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all YFN Poisson models.

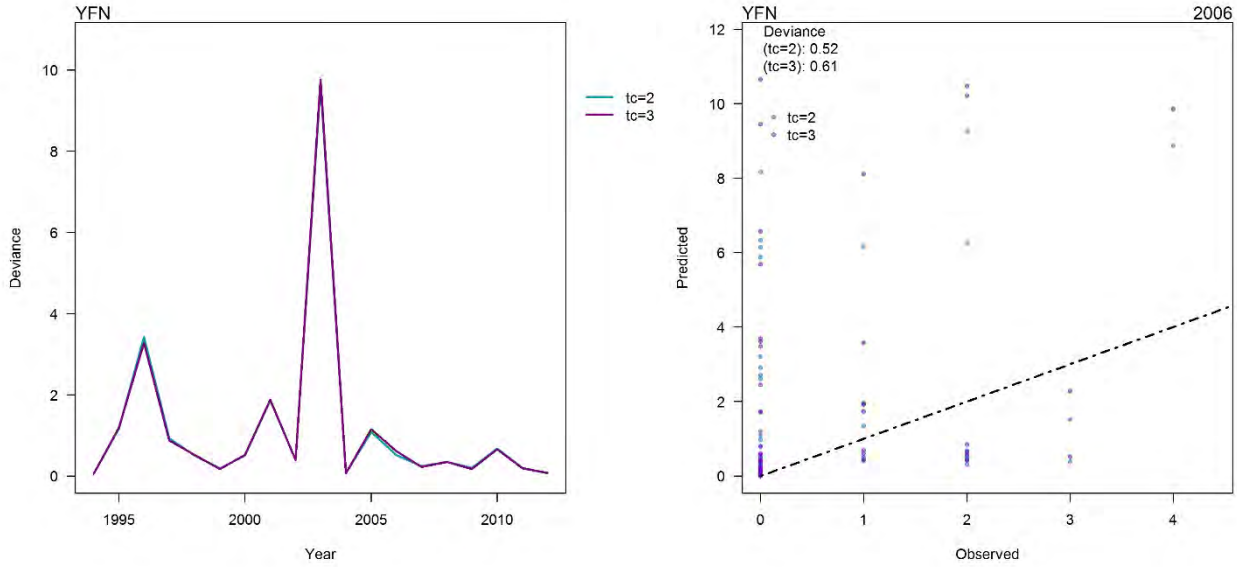


Figure 130: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2003 Poisson model (right) for species YFN.

Binomial

Increasing the *tc* from 2 to 3 made very little difference to the predictive deviance in all models, with a very slight decrease in the 2005, 2007 and 2008 models (Figure 131). It was not likely that increasing the *tc* further would improve the predictive ability and *tc*=2 has been used for the remainder of the analyses for all YFN Binomial models.

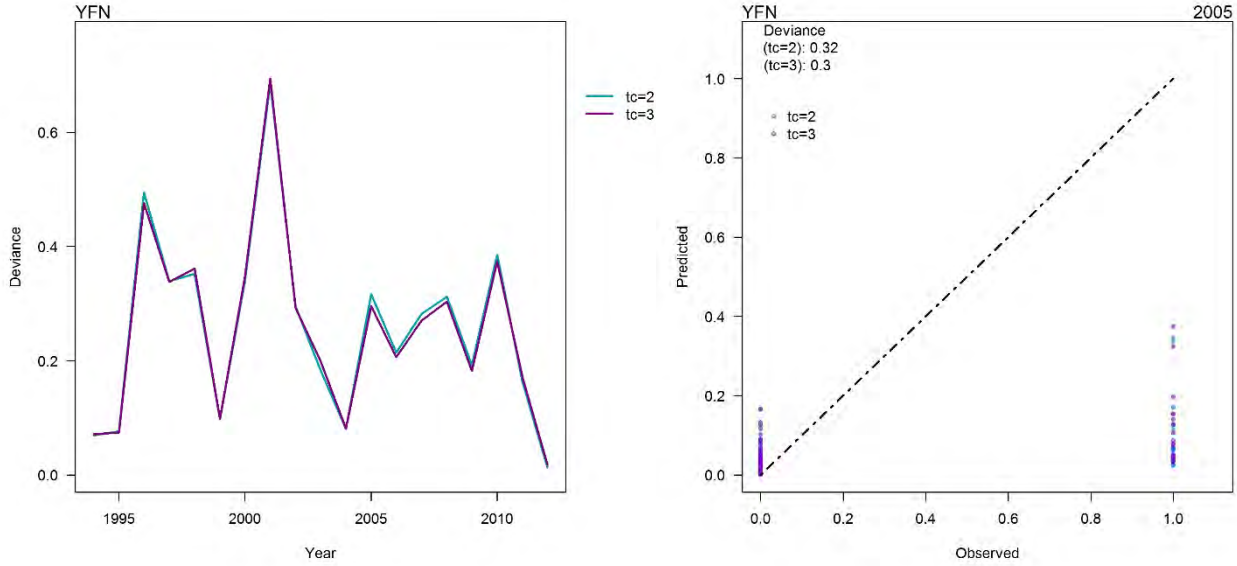


Figure 131: Predictive deviance using tree complexity of 2 and 3 across all years (left) and for the 2005 Poisson model (right) for species YFN.

Predictive ability

Poisson

Predictive ability was generally poor, and although sometimes fair this was generally when there were very small numbers observed (Figure 132). The 1999 model was one that seems fair, but there are few positive catches of YFN and only small numbers (Figure 134). The 1996 and 2003 models were typical levels of prediction for these models (Figure 133 and Figure 135).

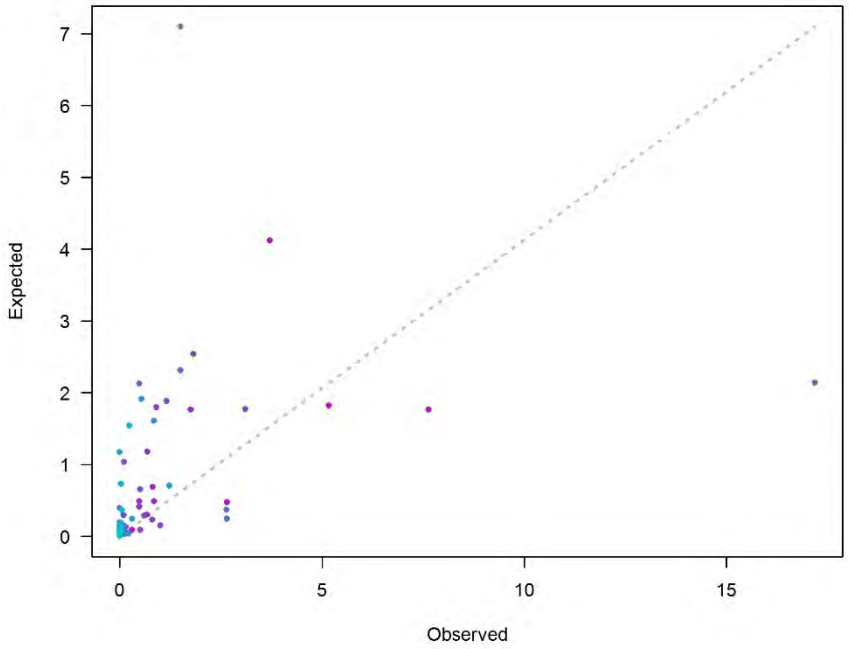


Figure 132: Observed and predicted counts of YFN for each year/subarea bin.

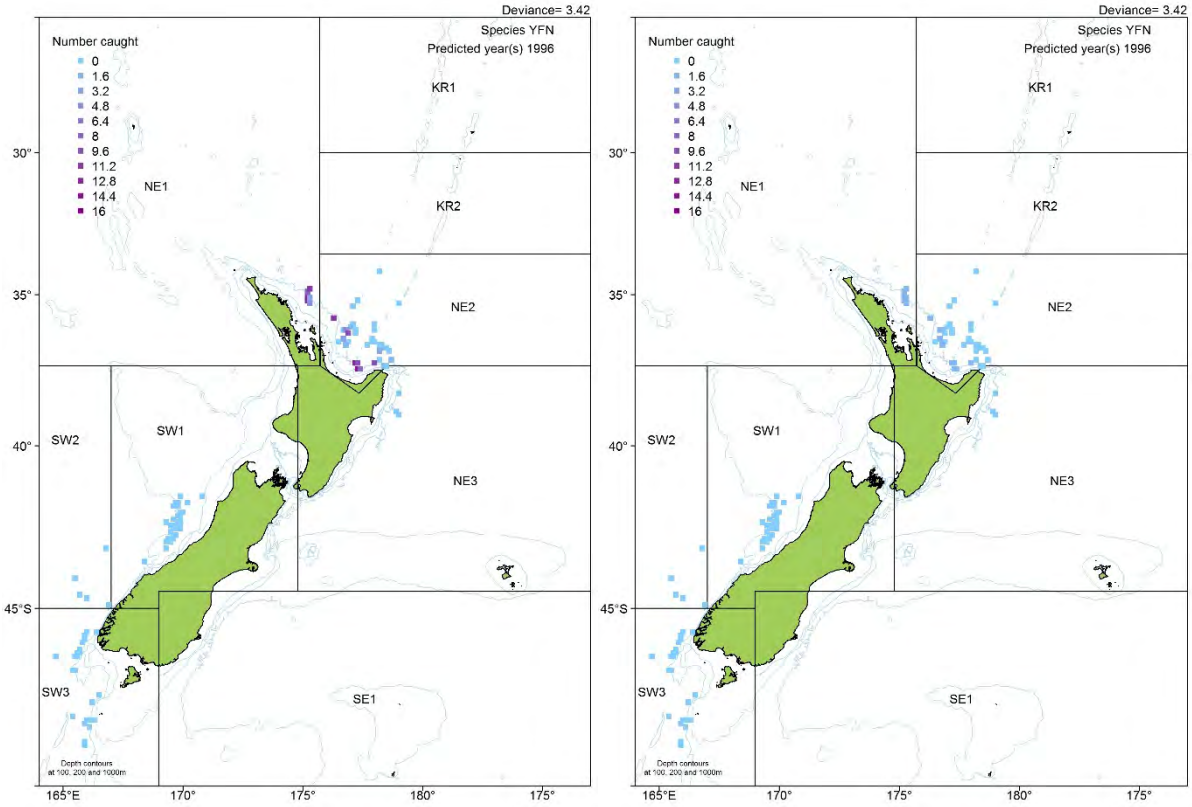


Figure 133: 1996 Poisson model observed (left) and predicted (right) numbers of YFN caught.

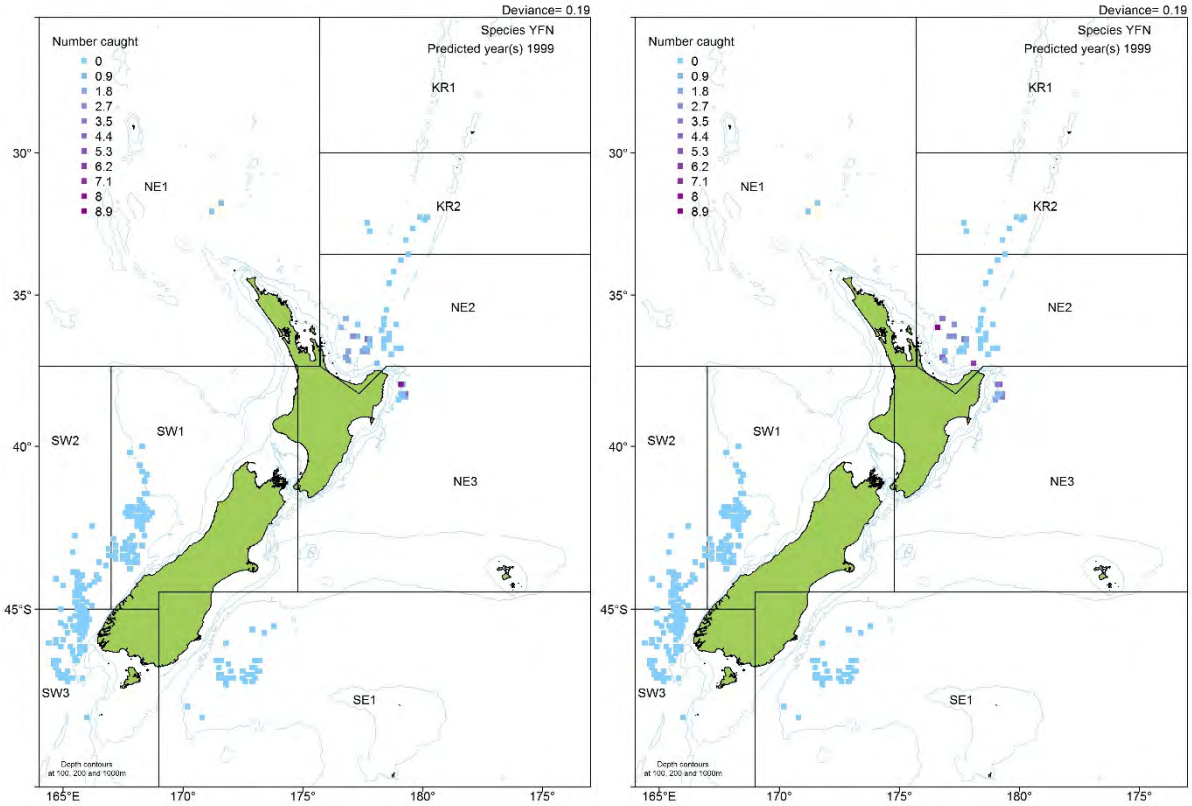


Figure 134: 1999 Poisson model observed (left) and predicted (right) numbers of YFN caught.

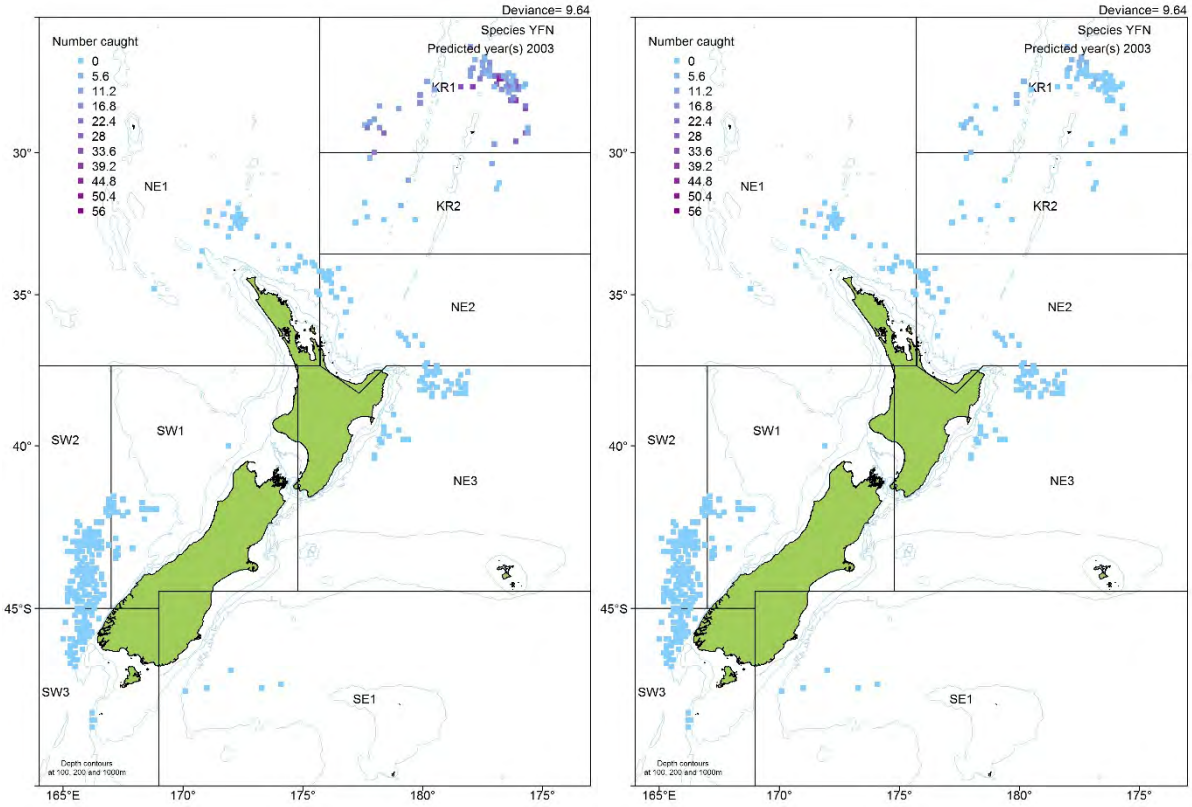


Figure 135: 2003 Poisson model observed (left) and predicted (right) numbers of YFN caught.

Binomial

Predictive ability was generally fair (Figure 136), except the 2005 and 2011 models which had poor predictive ability (Figure 137, Figure 138).

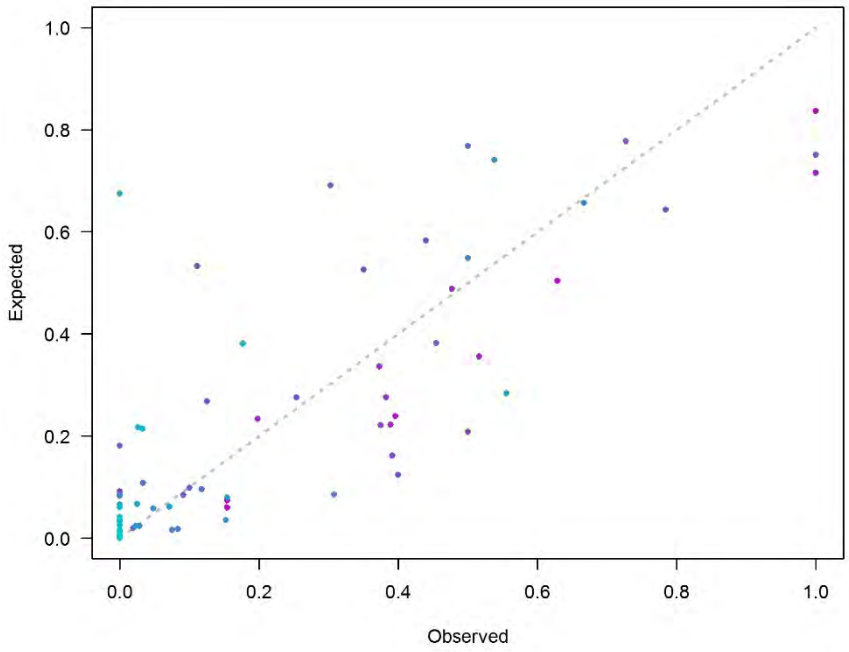


Figure 136: Observed and predicted probability of the presence of YFN for each year/subarea bin.

