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Assessment of the SNA 1 stocks in 2012

New Zealand Fisheries Assessment Report 2015/75

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EXECUTIVE SUMMARY

Francis, R.I.C.C.; McKenzie, J.R. (2015). Assessment of the SNA 1 stocks in 2012

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Snapper (*Pagrus auratus*) is New Zealand's most valuable commercial coastal marine species and, by virtue of its high abundance around the populous regions of northern New Zealand, it is also the nation's most important recreational species.

This report documents the stock assessment modelling carried out for SNA 1 during 2012. This modelling was useful in exploring the interactions between the fisheries and the complex stock structure in this area but did not produce results that were sufficiently robust to be useful for management of this stock.

The base model started in 1970 and described 20 fisheries acting on three fish stocks, with annual migrations between three areas (east Northland, Hauraki Gulf, and Bay of Plenty). This model was fitted to five types of observation: absolute biomass (from the 1984 Bay of Plenty tagging experiment); relative biomass (from longline and trawl catch per unit effort, CPUE); age compositions from commercial fisheries and research surveys; length compositions from recreational fisheries; and recaptures from tagging experiments in 1984 and 1993. The 142 parameters estimated for this model described the unfished size, initial depletion, and year-class strengths of each stock; the rates of migration; fishery and research selectivities; and catchabilities for the CPUE observations. Preliminary analyses are described which were useful in determining key aspects of the base model (including data weighting, the initial age structure, and trap shyness corrections for the tag recapture observations).

Point estimates from this model suggested that all stocks were already depleted in 1970, the first model year (with initial recruitment being 12–66% of that for the unfished stocks), and are currently even more depleted (with spawning biomass at 4–17% of its unfished value, B_0). However, posterior profiles showed that initial depletion was well estimated only for Hauraki Gulf. The percentage of fish migrating away from their spawning area was estimated to be low for east Northland and Hauraki Gulf (6% and 11%, respectively), but much higher for Bay of Plenty (30%, with 90% of migrators moving to Hauraki Gulf). Fits to most observations were adequate, being worst for some components of the tag recapture data. Short-term (3-year) projections suggested that, with current catch levels, biomass is likely to decline slightly for east Northland and Hauraki Gulf, and more rapidly for Bay of Plenty. Bayesian estimates for the base model were deemed unreliable because of poor diagnostics.

Sensitivity runs were used to explore the effect of uncertainty in key life history parameters (natural mortality and stock-recruit steepness) and the recreational catch. Results from the base model were shown to be broadly similar to those from simpler single-stock models.

Deterministic B_{MSY} was estimated to be 26%–27% B_0, but, because of the assumptions underlying the estimation, realistic management targets should be higher than this.

Two obvious major weaknesses of the current model were the estimation of initial depletion and very slow MCMC runs with poor diagnostics. Although the current modelling represents significant progress toward a robust SNA 1 assessment, further investigations were needed to resolve these issues before the results could be considered useful for management. The stock assessment was completed in 2013 and final results are presented in Francis & McKenzie (2015).

1 INTRODUCTION

Snapper (*Pagrus auratus*) is New Zealand's most valuable commercial coastal marine species and, by virtue of its high abundance around the populous regions of northern New Zealand, it is also the nation's most important recreational species (Hartill et al. 2007). Most New Zealand snapper stocks have been subject to significant exploitation for over a century; with commercial landings peaking in the 1970s at around 18 000 t per annum (Paul & Sullivan 1988; Ministry of Fisheries 2008). Commercial exploitation of snapper has been constrained by quota since the introduction of the Quota Management System (QMS) in 1986. Non-commercial snapper exploitation is not subject to quota, and is regulated primarily by minimum-legal-size and individual bag limits.

Under the QMS there are four snapper Quota Management Areas (QMAs) of commercial and non-commercial significance (Figure 1). The largest volume of catch, both commercial and non-commercial, comes from the north-east coast QMA known as SNA 1 (Figure 1).