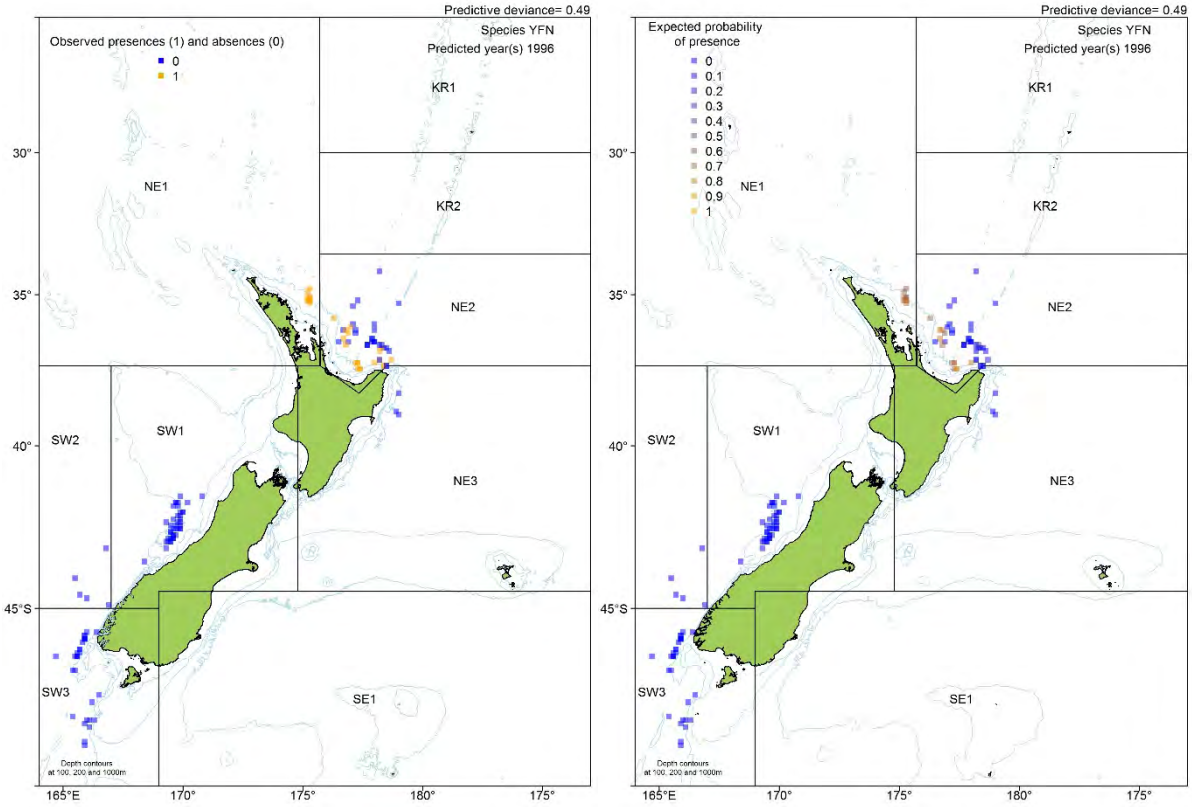


Figure 137: 1996 Binomial model observed (left) and predicted (right) presence/absence of YFN in the catch.

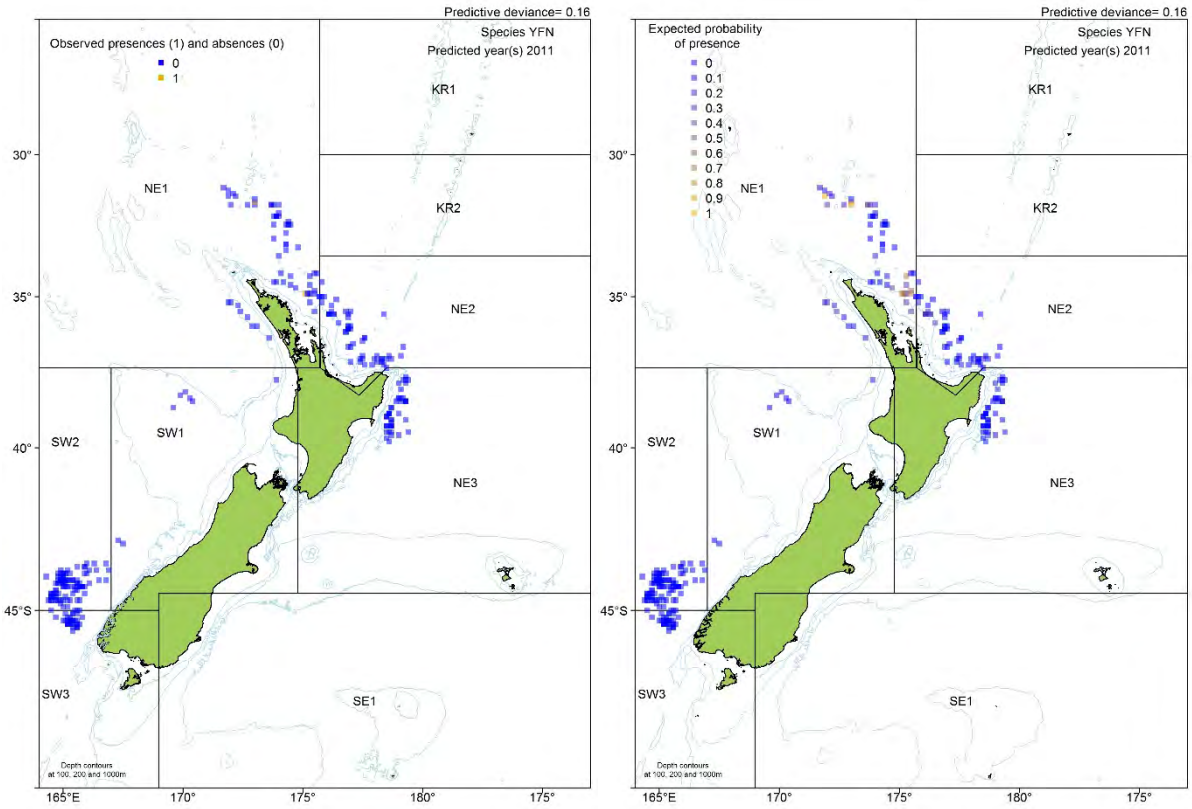


Figure 138: 2011 Binomial model observed (left) and predicted (right) presence/absence of YFN in the catch.

4. Variable influence and effects

The Binomial models were more consistent in terms of most influential variables than the Poisson models (Figures 139, 140 and Appendix B). In the Binomial models, sea surface temperature (SST) was the most influential variable for 9 out of the 13 species, subarea (sub_area) for 2 species, and start latitude (start_latitude) for 2 species. Also often influential in the Binomial models were hook number (hook_no), month (haul_month), time (time_haul), duration, and sea surface height (SSH).

In the Poisson models, the most influential variable was start latitude for 3 of the species, sea surface temperature, subarea, and time, each for 2 species, and duration, month, hook number and depth (hook_depth), each for 1 species. Sea surface height (SSH) and start longitude (start_longitude) were also often influential in the Poisson models.

In the Poisson and Binomial models moon phase (moon_ph) was rarely influential. It had a small influence in the BWS Binomial, POS Poisson and STN Poisson models (see Figures Figure, Figure and Figure). Sea surface temperature anomaly (SST_anomaly) and sea surface current (SST_mag_uv) were sometimes slightly influential in Binomial and Poisson models, such as the BWS models (Figure). Pie charts of the mean influence of each variable for each species and model type are in Figures Figure –Figure (Appendix B).

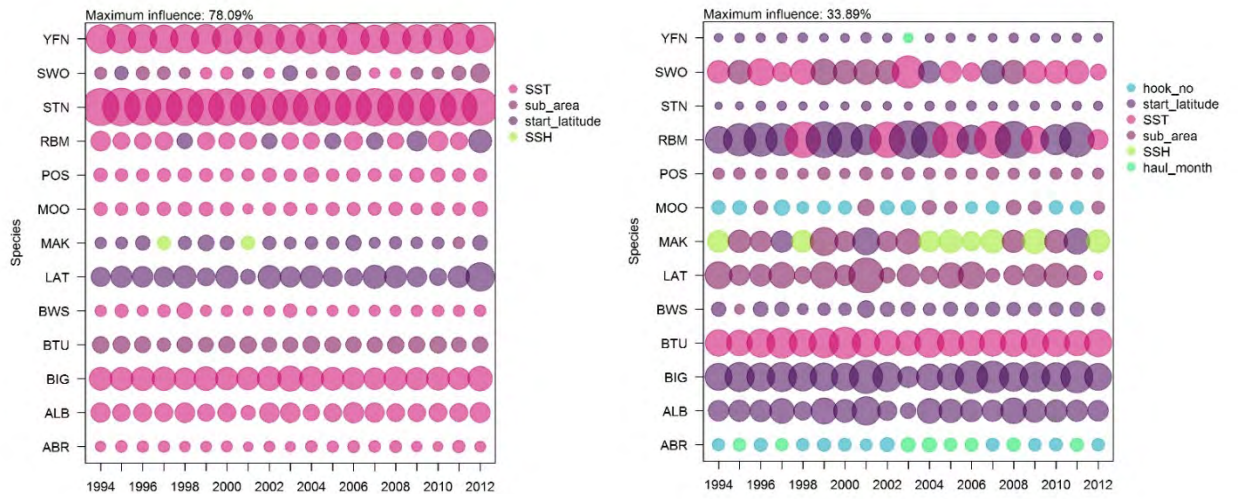


Figure 139: First (left) and second (right) most influential variables for Binomial models for all species across al years.

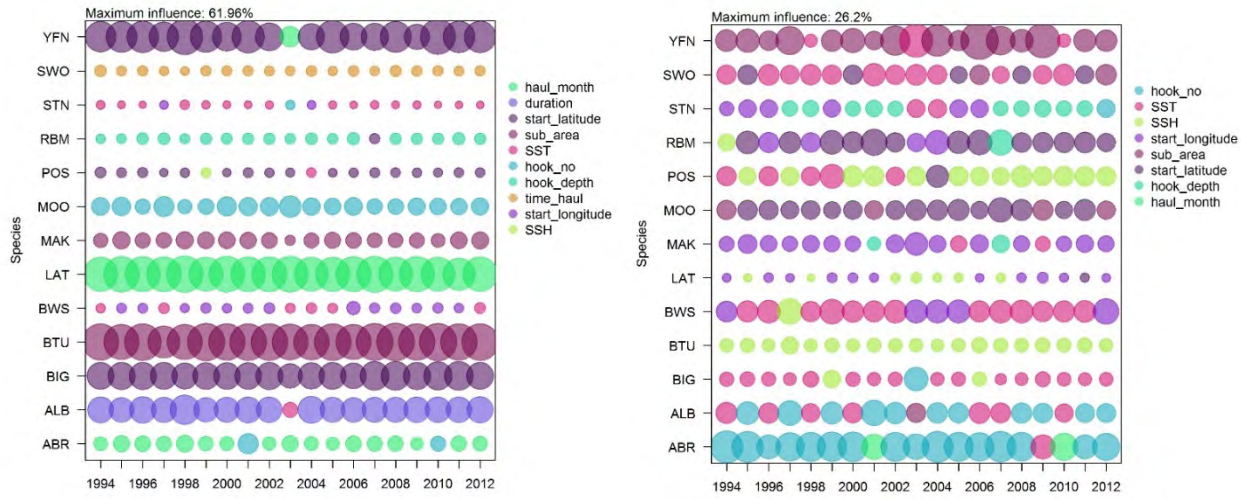


Figure 140: First (left) and second (right) most influential variables for Poisson models for all species across all years.

BTU	<17 °C	NA	SE1
BWS	12–17 °C	>-46 ° latitude	-
LAT	>18°C	>-40	KR2, SW1
MAK	13–20°C	>-40° latitude	NE1, NE2, NE3
MOO	>14°C	-35 to -32° latitude	KR2, NE1, NE3
POS	<17°C	<-42° latitude	NE2, NE3, SE1
RBM	<16°C	<-40° latitude	NE3
STN	<17°C	<-40° latitude	NE2, SW2, SW3
SWO	>14°C	>-42° latitude	KR2, NE1, NE2, NE3
YFN	>17°C	>-30° latitude	KR1, KE2

4.1 ALB

Sea surface temperature was the most influential variable in the Binomial models, contributing around 40% relative influence, and start latitude was the second most influential variable (Figure 141). The Poisson models had duration as the most influential variable followed by hook number and sea surface temperature.

The variable effect of sea surface temperature in both the Binomial and Poisson models increased from around 12–13°C, peaked at around 17–20°C and then dropped off (Figure 142). The variable effect of start latitude in the Binomial model indicated that ALB were more likely to be present at latitudes greater than -45° and less than -34° (Figure 143).

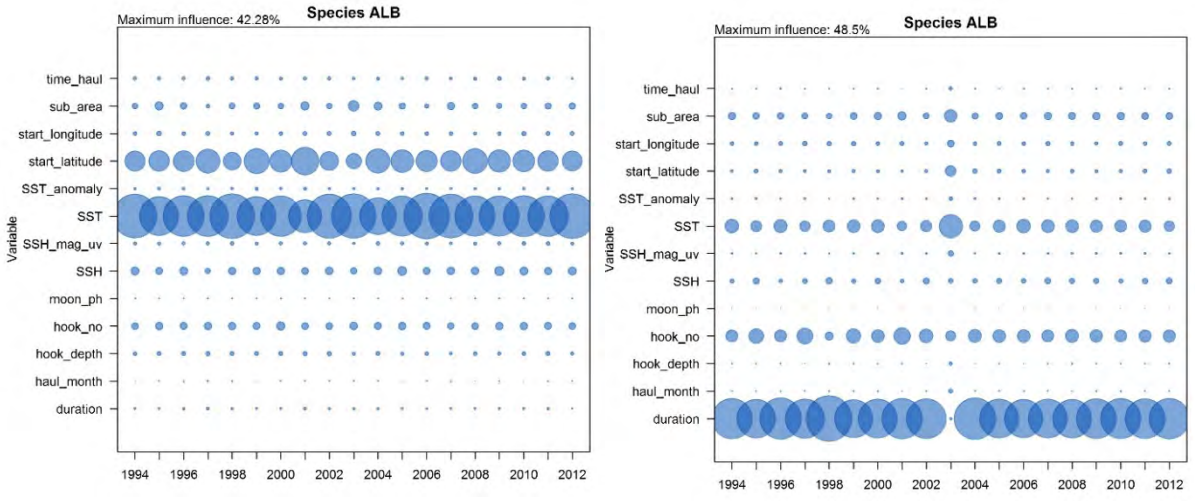


Figure 141: Relative influence of variables in ALB Binomial (left) and Poisson (right) models.

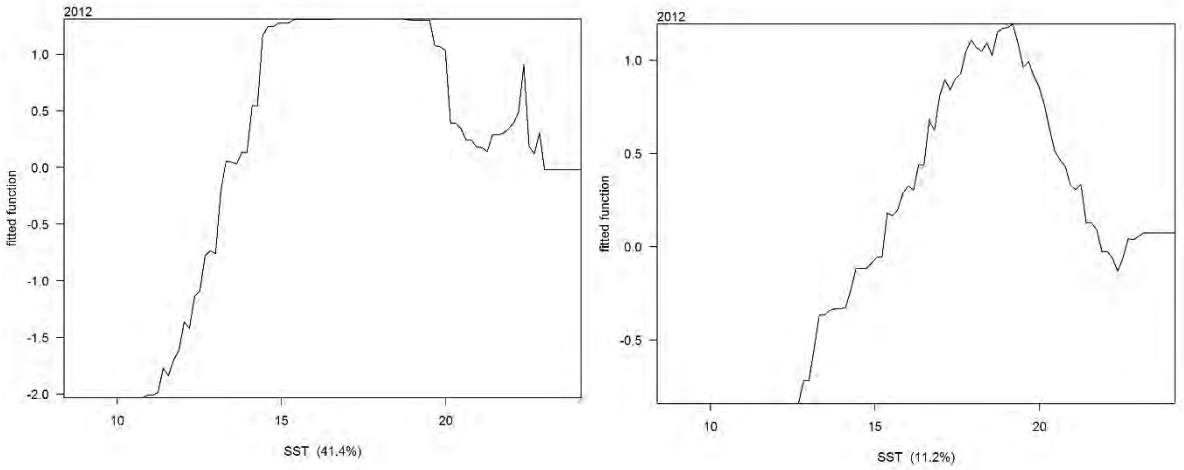


Figure 142: Variable effect of sea surface temperature in the ALB 2012 Binomial model (left) and ALB 2012 Poisson model (right).

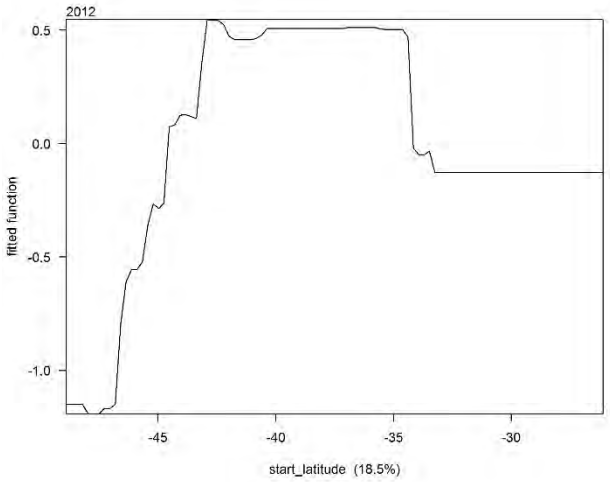


Figure 143: Variable effect of start latitude in the ALB 2012 Binomial model.

4.2 BIG

Sea surface temperature was the most influential variable in the Binomial models, contributing around 50% of the relative influence, and start latitude was the second most influential variable (Figure 144). The Poisson models had start latitude as the most influential variable, contributing around 50% of the relative influence, and sea surface temperature generally the second most influential variable, but it was much less influential than start latitude (Figure 144).

The effect of sea surface temperature suggested that BIG were most likely to be caught at temperatures greater than 16^{o}C (Figure 145). The start latitude effect suggested that BIG were most likely to be caught at latitudes greater than -36^{o} and less than -28^{o} (Figure 146).

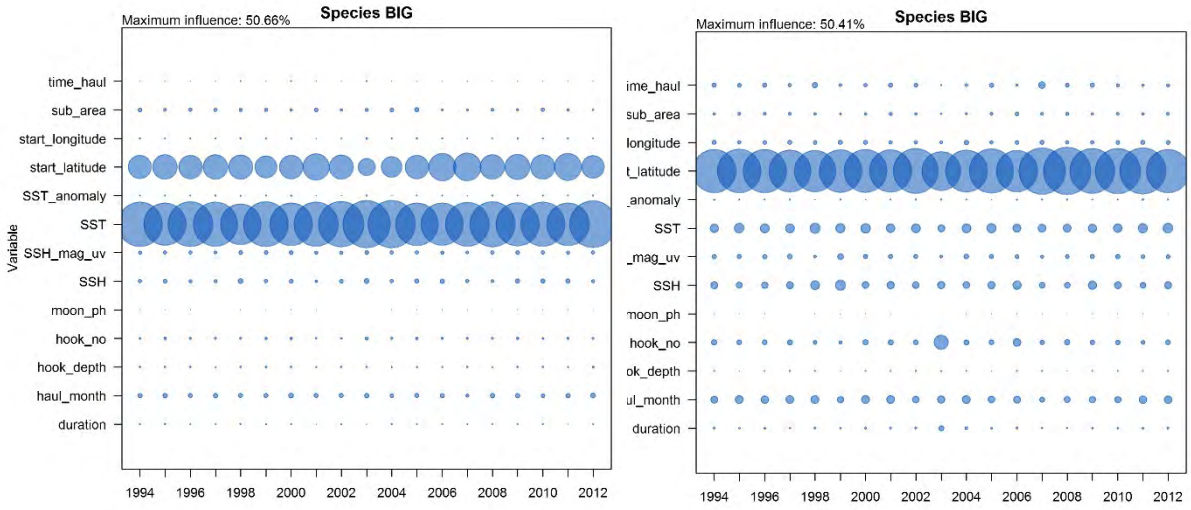


Figure 144: Relative influence of variables in BIG Binomial (left) and Poisson (right) models.

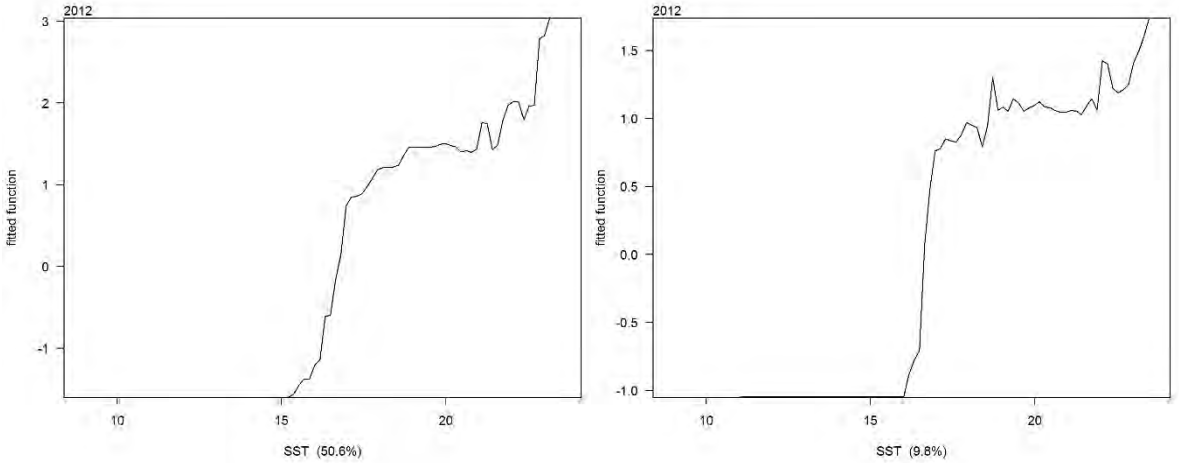


Figure 145: Variable effect of sea surface temperature in the BIG 2012 Binomial model (left) and BIG 2012 Poisson model (right).

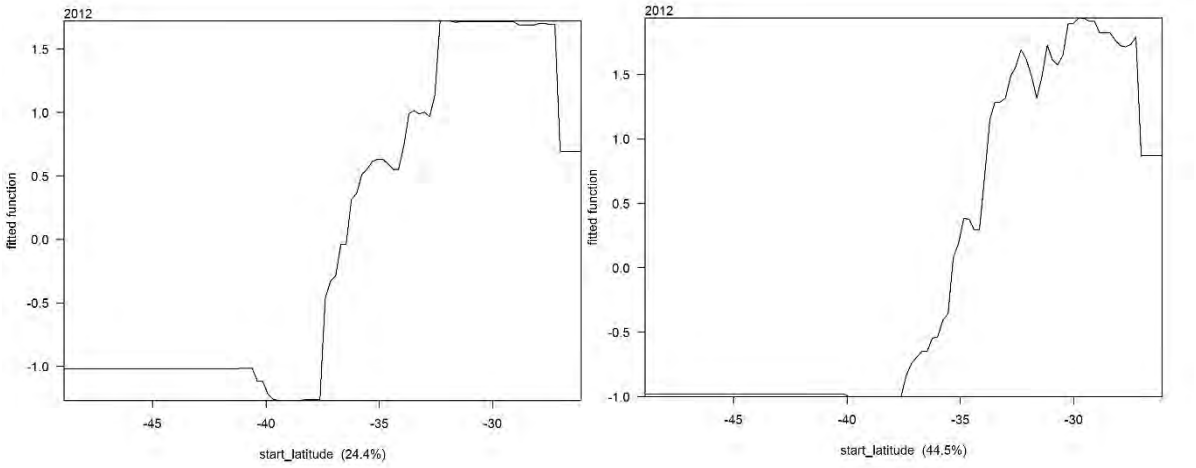


Figure 146: Variable effect of start latitude in the BIG 2012 Binomial model (left) and BIG 2012 Poisson model (right).

4.3 BTU

Subarea was the most influential variable for both the Binomial and Poisson models (Figure 147). Sea surface temperature was the second most influential variable for the Binomial models.

The variable effect for subarea suggested that subarea SE1 was by far most likely to have BTU present and with the greatest numbers caught (Figure 148). Subarea KR1 had a higher effect in the Binomial models than in the Poisson models.

The variable effect for sea surface temperature suggested that BTU were most likely at temperatures less than 18°C (Figure 149).

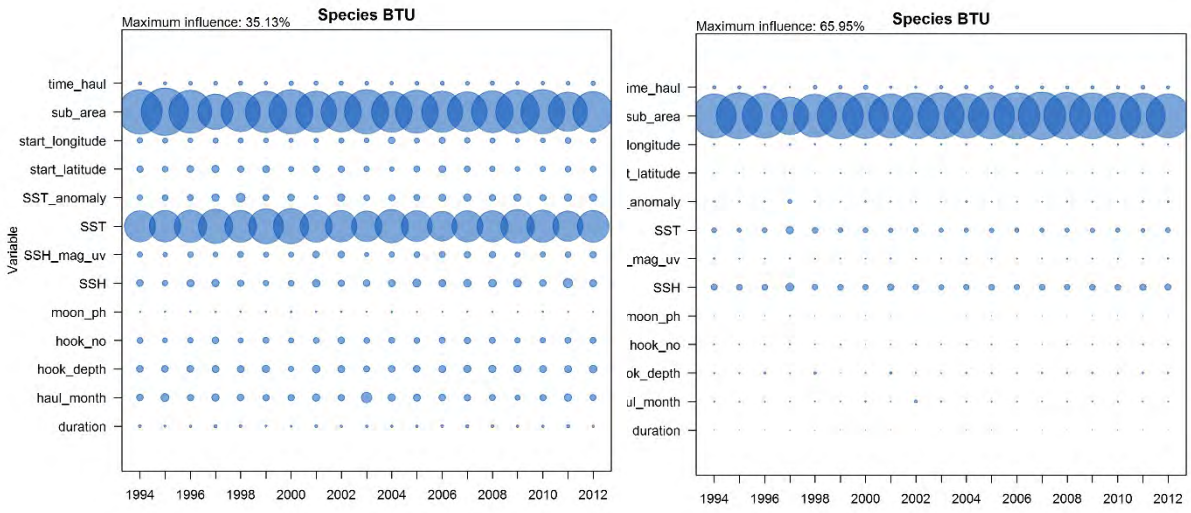


Figure 147: Relative influence of variables in BIG Binomial (left) and Poisson (right) models.

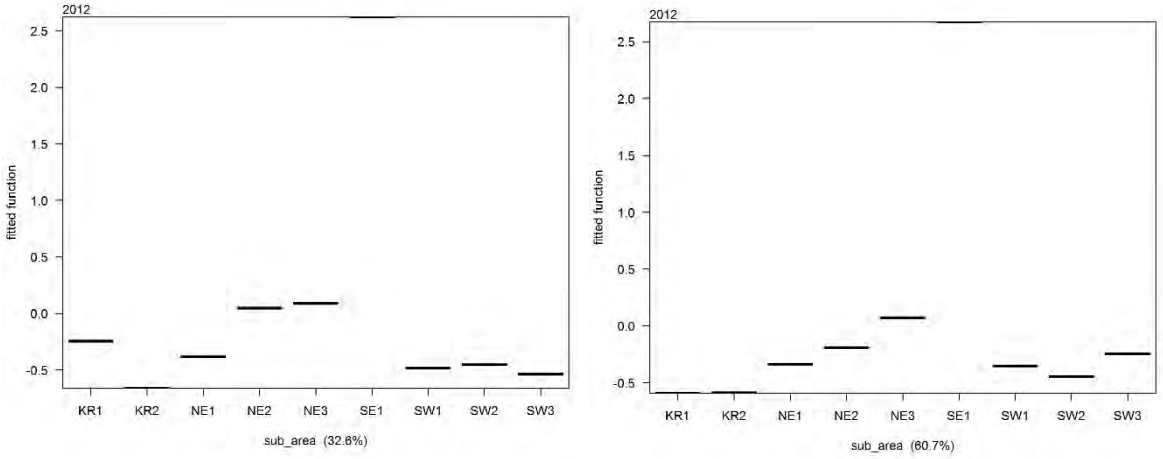


Figure 148: Variable effect of subarea in the BTU 2012 Binomial model (left) and BTU 2012 Poisson model (right).

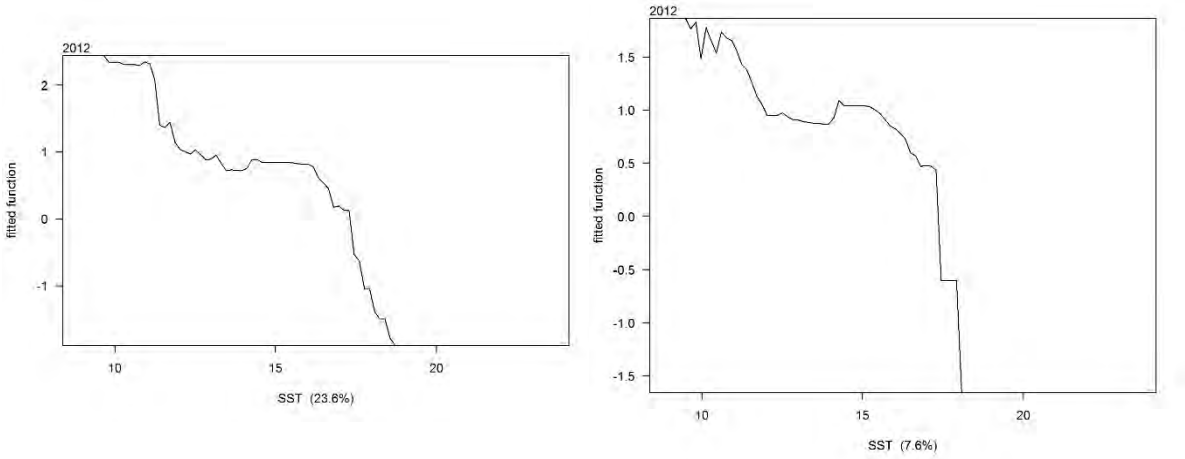


Figure 149: Variable effect of sea surface temperature in the BTU 2012 Binomial model (left) and BTU 2012 Poisson model (right).

4.4 BWS

Sea surface temperature was the most influential variable for the Binomial models, followed by start latitude. The Poisson models had sea surface temperature and start longitude as the most influential variables (Figure 150).

The variable effect for sea surface temperature suggested that BWS were more likely present and caught in larger numbers when the sea surface temperature was between 12°C and 17°C (Figure 151).

The variable effect for start latitude suggested BWS were most likely present north of -46° latitude (Figure 152).

The variable effect for start longitude suggested BWS were caught in larger numbers around 180° longitude (Figure 153).

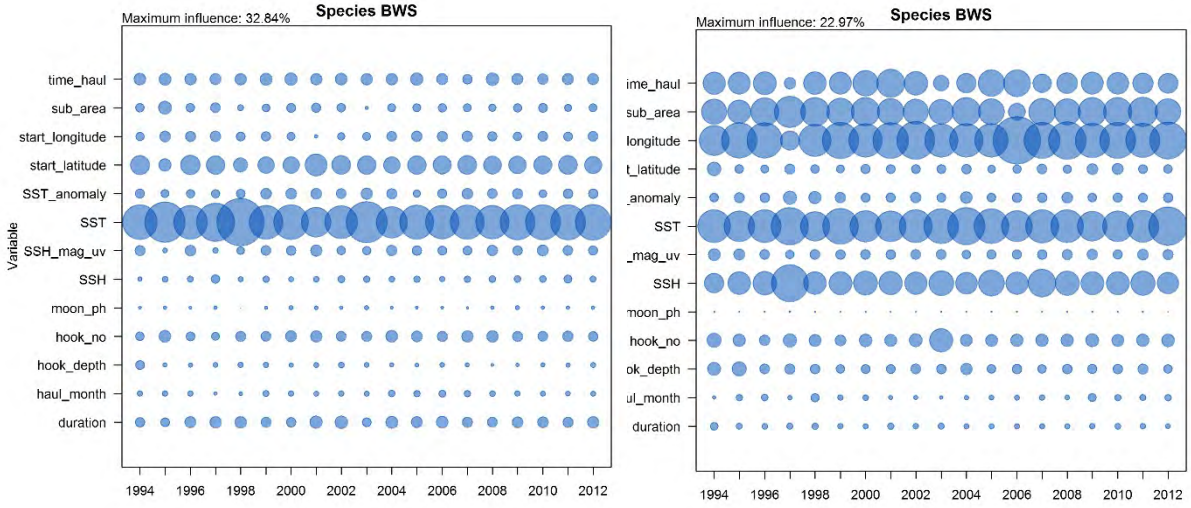


Figure 150: Relative influence of variables in BWS Binomial (left) and Poisson (right) models.

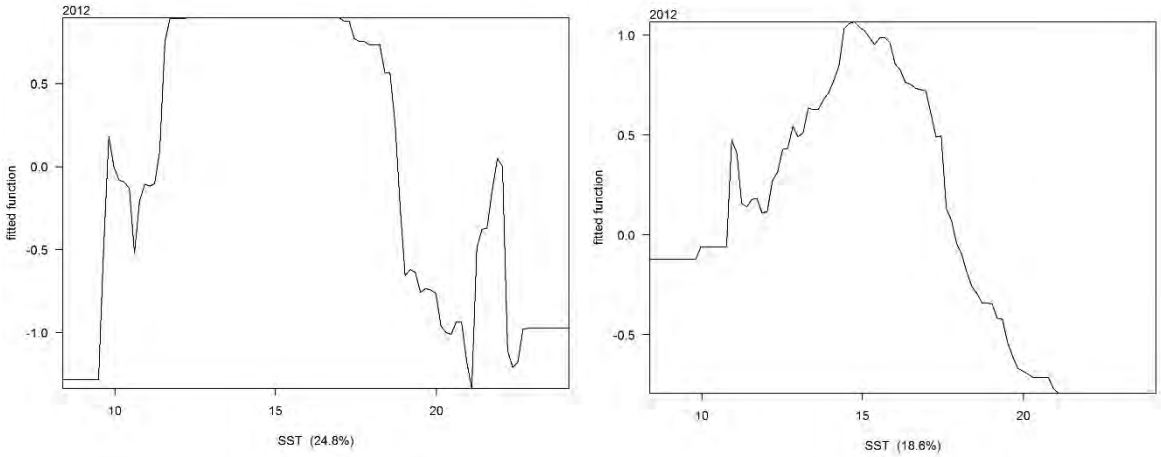


Figure 151: Variable effect of sea surface temperature in the BWS 2012 Binomial model (left) and BWS 2012 Poisson model (right).

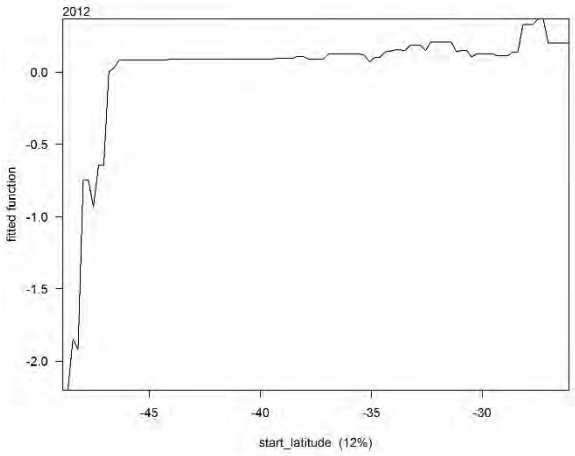


Figure 152: Variable effect of start latitude in the BWS 2012 Binomial model.

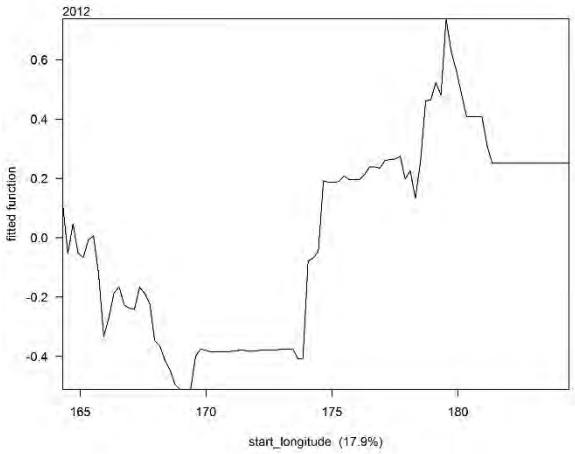


Figure 153: Variable effect of start longitude in the BWS 2012 Poisson model.

4.5 LAT

Start latitude was the most influential variable for the Binomial models, followed by subarea then sea surface temperature. The Poisson models were influenced most by month (Figure 154).

The variable effects of the Binomial models suggested LAT were most likely present at latitudes north of -45° latitude, in subareas KR2, SW1 and NE2 and somewhat more likely where the sea surface temperature was greater than 15°C and much more likely when it was over 20°C (Figures 155, 156 and 157).

The variable effects in the Poisson models suggested that LAT were caught in the greatest numbers in August-December (Figure 158).