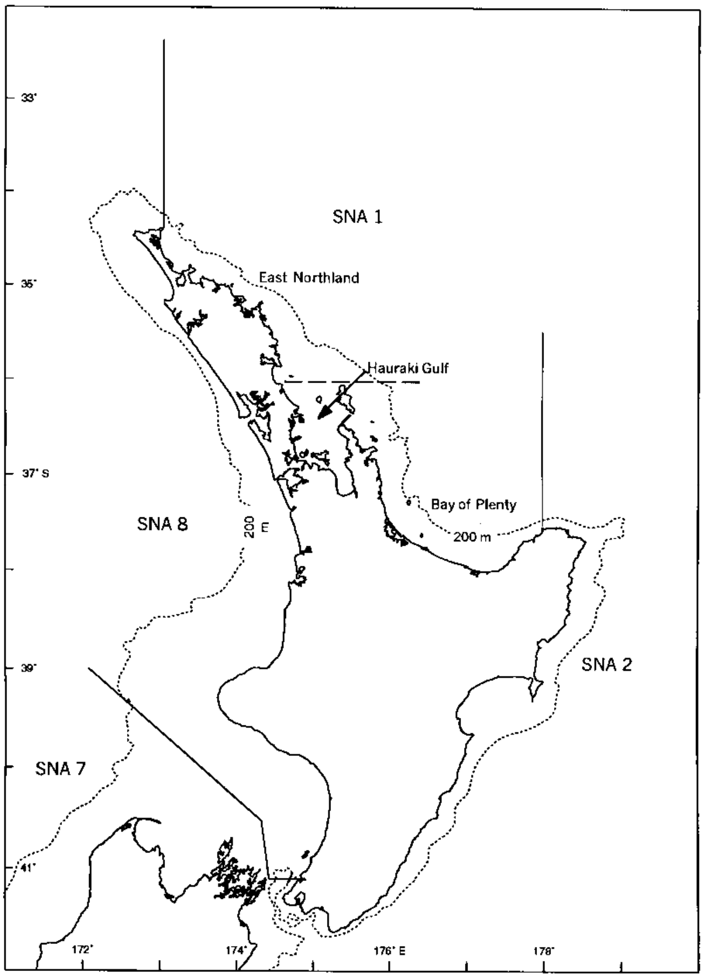

Figure 1: Boundaries for the snapper Quota Management Areas and three subareas within SNA 1: east Northland (EN), Hauraki Gulf (HG), and Bay of Plenty (BP).

Tagging movement, recruitment and growth data suggest that SNA 1 is productively distinct from the other three QMAs (Sullivan 1985; Walsh et al. 2011). Fishing pressure across SNA 1 has not been uniform and this is reflected in differences in age composition between SNA 1's three component sub-areas: east Northland (EN); Hauraki Gulf (HG); Bay of Plenty (BP) (Paul 1977; Sullivan 1985; Davies

& Walsh 1995: Figure 1). Recent east Northland longline catches show a wider range of age classes and a higher accumulation of biomass older than 20 years than catches from the other areas, suggesting that it has been less intensely fished (Walsh et al. 2011). The smallest proportion of biomass in the older age classes is seen in Bay of Plenty catches (Walsh et al. 2011), which is believed to be a legacy of a relatively high level of trawl fishing during the 1970s. Despite spatial differences in productivity, tagging observations suggest that the level of mixing between the three sub-stocks is significant (Sullivan et al. 1988; Gilbert & McKenzie 1999). The areas also appear to have similar recruitment characteristics (Walsh et al. 2011).

The spatial complexity of SNA 1 makes it difficult to assess as a unit stock. One approach has been to assess SNA 1 using amalgamated data from two or all sub-stocks. The other approach has been to model sub-stock productivity independently; the overall SNA 1 yield statistic being the combination of the individual assessments. Both approaches have limitations: amalgamation results in an assessment inherently more uncertain because spatial variability is unaccounted for; and assessing the sub-stocks independently, although accounting for spatial variability, largely ignores connectivity processes and may lead to a biased assessment.

Many millions of dollars have been spent monitoring SNA 1 since the early 1980s. Monitoring programmes have included commercial catch-at-age sampling, recreational harvest surveys, trawl surveys, and tagging programmes to derive estimates of biomass. Age-structured population modelling is used to estimate productivity and status.

The last formal SNA 1 stock assessment was undertaken in 1999 (Gilbert et al. 2000). The Hauraki Gulf/Bay of Plenty component of SNA 1 in the base-case run was predicted to have been at 0.80 B_{MSY} in 1999–2000; the sub-stock was predicted to rebuild over the following 20 years reaching about 1.73 B_{MSY} by 2019–20. The east Northland component of SNA 1 in the base-case run was predicted to have been at or slightly below B_{MSY} in 1999–2000; with 95% probability of the sub-stock biomass increasing over the following 20 years.

This report describes modelling carried out under MPI project SNA201101. The SNA201101 project had the following objectives:

1. *To collate and update catch histories through to 2010–11 and all observational data series required for the SNA 1 stock assessment.*

2. *To conduct a stock assessment for SNA 1 in the 2012 fishing-year using spatially disaggregated age-structured modelling, including estimating biomass and sustainable yields.*

In the rest of this report fishing years will be labelled by their end year (e.g., the 1999–2000 year will be labelled 2000).

The work in these report was reviewed and discussed by the Northern Inshore Working Group (henceforth denoted as Working Group).

The results presented in this work cover the assessment of the SNA 1 stock in 2012. A second assessment was completed in 2013 which built upon the conclusions and recommends given in this report. The 2013 SNA 1 assessment is presented in Francis & McKenzie (2015).

2 CATCH HISTORY

2.1 Commercial Catch

The SNA 1 commercial catch histories for the various method area fisheries after 1990 were derived from the Ministry for Primary Industries (MPI) catch effort reporting database (*warehou*). Historical catches for method and area, over the preceding two decades, were constructed on the basis of data contained in the fishery characterisation reports of King (1985; 1986), King et al. (1987) and Paul & Sullivan (1988). Area-method catches were prorated to the SNA 1 annual catch totals (Figure 2).

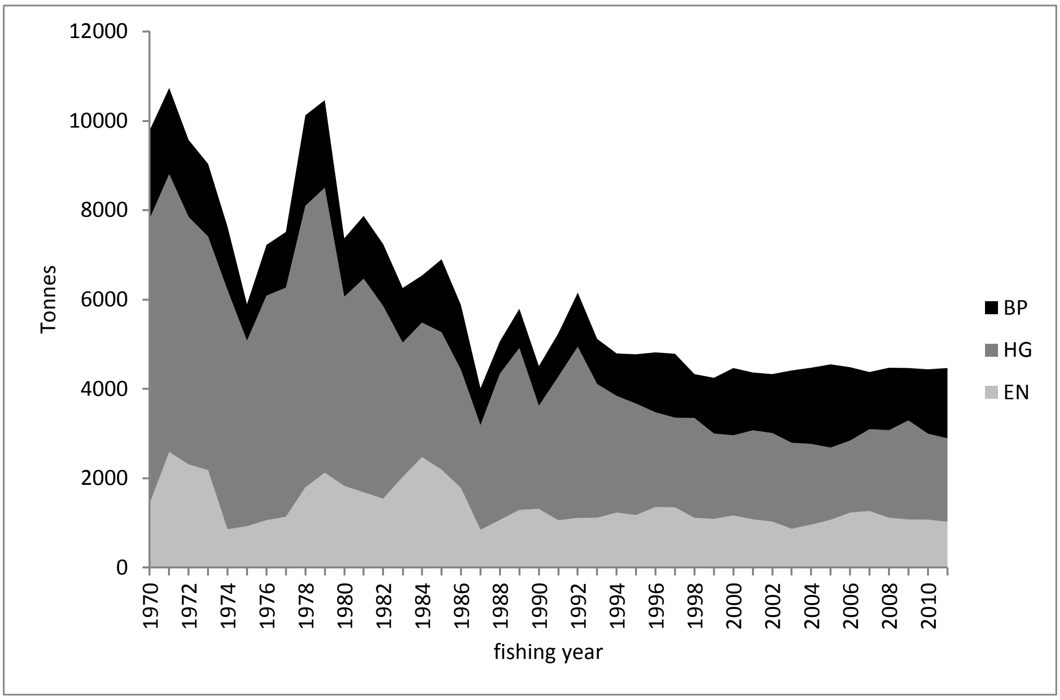

Figure 2: Area commercial catch histories (unadjusted for under reporting).

Since 1970 the dominant SNA 1 commercial fishing methods have been bottom longline (LL), bottom single trawl (ST), bottom pair trawl (PT) and Danish seine (DS) (Figure 3). For the purposes of the 2012 assessment all other methods were lumped into a single method class "other" (OTH); the predominant method under this class being setnet (Figure 3).