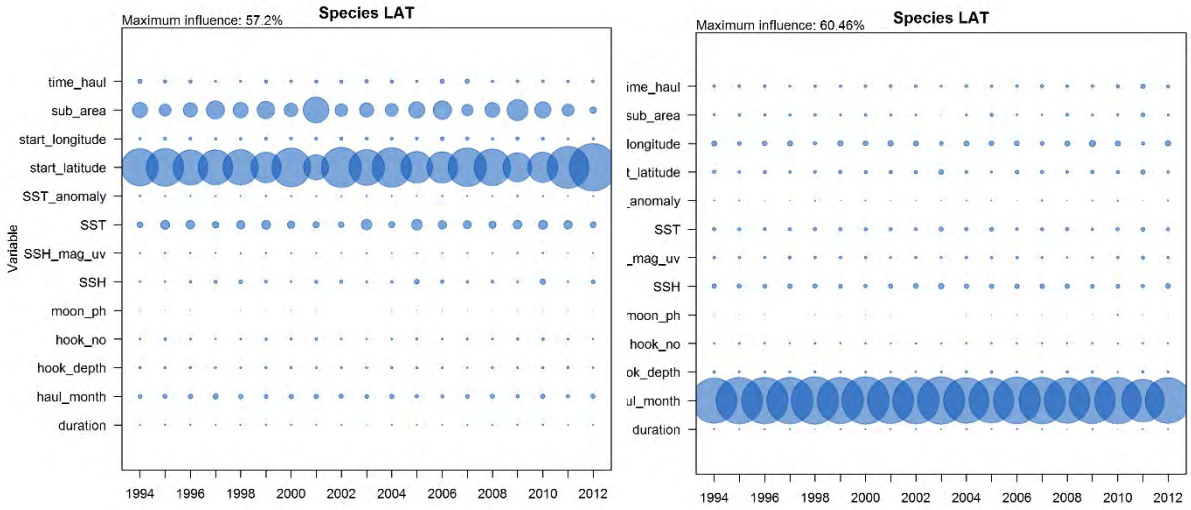


Figure 154: Relative influence of variables in BIG Binomial (left) and Poisson (right) models.

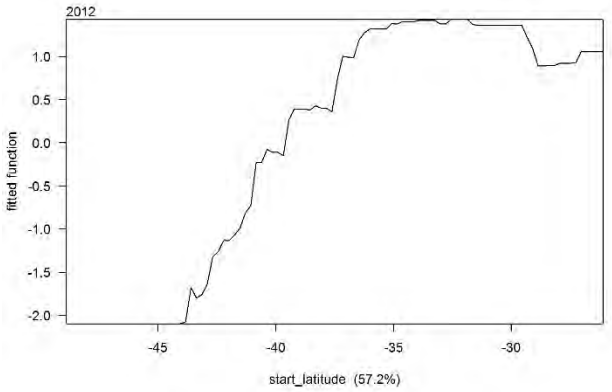


Figure 155: Variable effect of start latitude in the LAT 2012 Binomial model.

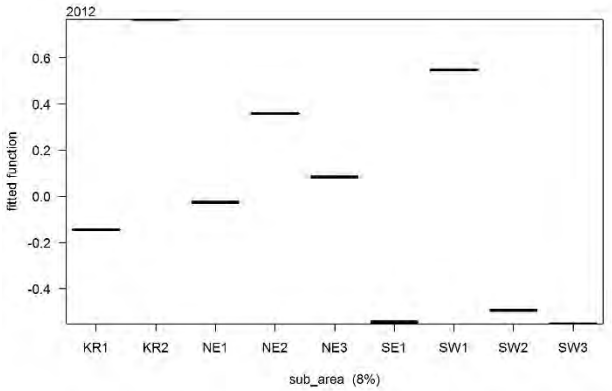


Figure 156: Variable effect of subarea in the LAT 2012 Binomial model.

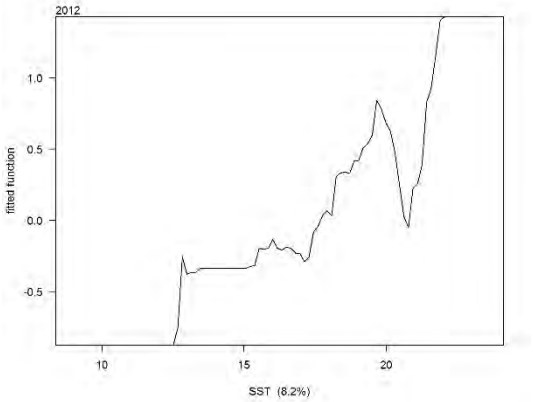


Figure 157: Variable effect of sea surface temperature in the LAT 2012 Binomial model.

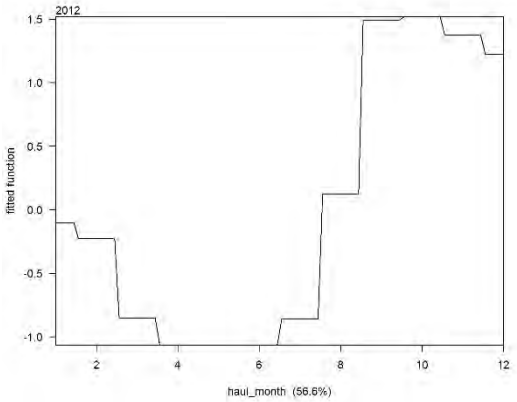


Figure 158: Variable effect of month in the LAT 2012 Binomial model.

4.6 MAK

Start latitude was the most influential variable for the Binomial models and subarea was most influential for the Poisson models (Figure 159). Subarea and sea surface height were the next most influential variables for the Binomial models. The Poisson models were influenced by start longitude, sea surface temperature, sea surface current and hook depth with fairly even influences.

In the Binomial and Poisson models, the effect of start latitude suggested that MAK were most likely north of about -42^{o} latitude (Figure 160). The subarea effect suggested MAK were most likely in NE1, NE2 and NE3 (Figure 161). In the Binomial models, the sea surface height effect suggested MAK were more likely to be present when the sea surface height was greater than 50 cm (Figure 162).

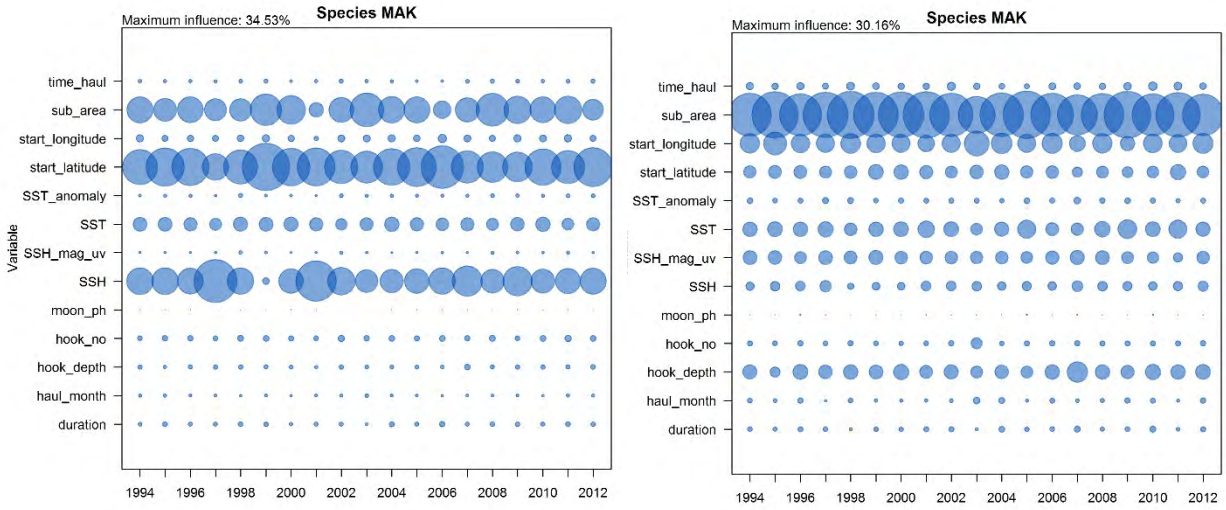


Figure 159: Relative influence of variables in MAK Binomial (left) and Poisson (right) models.

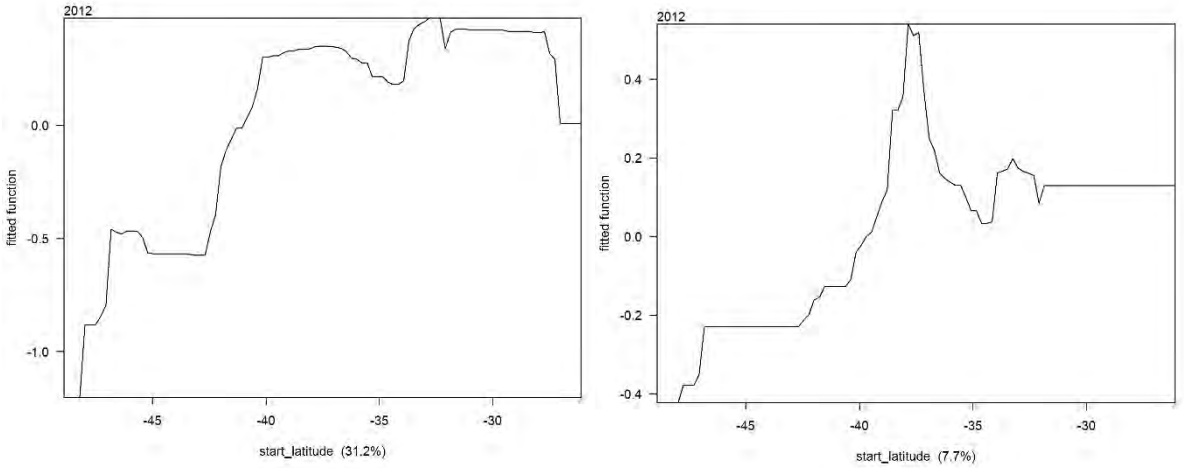


Figure 160: Variable effect of start latitude in the MAK 2012 Binomial model (left) and MAK 2012 Poisson model (right).

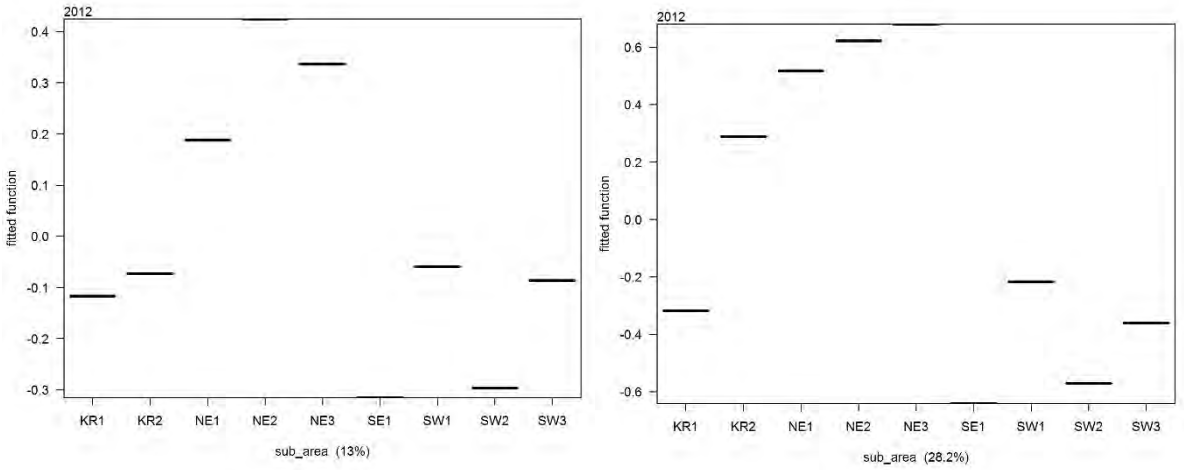


Figure 161: Variable effect of subarea in the MAK 2012 Binomial model (left) and MAK 2012 Poisson model (right).

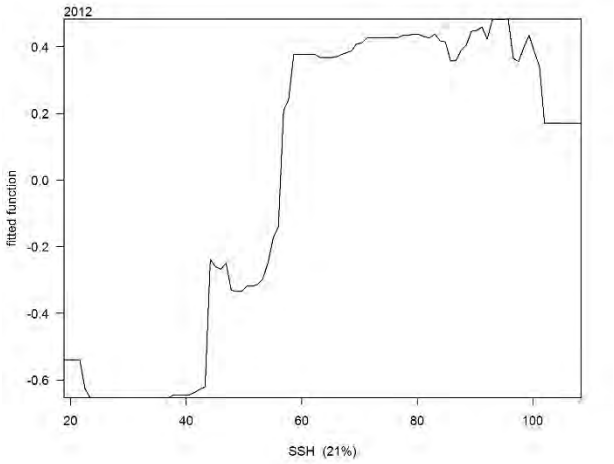


Figure 162: Variable effect of sea surface height in the MAK 2012 Poisson model.

4.7 MOO

Sea surface temperature was the most influential variable in the Binomial models, followed by subarea and hook number (Figure 163). The Poisson models were most influenced by hook number, then subarea and start latitude.

In the Binomial models, sea surface effects suggested that MOO were most likely present when the sea surface was greater than about 12°C (Figure 164).

The subarea effect was fairly consistent across Poisson models and suggested that MOO were caught in higher numbers in subareas NE3, KR2, NE1 and NE2 (decreasing order) (Figure 165). The subarea effect in the Binomial models was a bit more varied, sometimes matching that of the Poisson models such as the 2006 model (Figure 166) and sometimes with subarea NE1 more likely to have MOO present than KR2, such as in the 2012 model (Figure 165).

The start latitude effect for Binomial and Poisson models suggested that MOO were most likely to be present, and with highest catch numbers, at latitudes greater than -36° latitude and less than -32° latitude (Figure 167).

The hook number effect in the Poisson models suggested that MOO are more likely to be caught when more than 2000 hooks were set (Figure 168).

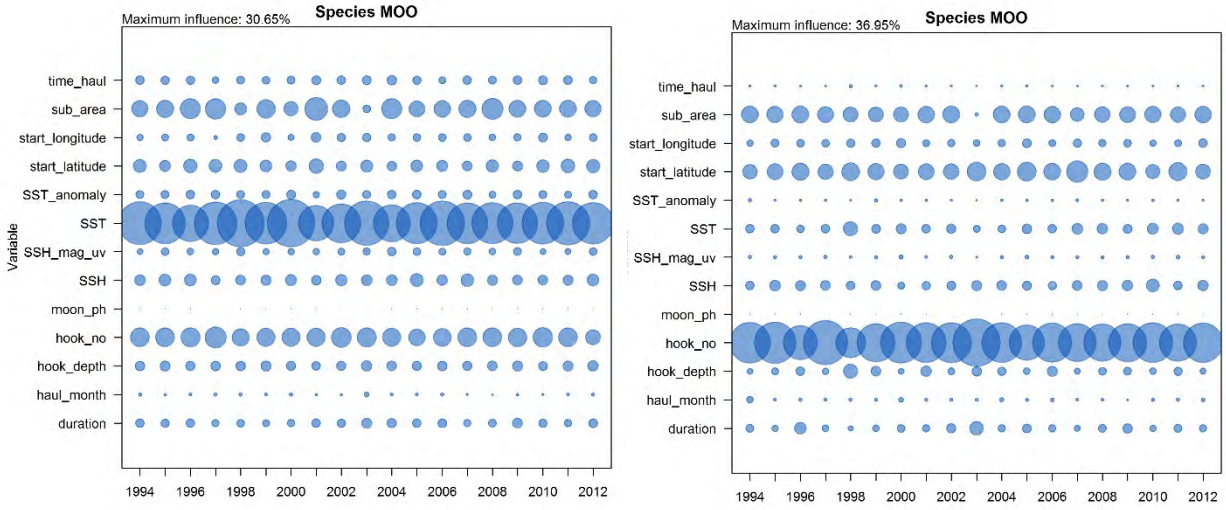


Figure 163: Relative influence of variables in MOO Binomial (left) and Poisson (right) models.

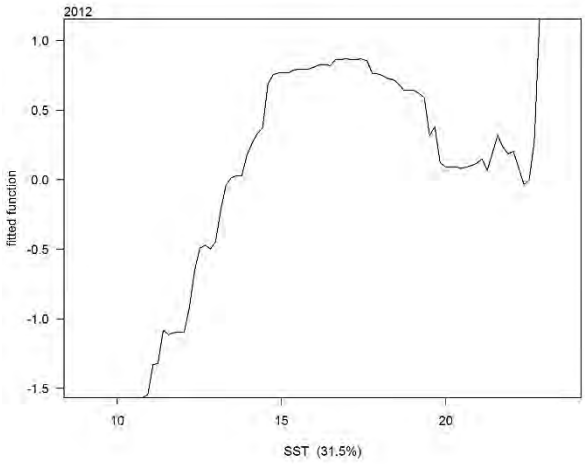


Figure 164: Variable effect of sea surface temperature in the MOO 2012 Binomial model.

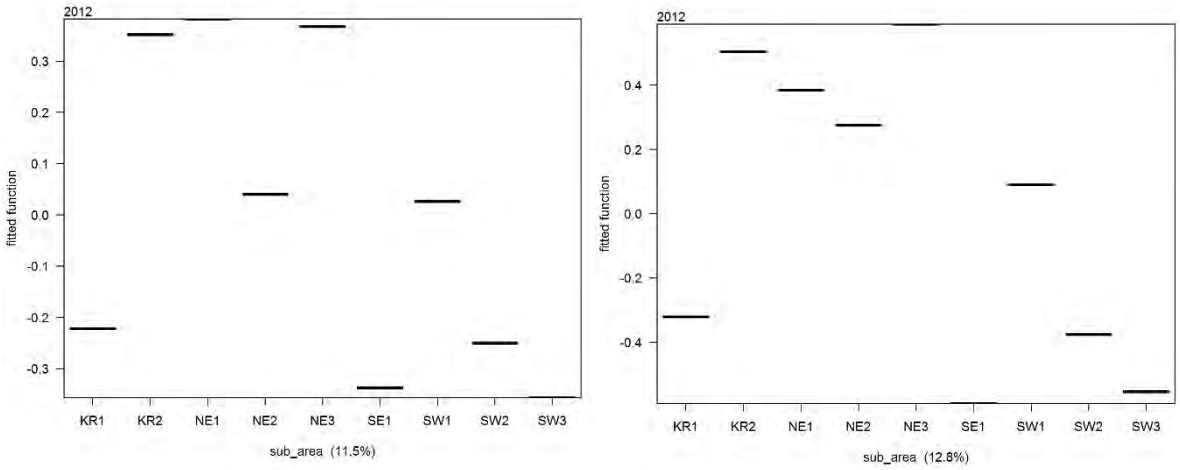


Figure 165: Variable effect of subarea in the MOO 2012 Binomial model (left) and MOO 2012 Poisson model (right).

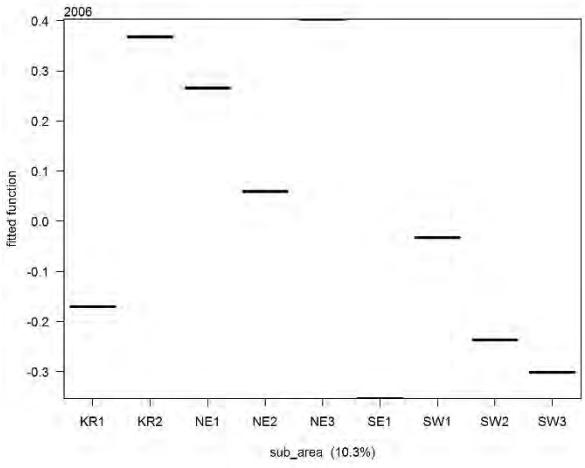


Figure 166: Variable effect of subarea in the MOO 2006 Binomial model.

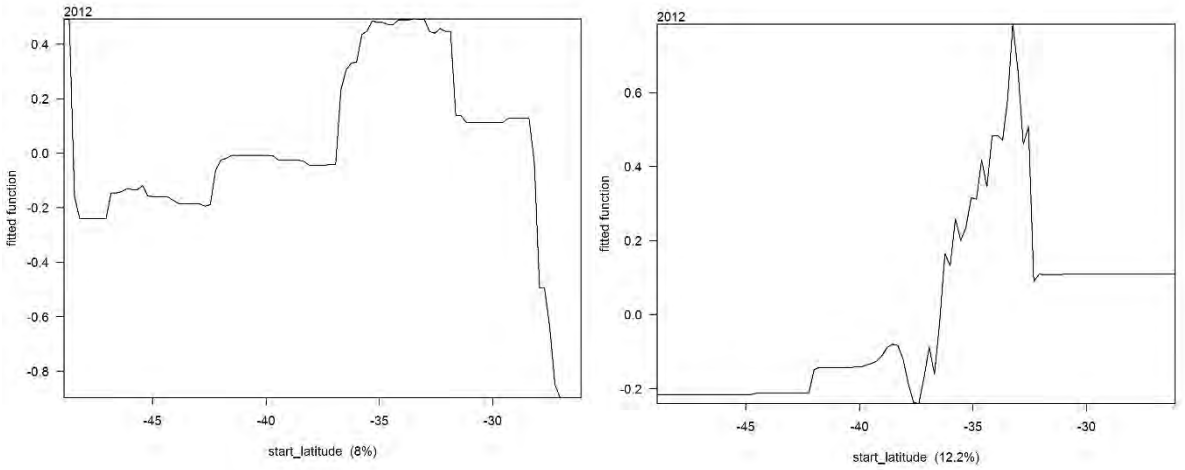


Figure 167: Variable effect of start latitude in the MOO 2012 Binomial model (left) and MOO 2012 Poisson model (right).

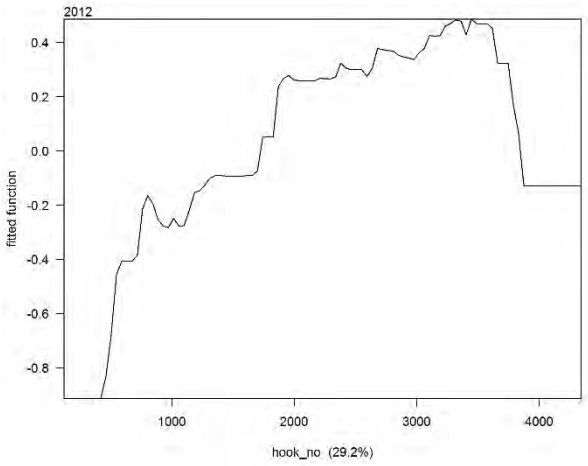


Figure 168: Variable effect of hook number in the MOO 2012 Poisson model.

4.8 POS

Sea surface temperature was the most influential variable for the Binomial models, followed by subarea. The Poisson models had start latitude as the most influential variable, followed by sea surface temperature and sea surface height (Figure 169).

The sea surface temperature effect from the Binomial and Poisson models suggested that POS were most likely to be present, and caught in higher numbers, when the sea surface temperature was less than 17^{o}C (Figure 170).

The variable effect of subarea in the Binomial models suggested that POS were most likely to be present in subareas NE2, NE3 and SE1 and least likely in subareas KR1, KR2 and NE1 (Figure 171). The start latitude effect in the Poisson models suggests POS were in greatest numbers south of -35^{o} latitude (Figure 172). This corresponds with POS being less likely in subareas KR1, KR2 and NE1, but doesn't differentiate between the west subareas SW1, SW2 and SW3 and the east subareas NE2, NE3 and SE1 as the Binomial models did.

The sea surface height effect in the Poisson models suggested that POS were caught in smaller numbers when the sea surface height was around 50 cm (Figure 173).

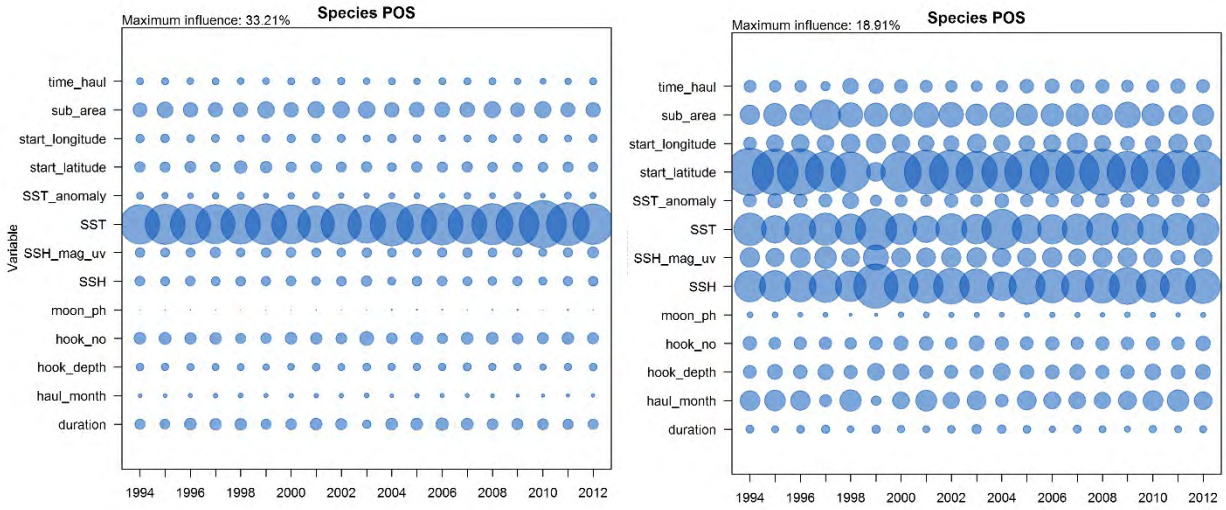


Figure 169: Relative influence of variables in POS Binomial (left) and Poisson (right) models.

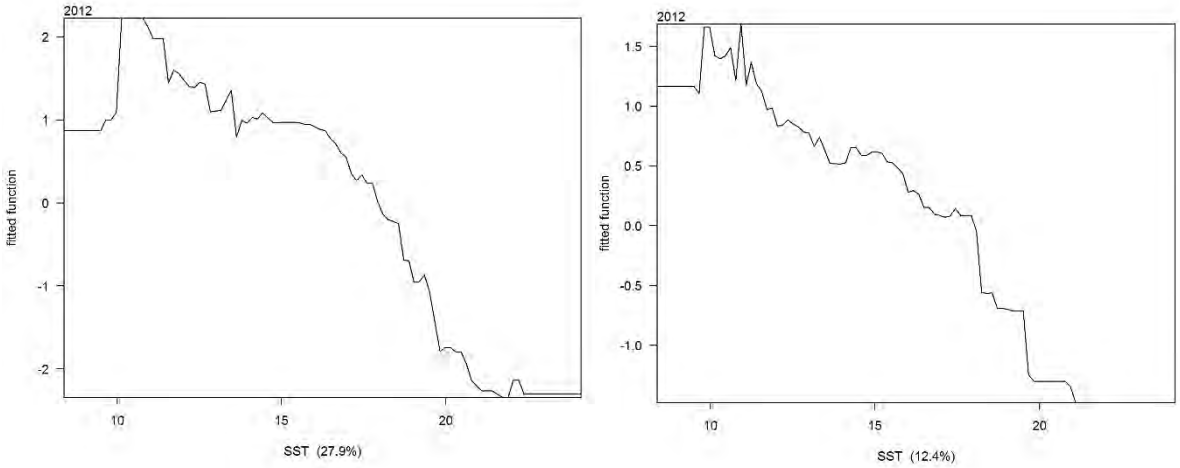


Figure 170: Variable effect of start latitude in the POS 2012 Binomial model (left) and POS 2012 Poisson model (right).

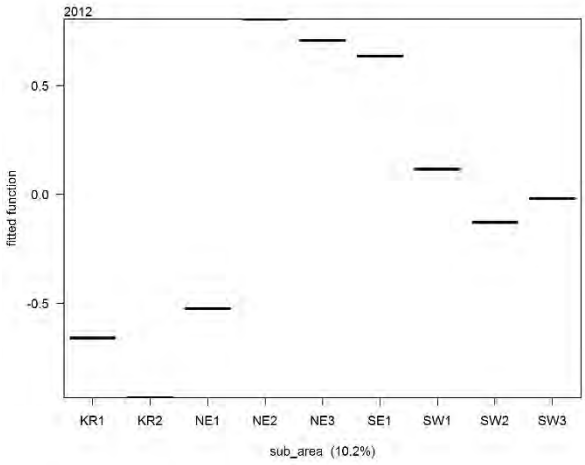


Figure 171: Variable effect of subarea in the POS 2012 Binomial model.

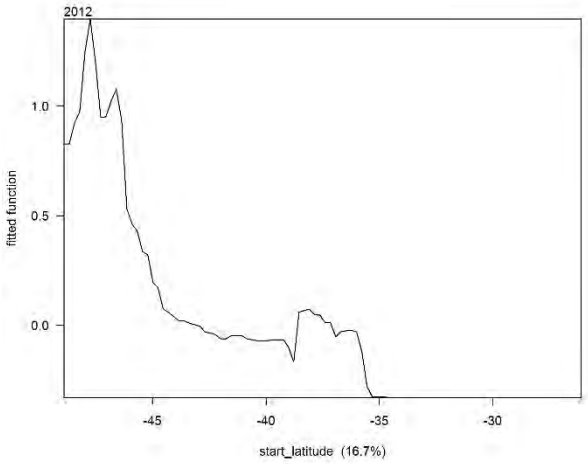


Figure 172: Variable effect of start latitude in the POS 2012 Poisson model.

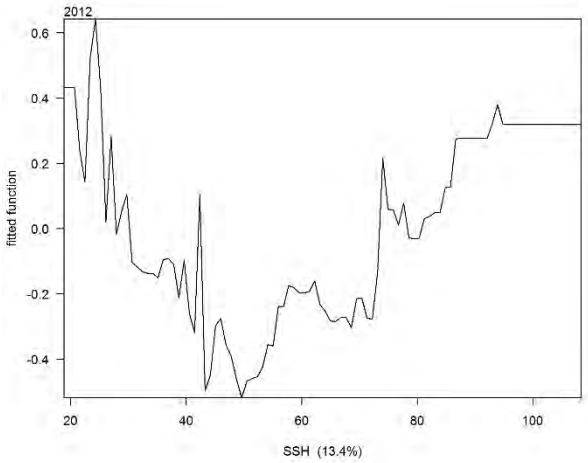


Figure 173: Variable effect of sea surface height in the POS 2012 Poisson model.

4.9 RBM

Sea surface temperature and start latitude were the most influential variables in the Binomial models. Hook depth, then start latitude and start longitude were the most influential variables in the Poisson models (Figure 174).

The variable effect of start latitude in the Binomial and Poisson models suggested that RBM were least likely to be caught around -40^{o} to -32^{o} latitude (Figure 175).

The variable effect of sea surface temperature in the Binomial and Poisson models suggested that RBM were most likely to be caught when the sea surface temperature was less than around 19^{o}C (Figure 176).

The variable effect of hook depth in the Poisson models was quite jagged, but suggested that the numbers of RBM caught were generally highest when the hook depth was 80–150 m (Figure 177).

The variable effect of start longitude in the Poisson models suggested that RBM were caught in higher numbers west of around 172^{o} longitude (Figure 178).

The variable effect of hook depth in the Poisson models suggested that the number caught increased when the hook depth was 50–150 m (Figure 177).

The variable effect of start longitude in the Poisson models was jagged, but suggested that RBM were least likely to be caught east of about 172° longitude and at around 168° longitude (Figure 178).

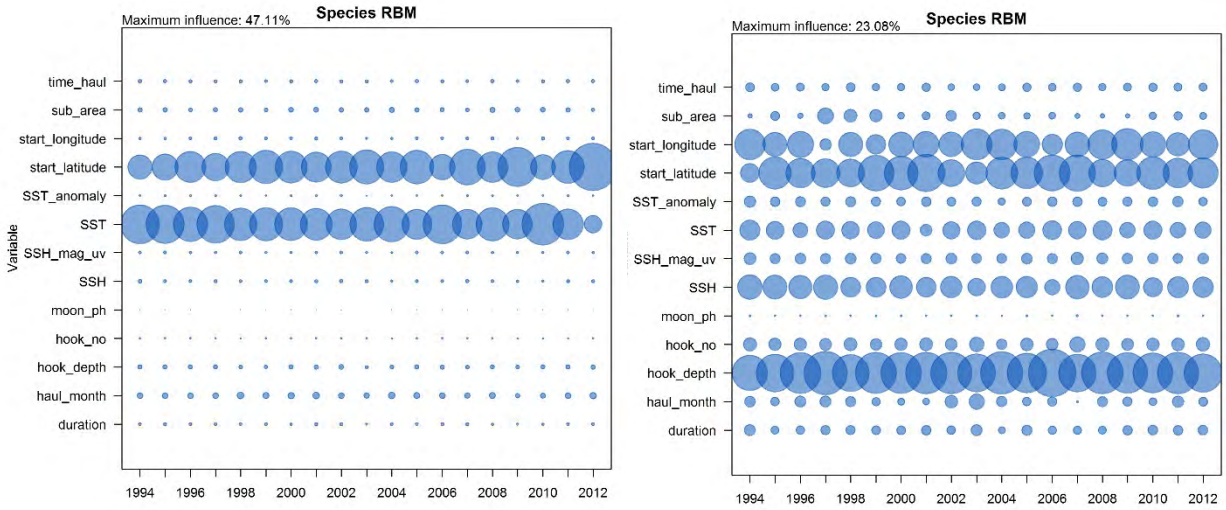


Figure 174: Relative influence of variables in RBM Binomial (left) and Poisson (right) models.

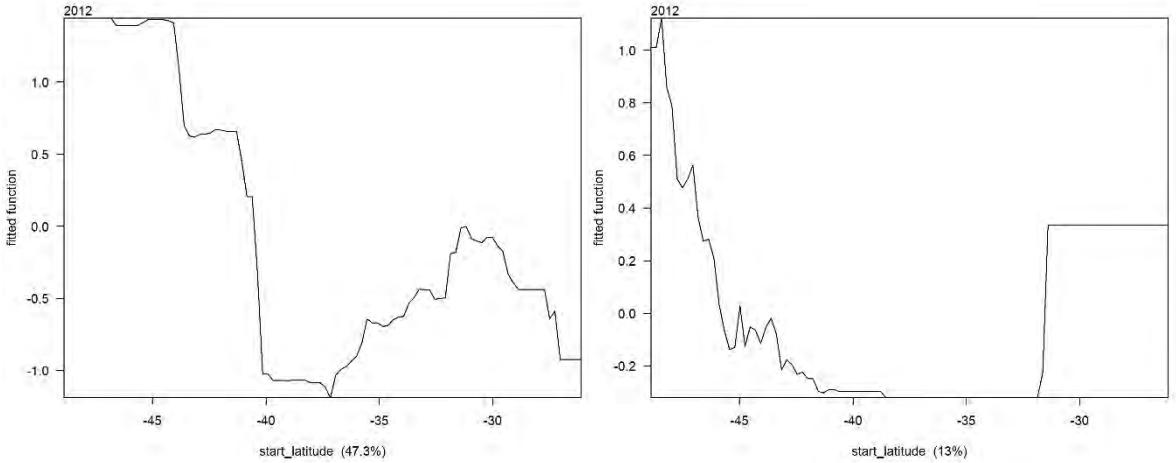


Figure 175: Variable effect of start latitude in the RBM 2012 Binomial model (left) and RBM 2012 Poisson model (right).

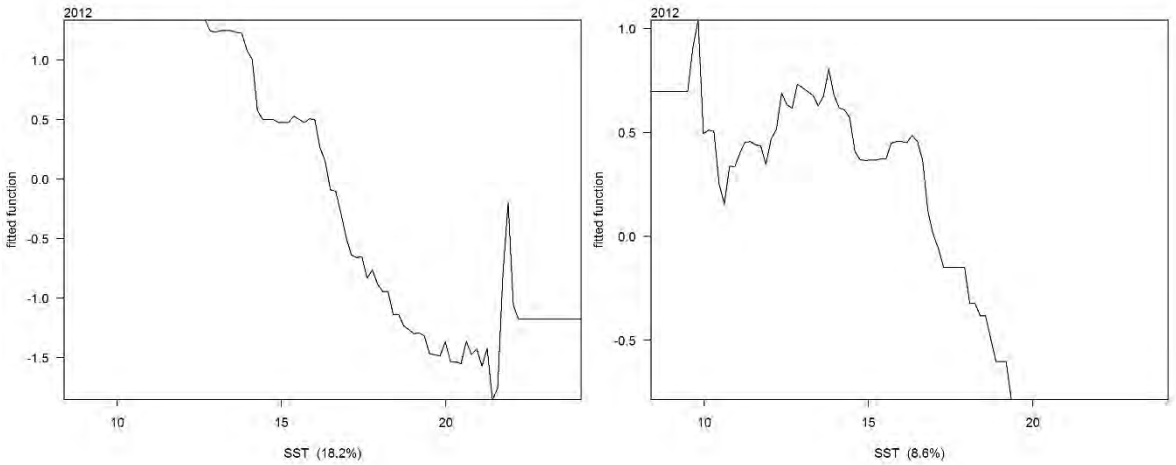


Figure 176: Variable effect of sea surface temperature in the RBM 2012 Binomial model (left) and RBM 2012 Poisson model (right).

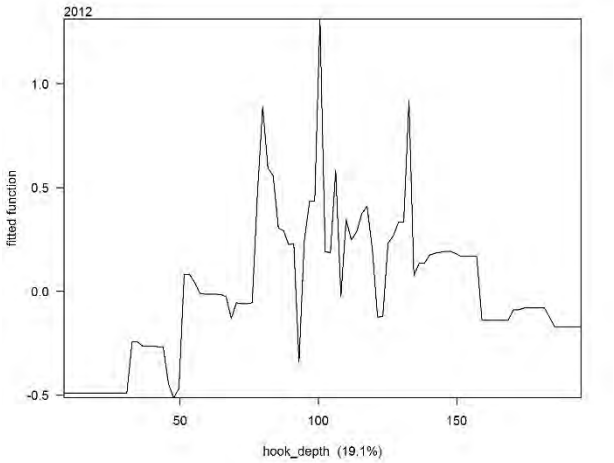


Figure 177: Variable effect of hook depth in the RBM 2012 Poisson model.