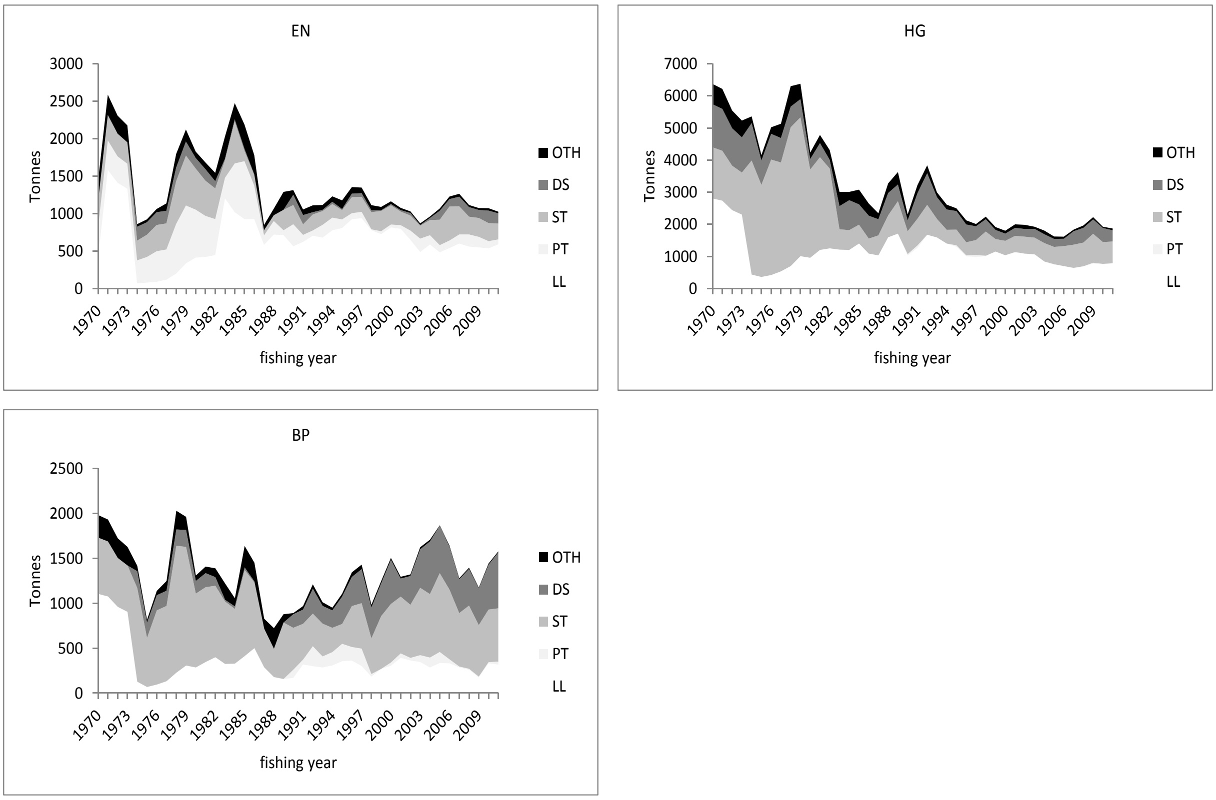

Figure 3: Method-area commercial catch histories (unadjusted for under reporting).

2.2 Illegal catch

The level of illegal catch in SNA 1 since 1970 is largely unknown but unlikely to be zero. As was done in previous assessments (Gilbert et al. 2000); commercial catch totals prior to the 1986 QMS year were adjusted upwards to account for an assumed 20% level of under-reporting. Catch totals post 1986 QMS were likewise scaled assuming 10% under-reporting.

2.3 Recreational and Customary catch

Annual recreational harvest estimates used in the 2012 model were constructed in three steps. First, catches for 1990–2011 for each stock were calculated by scaling the corresponding commercial longline CPUE index (Section 4.2.2) to the 2004–05 harvest estimates from the aerial over-flight survey by stock (Hartill et al. 2007). Second, estimates between 1989–90 and 1994–95 were scaled up by 10% to compensate for the lower MLS (25 cm), more hooks allowed per longline (50) and higher bag limit (15 per person) that was in place at that time. Third, catches for 1970–1989 were calculated by assuming that harvest by recreational fishers in 1970 was 70% of the 1990 estimate with a linear increase in annual catch across the intervening years (Figure **4**). The customary harvest is not known and is assumed to be included in the recreational catch.

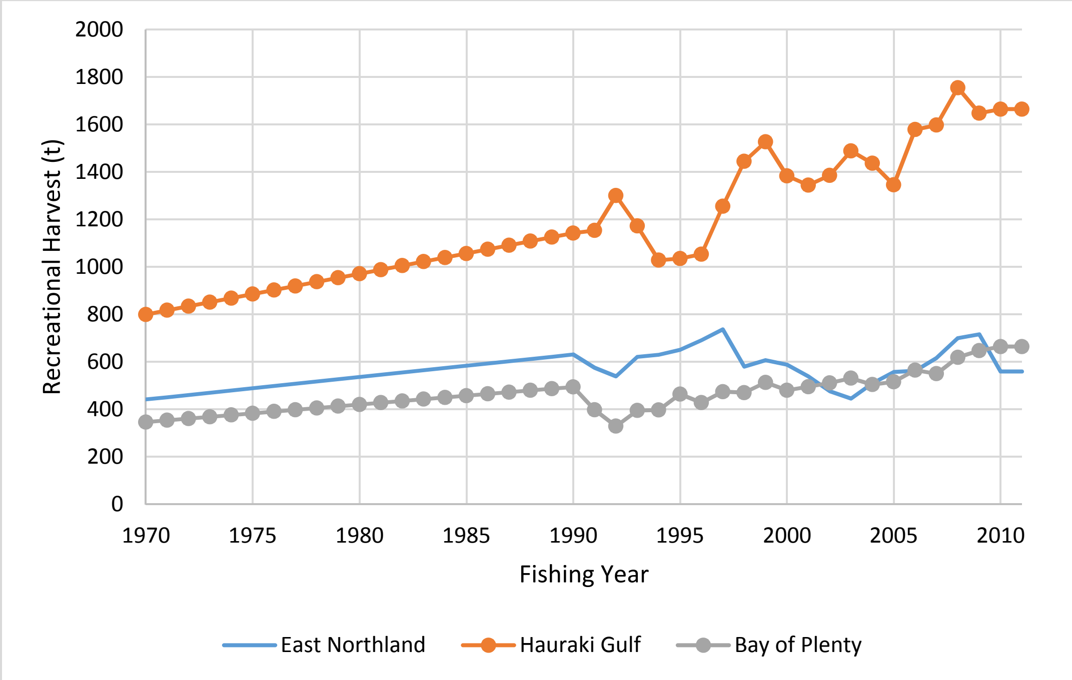

Figure 4: Recreational catch history used in the 2012 SNA 1 assessment model. Note that the 2005 catches are as estimated by Hartill et al. 2007.

2.3.1 Other sources of mortality

An at-sea study of the SNA 1 commercial longline fishery in 1997 (McKenzie 2000) found that 6–10% of snapper caught by number were under 25 cm (commercial minimum legal size). Results from a holding net study indicate that mortality levels amongst lip-hooked snapper caught shallower than 35 m were low (less than %10).

Recreational fishers release a high proportion of snapper catch most of which is less than 27 cm (recreational minimum legal size). An at sea study in 2006–07 recorded snapper release rates of 54.2% of the catch by trailer boat fishers and 60.1% of the catch on charter boats (Holdsworth & Boyd 2008). Incidental mortality, estimated from condition at release, was 2.7% to 8.2% of total catch by weight depending on (untested) assumptions used.

In the current modelling we have made no explicit allowance for incidental or unseen mortality. In doing this we reason that the combined effect of all historical mortality (both unseen and explicit) is reflected in the fitted observational data (i.e. abundance and compositional data) and therefore the unseen component is implicit in the modelling analysis. In other words, although unseen mortality is not included in the model catch history, the yield estimates the model produces as a result of fitting to the observational data still reflect unseen mortality. This assumption will be reasonable as long as there has been no substantial temporal trend in rates of incidental and unseen mortality.

2.3.2 Model catch history

In total the model recognised 20 area-method catch histories (Table 1).

Table 1: Model method-area fishery definitions.

Area	Method
East Northland (EN)	Longline (LL)
East Northland (EN)	Single Trawl (ST)
East Northland (EN)	Pair Trawl (PT)
East Northland (EN)	Danish seine (DS)
East Northland (EN)	Other commercial (OTH)
East Northland (EN)	Recreational (REC)*
Hauraki Gulf (HG)	Longline (LL)
Hauraki Gulf (HG)	Single Trawl (ST)
Hauraki Gulf (HG)	Danish seine (DS)
Hauraki Gulf (HG)	Other commercial (OTH)
Hauraki Gulf (HG)	Recreational (REC)*
Bay of Plenty (BP)	Longline (LL)
Bay of Plenty (BP)	Single Trawl (ST)
Bay of Plenty (BP)	Pair Trawl (PT)
Bay of Plenty (BP)	Danish seine (DS)
Bay of Plenty (BP)	Other commercial (OTH)
Bay of Plenty (BP)	Recreational (REC)*

* Represented as pre and post 1995 fisheries in the model with separate selectivities to account for 1995 MLS change.

3 MODEL STRUCTURE

We describe first the three-stock structure that was used for the base model and most sensitivity analyses, and then the much simpler one-stock structure that was used for some sensitivities.

3.1 The base model

The base model is a development of the spatially disaggregated model proposed by McKenzie (2012). The McKenzie model recognises SNA 1 as being comprised of three separate biological stocks and uses a home fidelity (HF) dynamic to model movement of these stocks between three spatial areas: East Northland, Hauraki Gulf; Bay of Plenty (Figure 1). Under the HF dynamic, movement is an attribute of the individual fish not the area in which it currently resides; stocks and areas can therefore be decoupled such that during some of the model time steps a given area may contain fish from one or more stocks. The HF decoupling property meant that the model could provide yield estimates (MSY, B_{MYS}, B_0, etc) relative to both stocks and areas. To avoid confusion about areas and stocks we will use two-letter abbreviations (EN, HG, BP) for areas, and longer abbreviations (ENLD, HAGU, BOP) to denote biological stocks.

The model structure is completely defined by the associated CASAL input file, population.csl, (given in Appendix 5) together with the CASAL User Manual (Bull et al. 2012). The model partitions the modelled population by age (ages 1–20, where the last age was a plus group), stock (three stocks, corresponding to the parts of the population that spawn in each of the three subareas of SNA 1 shown in Figure 1), area (the three subareas), and tag status (grouping fish into six categories – one for untagged fish, and one for each of five tag release episodes [which are described below in Section 4.5]). That is to say, at any point in time, each fish in the modelled population would be associated with one cell in a

20 × 3 × 3 × 6 array, depending on its age, the stock it belonged to, the area it was currently in, and its tag status at that time.