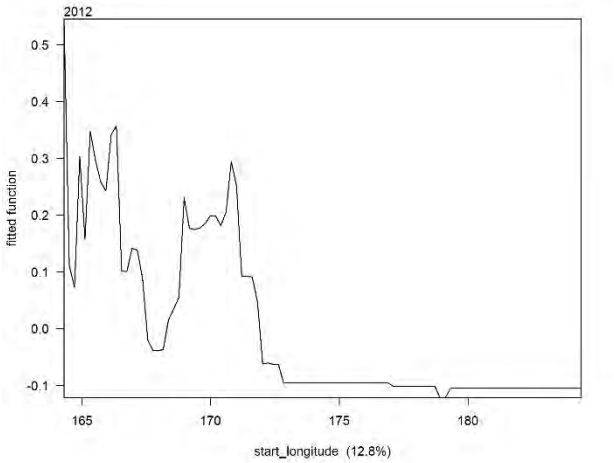


Figure 178: Variable effect of start longitude in the RBM 2012 Poisson model.

4.10 STN

Sea surface temperature was by far the biggest contributor in terms of relative influence in the Binomial models (Figure 179). Start latitude was the second most influential variable in the Binomial models. The Poisson models were influenced most by sea surface temperature, hook number, hook depth and start longitude (Figure 179).

The sea surface temperature effect of the Binomial models and Poisson models suggested that STN were most likely when the sea surface temperature was less than about 19^{o}C (Figure 180).

The start latitude effect of the Binomial models and Poisson models suggested that STN were most likely south of about -35^{o} latitude (Figure 181).

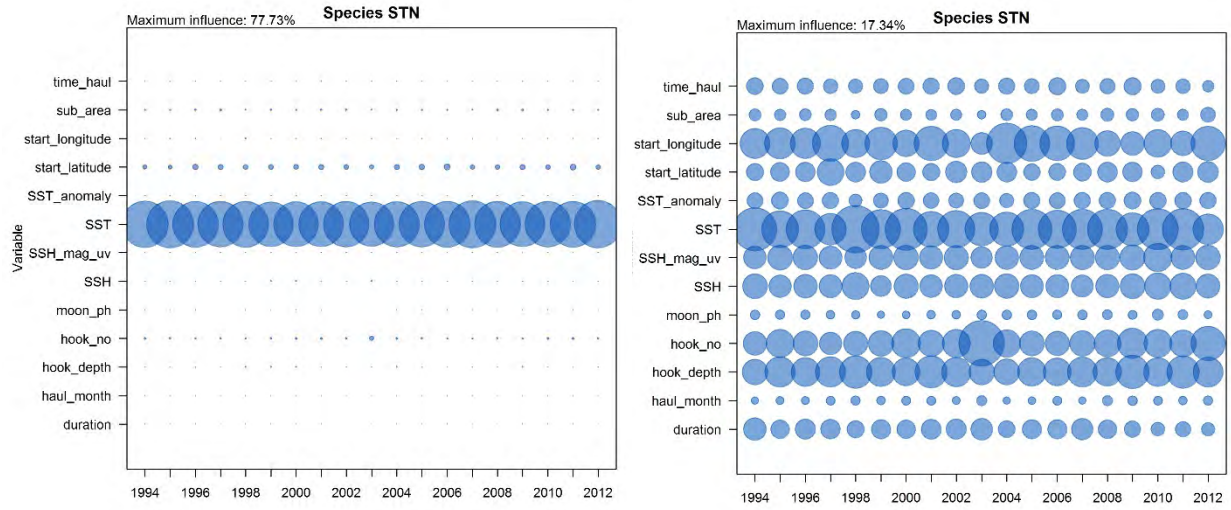


Figure 179: Relative influence of variables in STN Binomial (left) and Poisson (right) models.

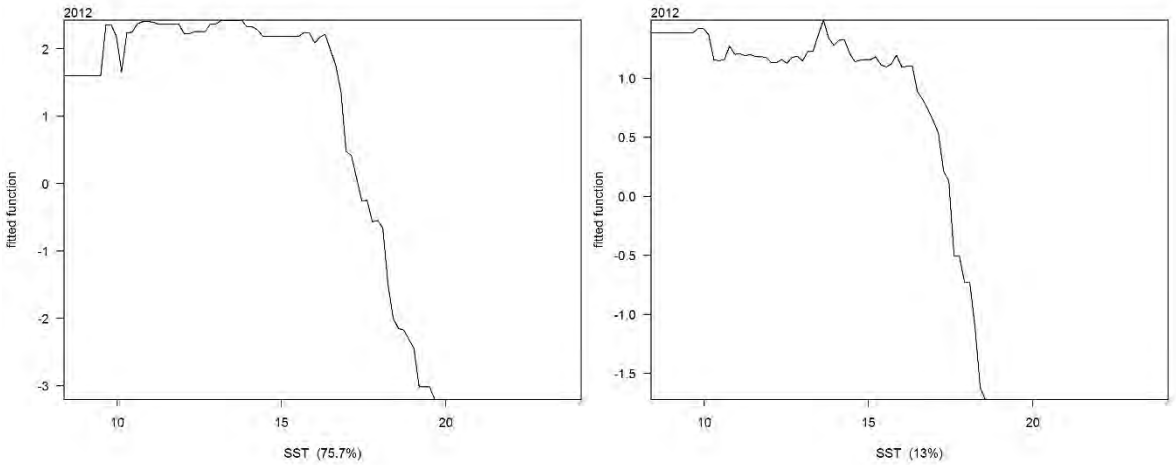


Figure 180: Variable effect of sea surface temperature in the STN 2012 Binomial model (left) and RBM 2012 Poisson model (right).

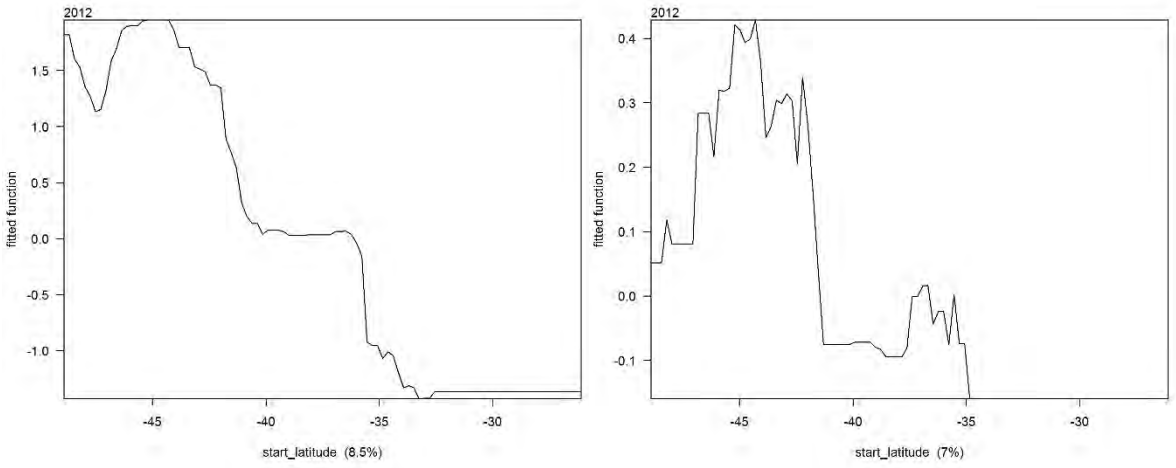


Figure 181: Variable effect of start latitude in the STN 2012 Binomial model (left) and STN 2012 Poisson model (right).

4.11 SWO

Subarea, sea surface temperature and start latitude were the most influential variables for the Binomial models (Figure 182). Time haul, sea surface temperature and start latitude were the most influential variables in the Poisson models (Figure 182).

The sea surface temperature effect in the Binomial and Poisson models suggested that SWO were most likely to be caught when the sea surface temperature was greater than about 14^{o}C (Figure 183).

The start latitude effect in the Binomial and Poisson models suggested that SWO were most likely north of -42^{o} latitude (Figure 181).

The subarea effect in the Binomial models suggested SWO were most likely to be caught in subareas KR2, NE1, NE2 and NE3 (Figure 185).

The time haul effect in the Poisson models suggested that the numbers of SWO caught decreased throughout the day (Figure 186).

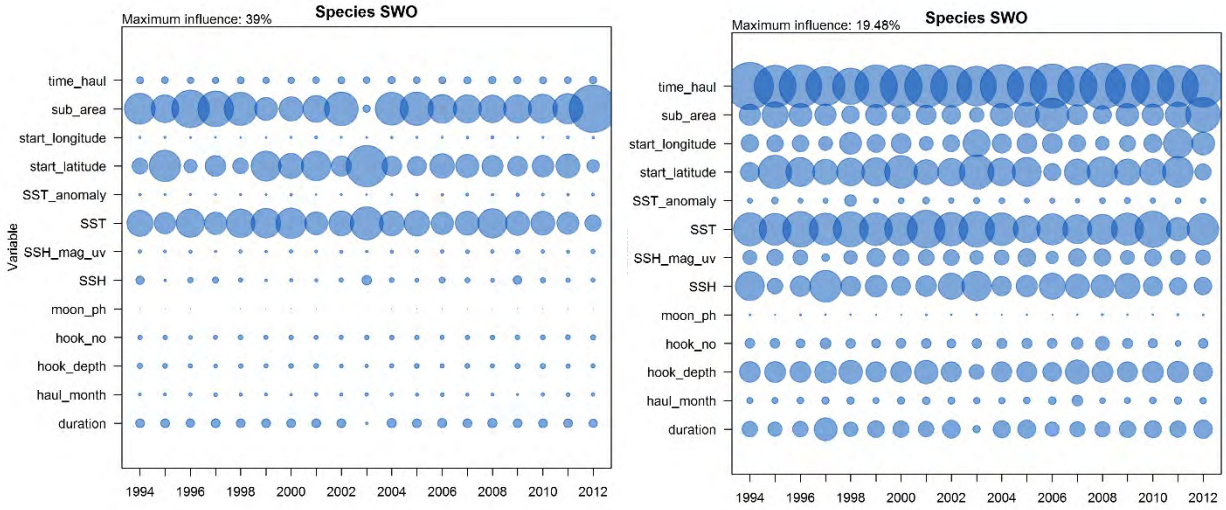


Figure 182: Relative influence of variables in SWO Binomial (left) and Poisson (right) models.

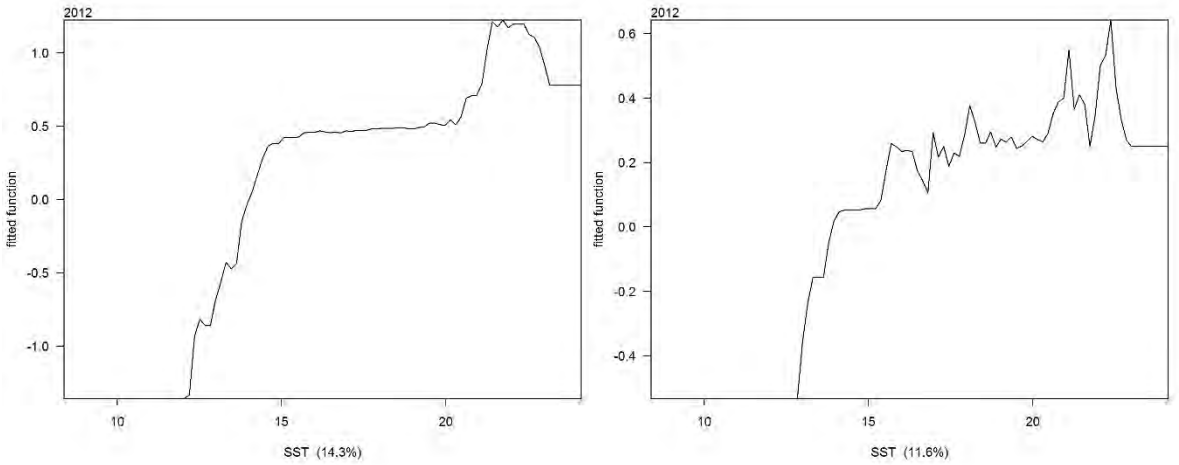


Figure 183: Variable effect of sea surface temperature in the SWO 2012 Binomial model (left) and SOW 2012 Poisson model (right).

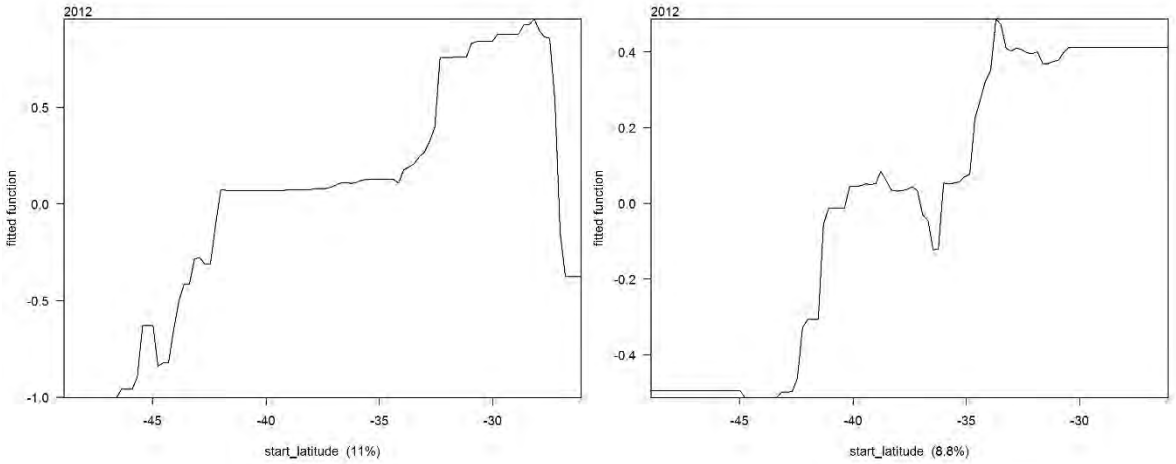


Figure 184: Variable effect of start latitude in the SWO 2012 Binomial model (left) and SOW 2012 Poisson model (right).

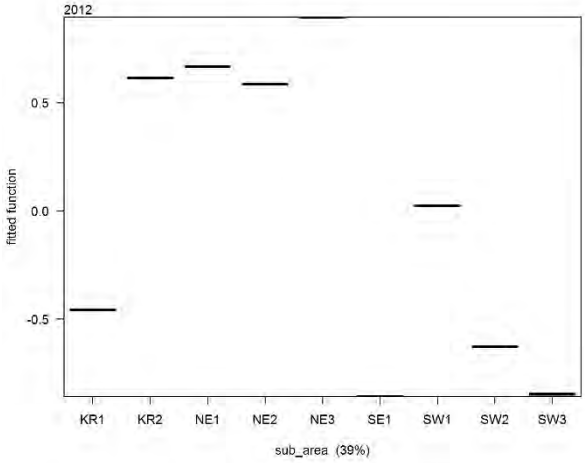


Figure 185: Variable effect of subarea in the SWO 2012 Binomial model.

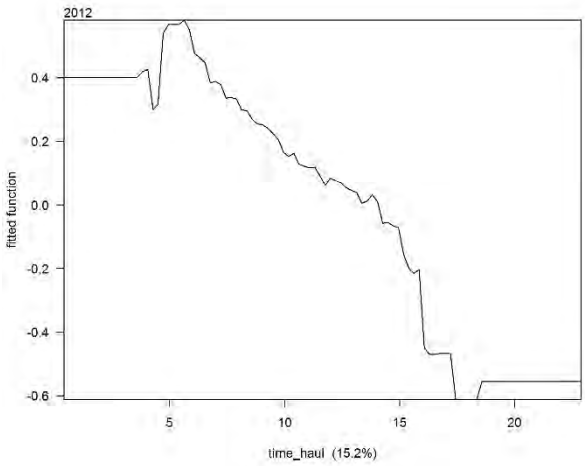


Figure 186: Variable effect of subarea in the SWO 2012 Poisson model.

4.12 YFN

Sea surface temperature was the most influential variable for the Binomial models followed by start latitude (Figure 187). Start latitude was the most influential variable for the Poisson models, followed by subarea then sea surface temperature (Figure 187).

The sea surface temperature effect in the Binomial and Poisson models suggested that YFN were most likely when the sea surface temperature was greater than about 17°C (Figure 188).

The start latitude effect in the Binomial and Poisson models suggested that YFN were most likely north of about -32° latitude (Figure 189).

The subarea effect in the Poisson models suggested that YFN were most likely to be caught in subareas KR2 and KR1 (Figure 190).

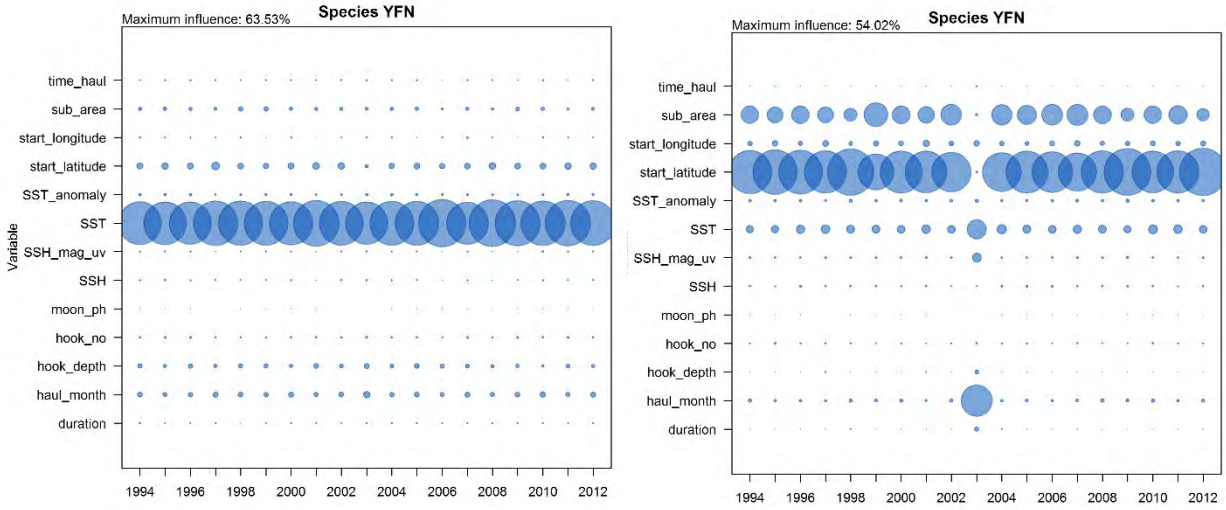


Figure 187: Relative influence of variables in YFN Binomial (left) and Poisson (right) models.

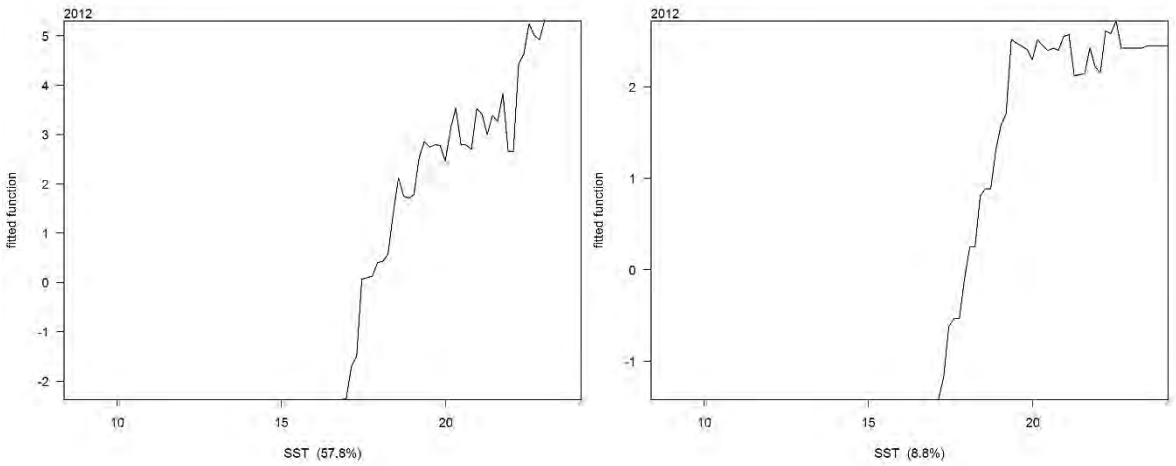


Figure 188: Variable effect of sea surface temperature in the YFN 2012 Binomial model (left) and YFN 2012 Poisson model (right).

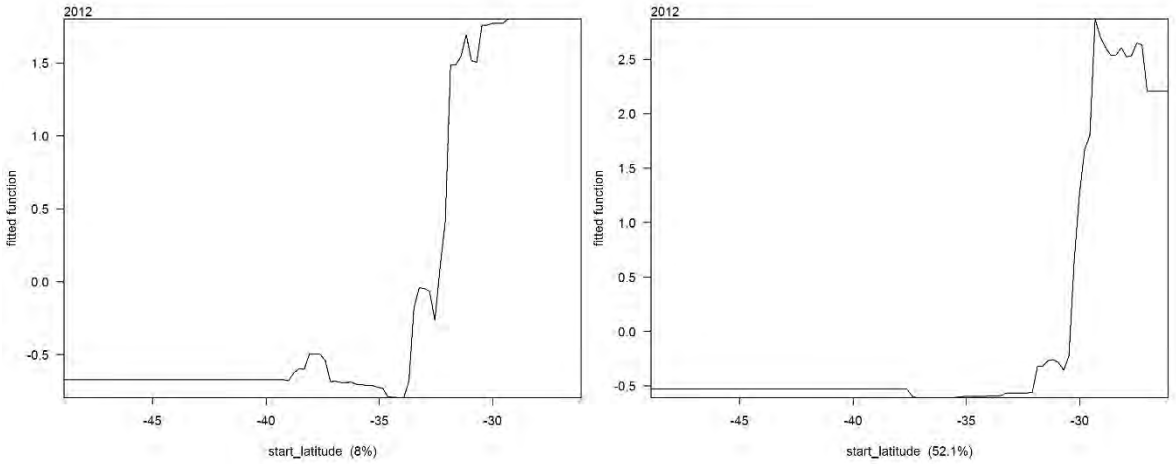


Figure 189: Variable effect of sea surface temperature in the YFN 2012 Binomial model (left) and YFN 2012 Poisson model (right).

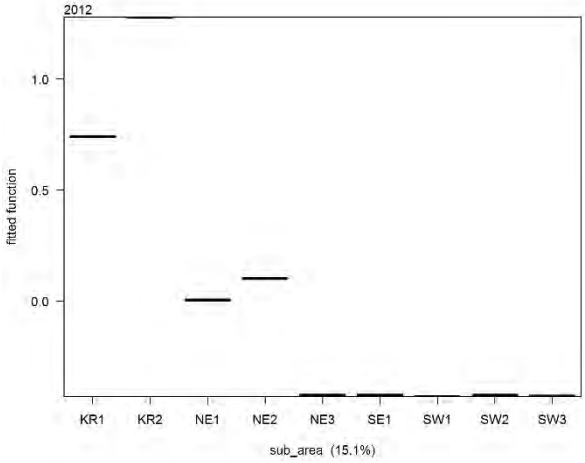


Figure 190: Variable effect of subarea in the YFN 2012 Poisson model.

5. DISCUSSION

It has often been suggested that the schooling and migration of large pelagic fishes, primarily tunas, is related to environmental cues, particularly water temperature (e.g., Humston et al. 2000), and often to the presence of thermal fronts (e.g., Lutcavage et al. 2000). However, some studies suggest that temperature is not a determining factor in the distribution of tuna, and that areas of high biological productivity are more important (De Anda-Montañez et al. 2004). In addition, parameters such as the levels of chlorophyll-*a* and dissolved oxygen, and distance from thermal fronts have also been found to explain much of the variation in distribution and abundance of these species (e.g., Schick et al. 2004, Song & Zhou 2010). For large sharks, spatial and temporal factors were generally the most influential on distribution and abundance (e.g., Carvalho et al. 2011), and while temperature at depth could be a significant modifier of catch rate, SST was a poor predictor (Campana& Joyce 2004).

For the current work, temporal and spatial variables were available, as was sea surface temperature. However, temperature at capture depth, chlorophyll-*a*, dissolved oxygen, and distance from a thermal front were not available. Consequently, the conclusions drawn from these analyses probably comprise an incomplete explanation of what influences the species distributions. For example, available

variables like sea surface temperature or latitude could be acting as proxies for water temperature at capture depth as there is likely to be reasonable correlation between them. So although a spatial variable (e.g., latitude) may provide the greatest predictive power, the variable that is actually paramount may be an environmental one (e.g., temperature at capture depth). Determining the factors that truly influence distribution and abundance is clearly a complex process.

Generally the Binomial models had greater predictive power than the Poisson models. The Binomial models only needed to predict the probability a species was present for each data point. The Poisson models needed to predict not only presence, but also the number caught for each data point.

The species that generally had less than 100 presences per year (ABR, BIG and YFN) had the least predictive power in the Poisson models, and in the case of ABR, in the Binomial models as well. These three species were all caught from around the North Island (Figur) and they had low numbers caught in each year (Figure A2). Species BTU and LAT also had fairly low numbers of presences (generally less than 150 per year (Figure)), and BTU had low numbers caught (Figure A2), but the spatial distribution of presences for both these species extended to around both North and South Islands (Figur), and the predictive power of the Poisson models for these species was much better than that of ABR, BIG and YFN. It seems that the combination of low numbers of presences, low numbers caught, and the limited spatial distribution of the presences contributed to the poor predictive power of the Poisson models.

The models with best predictive power across both model types were the Binomial models for species ALB, BIG, BTU and LAT. BIG was interesting as it had a small number of presences in each year, small numbers caught in each year, more limited spatial distribution than most other species, and was one of the poorest performers in terms of predictive power in the Poisson models, yet its Binomial model had relatively good predictive power. In contrast, ALB was one of the biggest datasets in numbers of presences and numbers caught, extensive spatial distribution (Figures Figure , Figure A2 and Figur) and fair predictive power in the Poisson models.

The predictive power of the models was vulnerable to shifts in the data to a new area. This was evident when predicting the 2003 data which had a lot more data in subarea KR1 than any of the other years. Many of the models had difficulty predicting presence/absence or number caught in subarea KR1 in 2003. This area effect was evident here as the predictive performances were analysed in terms of the spatial distributions. It is likely that the predictive power of these models is also sensitive to shifts in the data with respect to any of the main influential variables, such as sea surface temperature start latitude, or month. It is therefore recommended that the models are only used for predictions where the influential variables fall within the ranges of those the models have been fitted to.

The Binomial models were more consistent in terms of most influential variables, as these models were only fitting to where the fish were, not how many there were. The Poisson models required influence from variables to determine where the fish were, and also what quantities they were in.

In the Binomial models, the variables contributing to most of the influence were fairly consistent and generally included sea surface temperature, start latitude and subarea. Hook number also contributed in the MOO and POS Binomial models, and sea surface height in the LAT Binomial models.

The Poisson models tended to have more variables influencing the models, and the order of the variables in terms of relative influence varied a lot between species. The influence of the variables did not vary for the models within any one species. Hence, the variables selected for each species are helpful, but it is not as clear what the effects are when there are so many influencing the model.

In the Binomial and Poisson models the variable effects were generally consistent for all models for each species. The 2003 model was sometimes an exception, highlighting the concern in using these models to predict outside their fitted range.

A limitation of these models is that they lack a run where only the main variables are offered as predictors. It is possible that the predictive ability of these models would be almost as good as the full models, and the effects of the variable may be clearer, as well as establishing whether the minor variables are required.

6. ACKNOWLEDGMENTS

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APPENDIX A: Fishery data

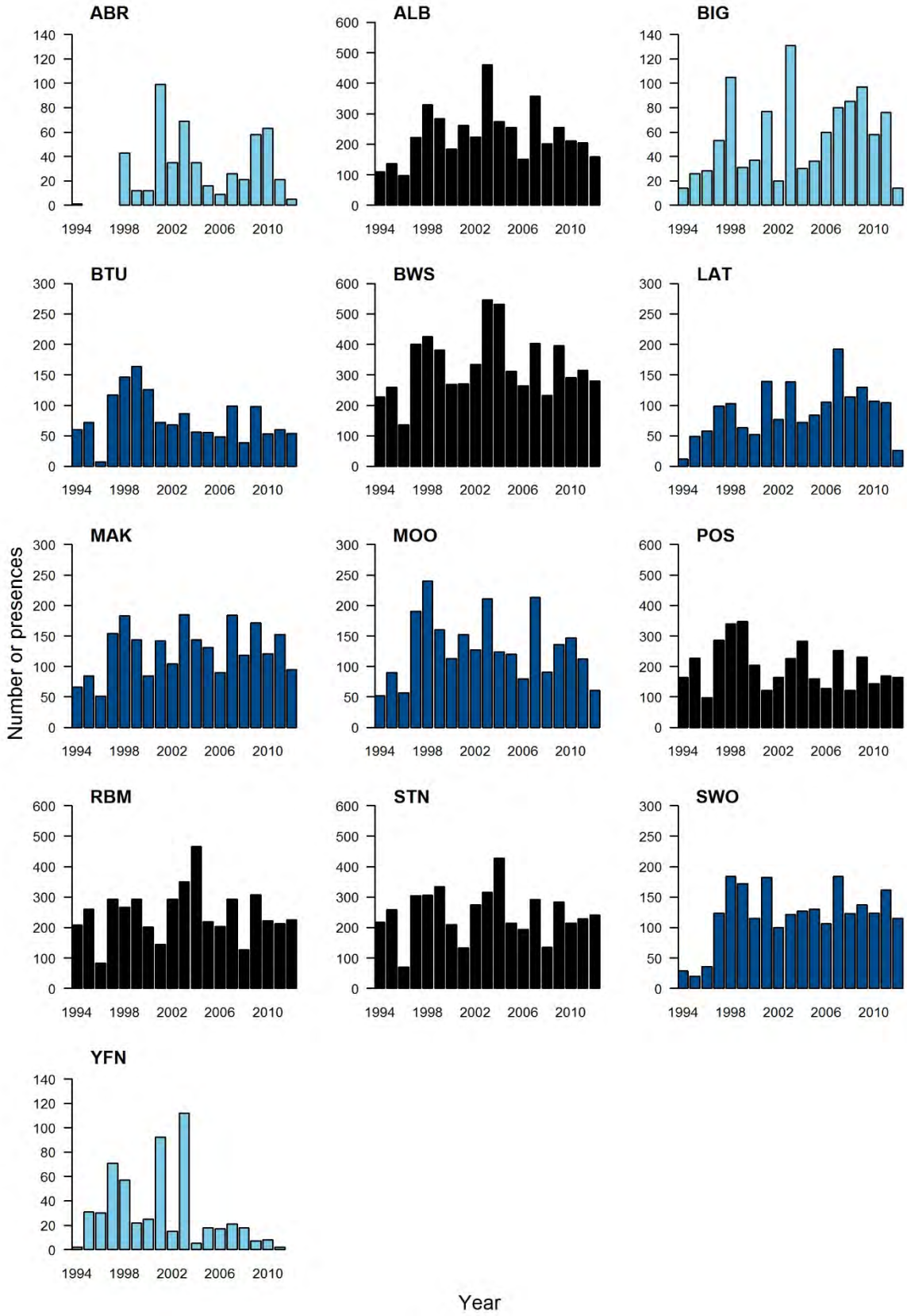

Figure A1: Number of presences by year for each species.

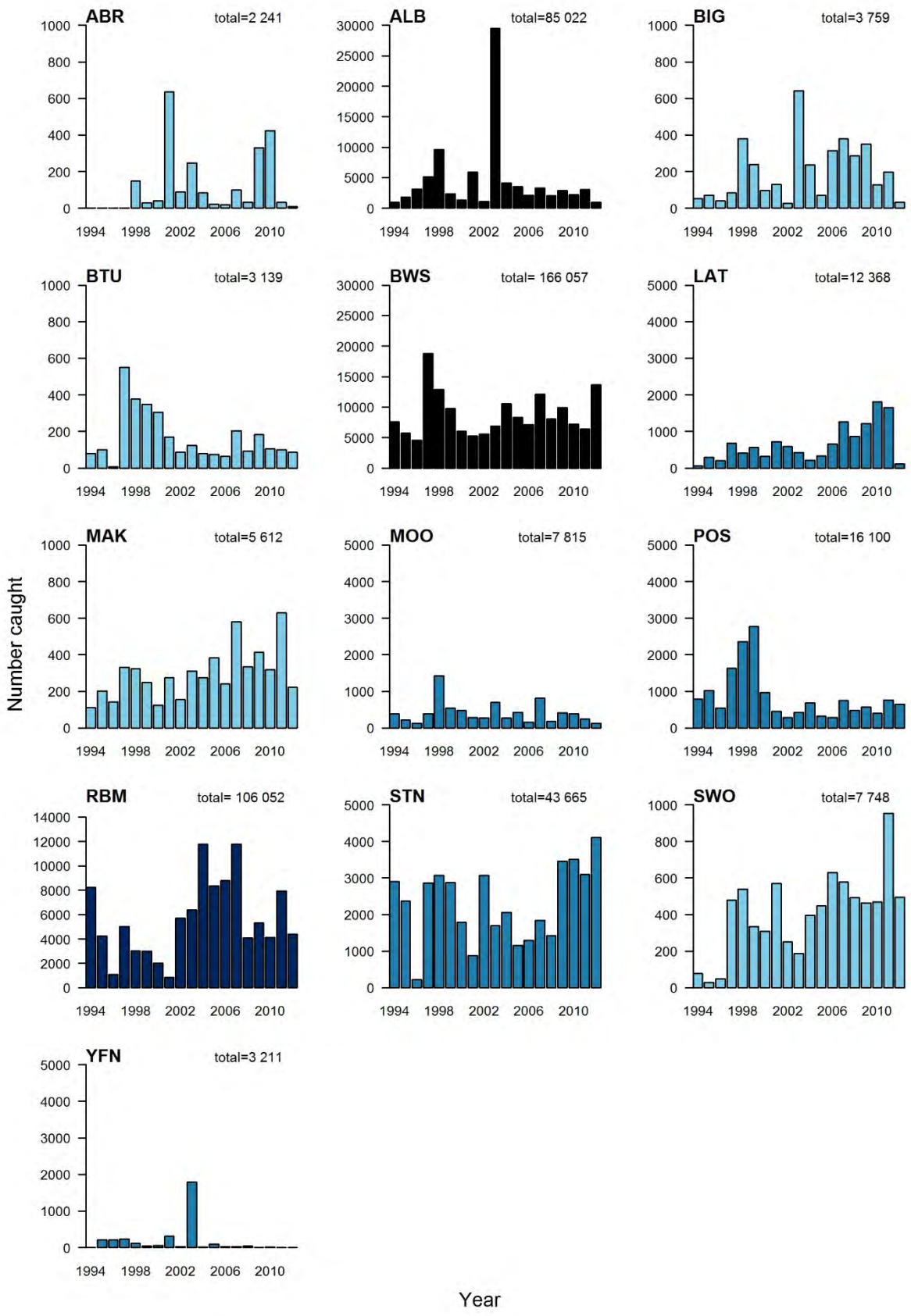

Figure A2: Number of fish caught by year for each species.

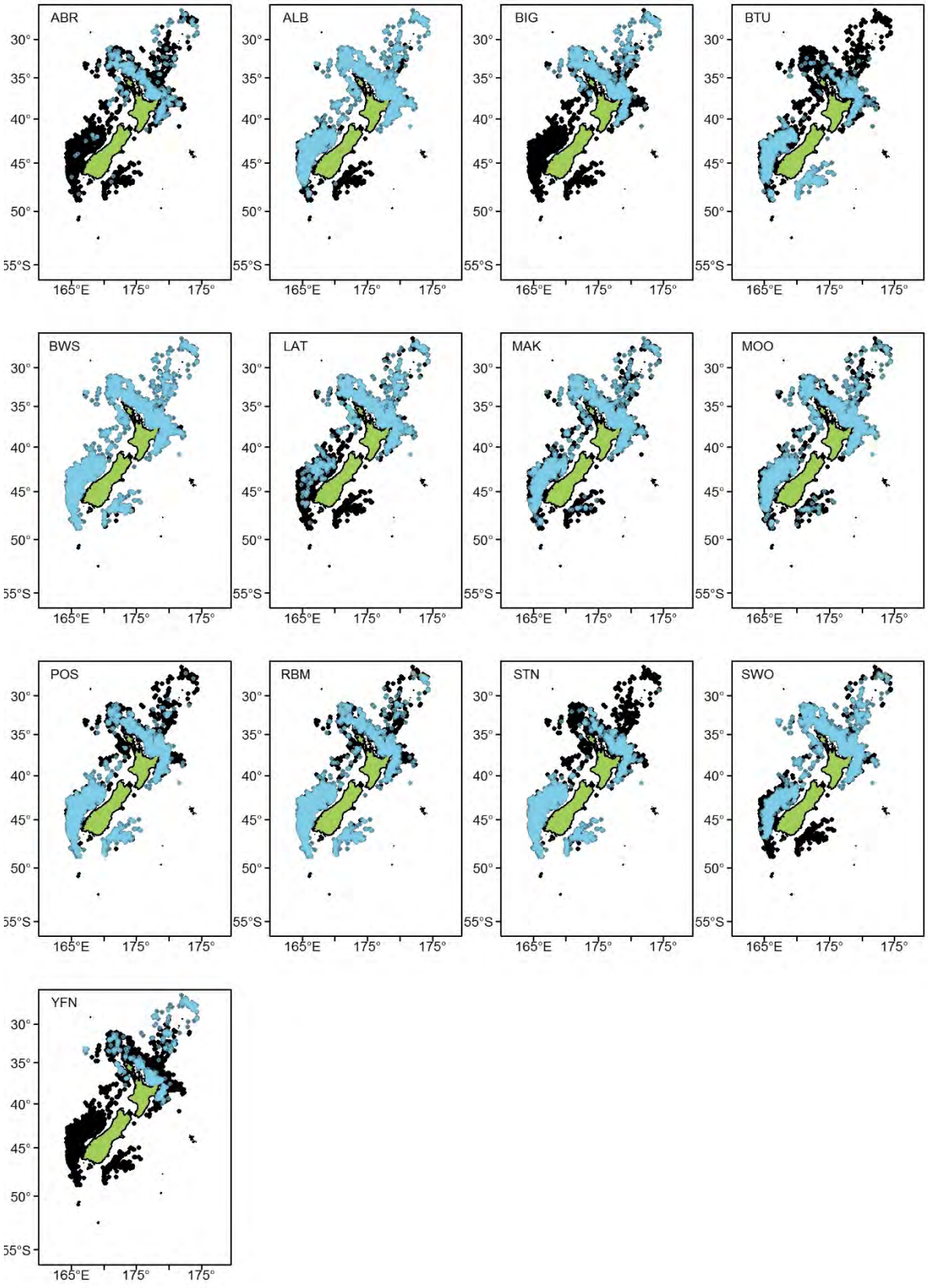

Figure A3: Spatial distribution of presences for each species for years 1994–2012. Black dots are the set positions of all longline sets, blue dots are the set positions of the longline sets that caught each species.