As with previous snapper models (e.g., Gilbert et al. 2000), this model did not distinguish fish by sex. The model covered the time period from 1970 to 2011, with two time steps in each year (Table 2).

There were two sets of migrations: in time step 1, all fish returned to their home (i.e., spawning) area just before spawning; and in time step 2, some fish moved away from their home area into another area. This second migration may be characterised by a 3 × 3 matrix, in which the *ij*th element, p_{ij}, is the proportion of fish from the *i*th area that migrate to the *j*th area.

There are three key assumptions of the base model (Table 3) that were found necessary in order to allow an assessment. There is no evidence for the first two of these, and the third is simply a convenience.

Table 2: The time steps in each year of the base model, and the model processes and observations that occur at each step.

Time step	Model processes (in temporal order)	Observations[2,3]
1	age incrementation, migration to home area, recruitment, spawning, tag release	
2	migration from home area, natural and fishing mortality[1]	biomass, length and age compositions, tag recapture

[1]Fishing mortality for each of the 20 fisheries (see Section 2) was applied after half the natural mortality
[2]The tagging biomass estimate was assumed to occur immediately before the mortality; all other observations occurred half-way through the mortality
[3]See Section 4 for more details of all observations

Table 3: Three key assumptions of the base model.

1. All fish were in their home grounds at the time of tagging
2. The proportions migrating at time step 2, p_{ij}, were the same each year
3. All tag recaptures in any year occurred in time step 2 after the migration away from the home area

3.1.1 Model parameters

A total of 142 parameters were estimated in the base model (Table 4).

One important decision was how to parameterise the initial (1970) age structure of each stock, given that all stocks were fished for many years before this. It was assumed that each stock had the stable age distribution which would arise if in the preceding years its recruitment was constant at some fraction (Rinitial) of the mean unfished recruitment (R0) and there was no fishing (see Section 5.4 for discussion of an alternative parameterisation).

The six migration parameters define the 3 × 3 migration matrix described above (there are only six parameters because the proportions in each row of the matrix must sum to 1).

Selectivities were assumed to be age-based and double normal, and to depend on fishing method but not on area. Three selectivities were estimated for commercial fishing (for longline, single trawl, and Danish seine); one for the (single trawl) research surveys; and two for recreational fisheries (for before and after a change in recreational size limit in 1995). All priors on estimated parameters were uninformative, except for the usual lognormal prior on year-class strengths (with coefficient of variation (CV) 0.6), and arbitrary normal priors which were found necessary to constrain the recreational selectivities, which were not well estimated (because no age samples were available for recreational catches and length frequencies varied greatly from year to year).

Table 4: Details of parameters that were estimated in the base model

Type	Description	No. of parameters	Prior
R0	Mean unfished recruitment for each stock	3	uniform-log
Rinitial	Pre-1970 recruitment (as proportion of R0)	3	uniform
YCS	Year-class strengths by year and stock	115[1]	lognormal[2]
Migration	Proportions migrating from home grounds	6	uniform
Selectivity	Proportion selected by age by a survey or fishing method	18	uniform[3]
q	Catchability (for relative biomass observations)	5	uniform-log
		142	

[1]YCSs were estimated for years 1969–2007 (for ENLD and HAGU) and 1971–2001 (for BOP)
[2]With mean 1 and coefficient of variation 0.6
[3]Except for the recreational selectivities, where normal priors were assumed for each parameter with means 4.55, 0.50, 10.24 (pre-1995) and 5.30, 0.50, 10.40 (post-1995) and coefficients of variation 0.20, 0.05, and 0.05 (both pre- and post-1995)

Some parameters were fixed, either because they were not estimable with the available data (notably natural mortality and stock-recruit steepness were fixed at values determined by the Working Group), or because they were estimated outside the model (Table 5). Mean length at age was specified by yearly values (rather than a von Bertalanffy curve) because these values showed a strong trend for the older ages (Figure 5). Mean length at age data were available for 1994–2010 for ENLD, and for 1990–2010 for HAGU, so earlier values were set equal to those in the first year available and 2011 values were set equal to those for 2010.

Table 5: Details of parameters that were fixed in the base model.

Natural mortality	$0.075\ y^{-1}$
Stock-recruit steepness	0.85
Tag shedding (instantaneous rate, 1985 tagging)	$0.486\ y^{-1}$
Tag detection (1985 and 1994 tagging)	0.85
Proportion mature	0 for ages 1–3, 0.5 for age 4, 1 for ages > 4
Length-weight [mean weight (kg) = a (length (cm))^b]	$a = 4.467 \times 10^{-5}$, $b = 2.793$
Mean lengths at age	provided for years 1989-2011
Coefficients of variation for length at age	0.10 at age 1, 0.20 at age 20
Pair trawl selectivity	$a_1 = 6$ y, $\sigma_L = 1.5$ y, $\sigma_R = 30$ y
Selectivity for other fishing methods	$a_1 = 7$ y, $\sigma_L = 2$ y, $\sigma_R = 6.5$ y