APPENDIX B: Variable effects

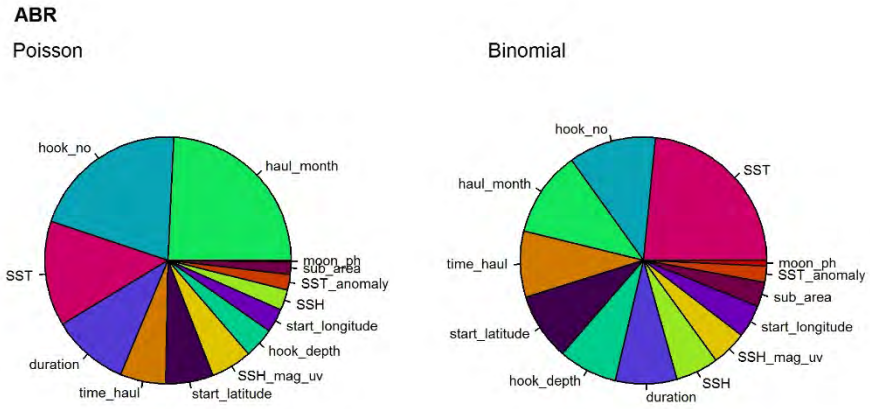

Figure B1: Mean influence of each variable for ABR Poisson (left) and Binomial (right) models.

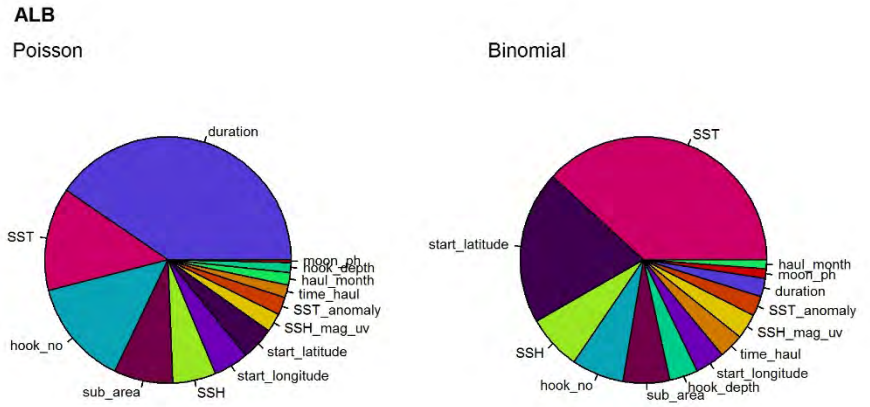

Figure B2: Mean influence of each variable for ALB Poisson (left) and Binomial (right) models.

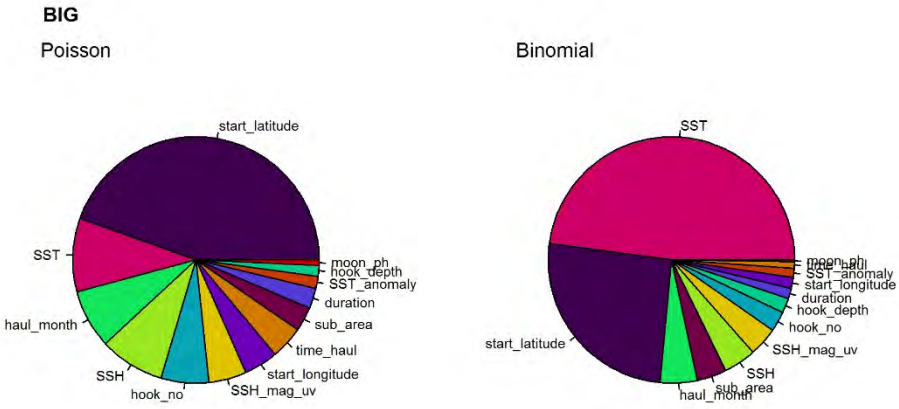

Figure B3: Mean influence of each variable for BIG Poisson (left) and Binomial (right) models.

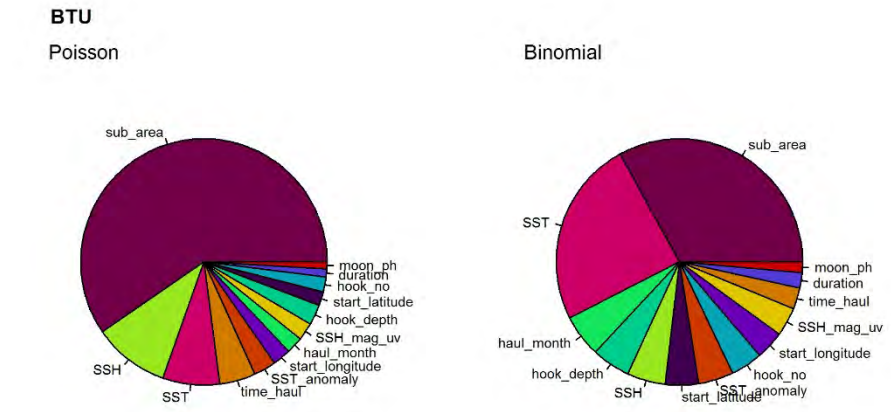

Figure B4: Mean influence of each variable for BTU Poisson (left) and Binomial (right) models.

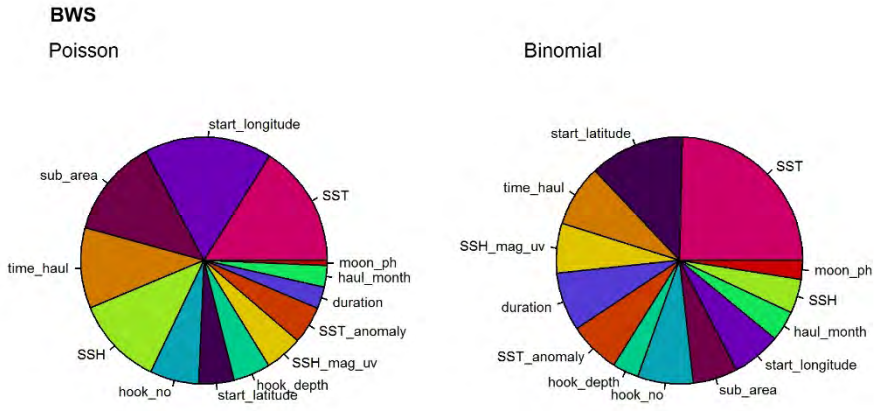

Figure B5: Mean influence of each variable for BWS Poisson (left) and Binomial (right) models.

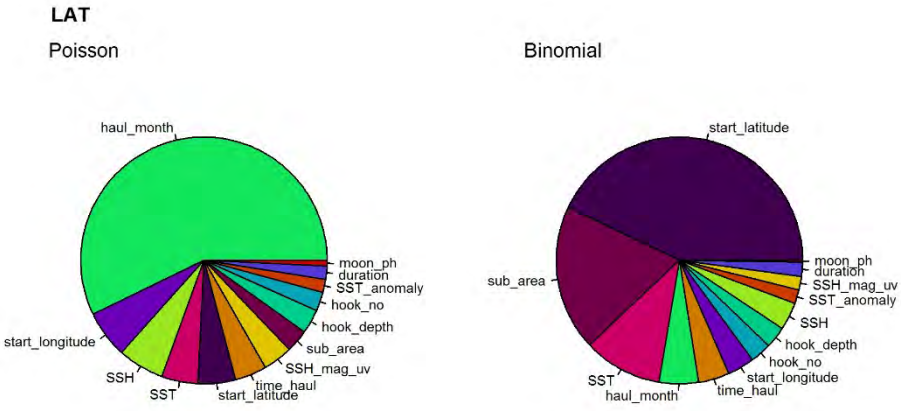

Figure B6: Mean influence of each variable for LAT Poisson (left) and Binomial (right) models.

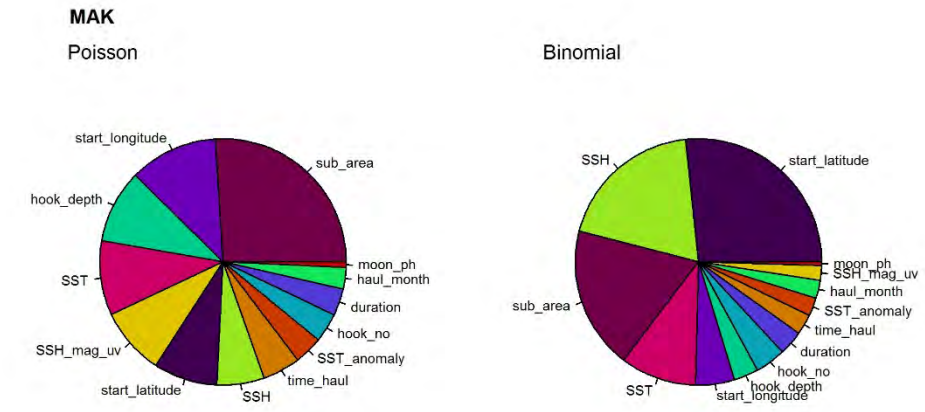

Figure B7: Mean influence of each variable for MAK Poisson (left) and Binomial (right) models.

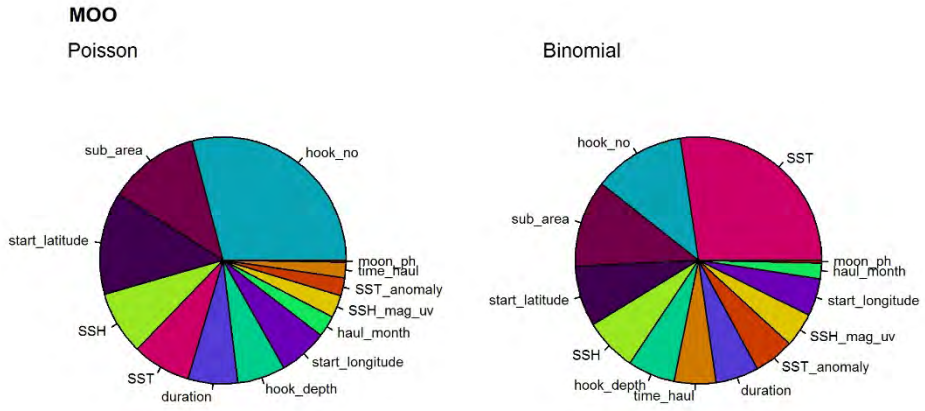

Figure B8: Mean influence of each variable for MOO Poisson (left) and Binomial (right) models.

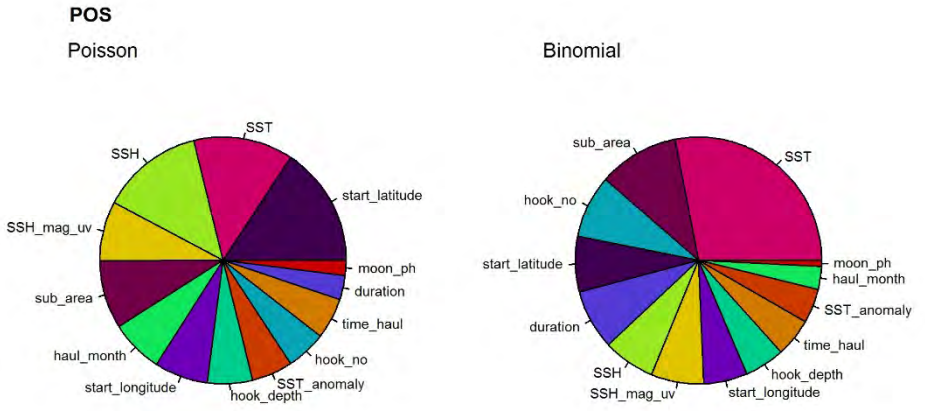

Figure B9: Mean influence of each variable for POS Poisson (left) and Binomial (right) models.

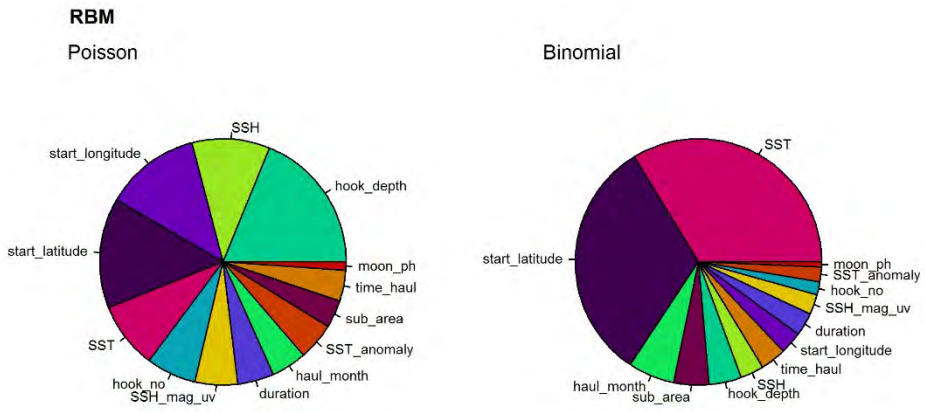

Figure B10: Mean influence of each variable for RBM Poisson (left) and Binomial (right) models.

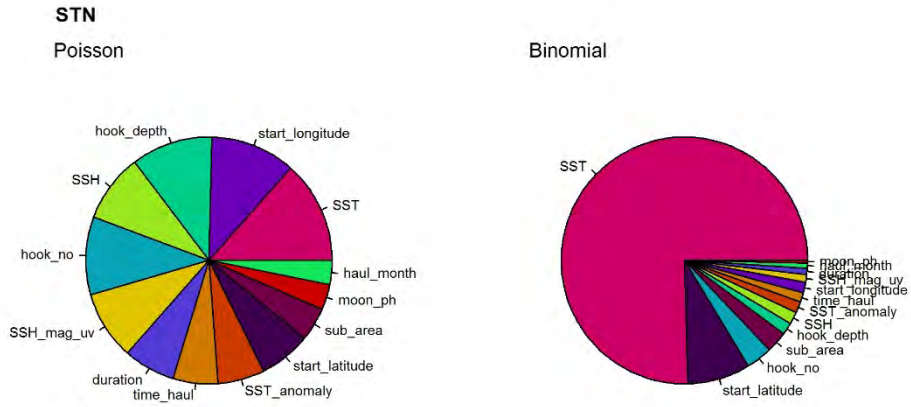

Figure B11: Mean influence of each variable for STN Poisson (left) and Binomial (right) models.

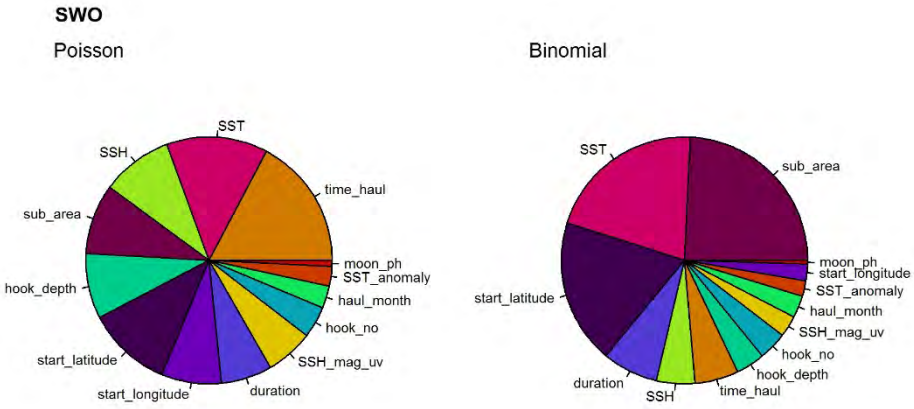

Figure B12: Mean influence of each variable for SWO Poisson (left) and Binomial (right) models.

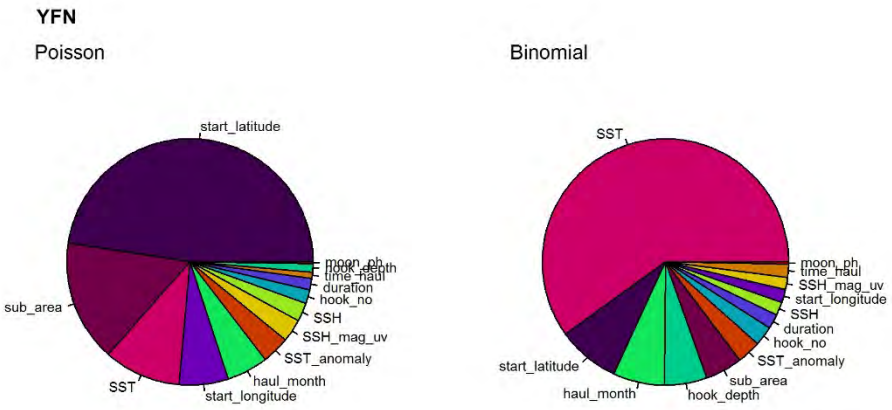

Figure B13: Mean influence of each variable for YFN Poisson (left) and Binomial (right) models.