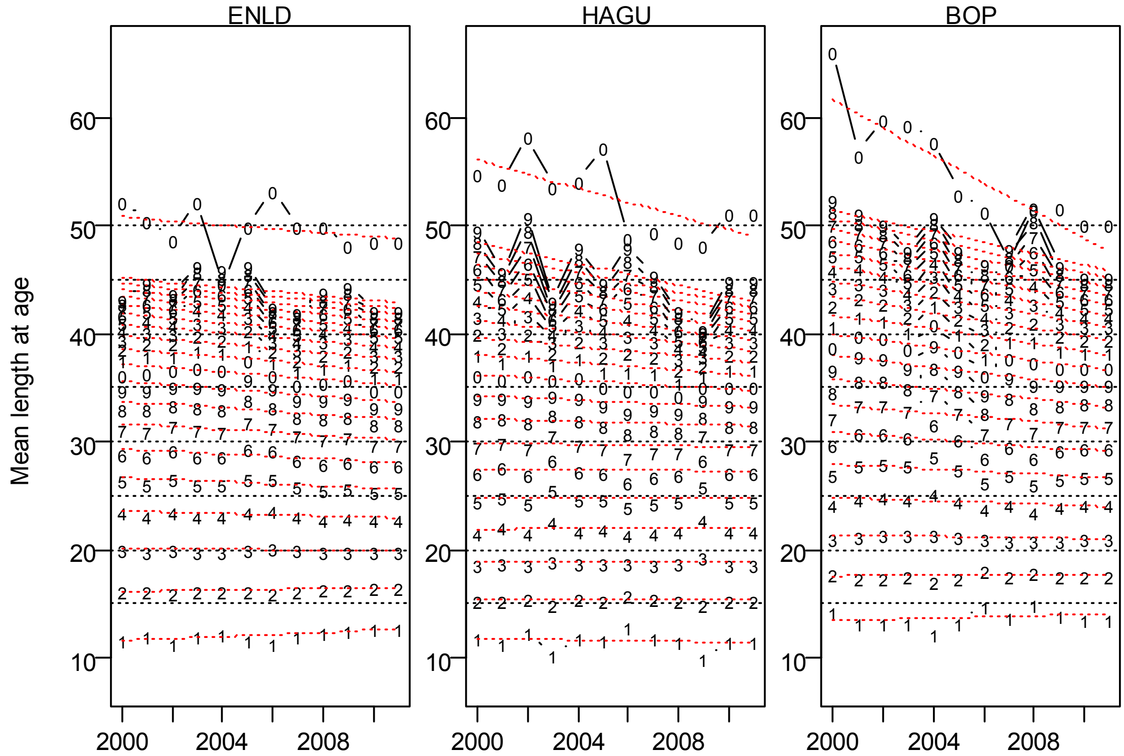

Figure 5: Mean lengths at age (for ages 1 to 20+) by stock, as used in the base model. The plotting symbols identify the age class (e.g., '1' is used both 1- and 11-year olds). Trends in these mean lengths are shown by regression lines (red dotted lines).

3.2 One-stock models

Some sensitivity runs were carried out using a separate model for each stock, with the simplifying assumption that movement between stocks is sufficiently minor to be ignored. Each such model was restricted to the area associated with that stock, so the model partitioned fish only by age and tag status, and there were no migrations. Parameters estimated for each of these models were: the R0, Rinitial, and YCSs for the stock; selectivities (as for the base model, except that in ENLD single trawl and Danish seine selectivities had to be fixed); and a catchability for each relative biomass series.

Accounting for recovered tags that moved between areas in the single stock models was problematic. The approach taken was to correct the initial area tag release numbers for movement while assigning all tag recovery observations to the area of recovery regardless of release area

4 OBSERVATIONS

Five types of observational data were used to inform the assessment: absolute biomass; relative biomass indices; age and length compositional data; and mark recapture data (Table 6).

Table 6: Details of observations used in the base stock assessment model. Areas are East Northland (EN), Hauraki Gulf (HG), and Bay of Plenty (BP).

Type	Likelihood	Area	Source	Range of years	No. of years
Absolute biomass	Lognormal	BP	1984 tagging	1983	1
Relative biomass[1]	Lognormal	BP	longline	1990–2011	22
		EN	longline	1990–2011	22
		HG	longline	1990–2011	22
		BP	single trawl	1996–2011	16
		HG	research survey	1983–2001	13
Age composition	Multinomial	HG	longline	1985–2010	22
		BP	longline	1990–2010	19
		EN	longline	1985–2010	18
		HG	Danish seine	1970–1996	11
		HG	research survey	1985–2001	10
		HG	single trawl	1975–1994	6
		BP	single trawl	1990–1995	4
		BP	research survey	1990–1996	3
		EN	research survey	1990	1
		BP	Danish seine	1995	1
Length composition	Multinomial	BP	recreational fishing	1991–2011[2]	13
		EN	recreational fishing	1991–2011[2]	13
		HG	recreational fishing	1991–2011[2]	13

		Area tagged	**Year tagged[3]**	**Areas recaptured**	**Years recaptured**
Tag recapture	Binomials	EN	1985	EN, HG	1985, 1986
		HG	1985	EN, HG	1985, 1986
		EN	1994	EN, HG, BP	1994, 1995
		HG	1994	EN, HG, BP	1994, 1995
		BP	1994	EN, HG, BP	1994, 1995

[1] CPUE (catch per unit effort) or single trawl research survey
[2]All length composition data sets were split into pre-1995 (2 years) and post-1995 (11 years) because recreational selectivity was assumed to change in 1995
[3]Fish labelled as tagged in 1984 were tagged between 21 October and 8 December in that year; those labelled 1993 were tagged between 27 October 1993 and 15 January 1994

4.1 Absolute biomass

A biomass estimate for the Bay of Plenty in the 1983–84 fishing year was derived by Petersen mark recapture (Appendix 2). None of the raw data from this tagging programme remains; the biomass estimate, however, was reported in Sullivan (1985) and updated in Sullivan et al. (1988).

4.2 Relative biomass

4.2.1 Research (trawl) survey indices

Relative abundance indices are available from thirteen Hauraki Gulf research trawl programmes undertaken between 1983 and 2001(Appendix 2).

4.2.2 Longline and trawl CPUE indices

East Northland, Hauraki Gulf and Bay of Plenty longline CPUE indices and a Bay of Plenty bottom trawl CPUE index are published in McKenzie & Parsons (2012); the indices covering the fishing years 1989–90 to 2009–10. These indices were updated for the 2012 assessment, in accordance with the McKenzie & Parsons (2012) methodologies, to include the 2010–11 fishing year. No new vessels were added into the updated analysis. The Working Group accepted the updated indices (Appendix 2) as indices of abundance.

4.3 Age composition

4.3.1 Commercial fisheries

Catch-at-age observations are intermittently available from the 1970s and 80s. Between 1989–90 and 2009–10 catch-at-age data were collected annually from most SNA 1 sub-stocks. The majority of the SNA 1 catch-at-age data is longline; the main justification being that this method is believed to select a broad range of age classes and hence the age composition of the catch is more reflective of the underlying population age structure than the catches of the other methods (trawl; Danish seine; setnet). Limited catch at age data is available from trawl and Danish seine fisheries prior to 1995 but only for the Hauraki Gulf and Bay of Plenty areas (Table 6).

4.3.2 Research Trawl

In addition to the Hauraki Gulf research trawl series, catch-at-age observations are available from three Bay of Plenty surveys and one east Northland survey (Table 6).

4.4 Length composition

4.4.1 Recreational fisheries

Length compositional data is available from recreational boat-ramp surveys conducted in all three areas between 1991 and 2011 (Table 6). Length compositional data is available from all three areas in both historical periods (Table 6).

4.5 Tag recapture

The 1985 and 1994 tagging experiments differed in three important ways. First, the former excluded the Bay of Plenty. Second, the former used external dart tags, whereas the latter used internal coded wire tags. Finally, tags were returned by fishers in the 1985 experiment (so it was assumed that all captured fish were checked for tags), whereas in the 1994 experiment, tags could be detected and returned only for the fraction of the catch that was scanned (in fishing sheds) for tags using specialist equipment. In most other respects the two experiments were similar, i.e. thirteen month recovery period, recaptures being restricted to commercial methods, the collection of length data to convert scanned catch weights to length frequencies. The total tonnage of catch examined for tags was lower in the 1994 programme, but this figure was more precisely determined.

Between 3 600 and 13 500 fish were tagged in each area in the two experiments; because of the difference in tag types return rates were higher in the earlier experiment (7.8% overall, compared to 2.1% in 1994); and most returned tags were from fish recaptured in the area of tagging (Table 7).

Table 7: Numbers of fish tagged and recaptured by area in the 1985 and 1994 tagging experiments

			Recaptured		
1985		Tagged	EN	HG	BP
	EN	6782	418	29	-
	HG	12046	47	974	-
1994					
	EN	8190	129	10	5
	HG	13466	20	272	17
	BP	3630	2	25	41

The tagging data enter the model in two parts: (i) for each tagging event (a combination of area and tagging year), the number tagged and their length composition, and (ii) for each combination of tagging event, recapture area, recapture year, and length bin, the number of fish scanned for tags and the number of tags detected. For the early tagging experiment the length distribution at recapture was assumed to be the same as at tagging because recapture lengths were unknown for most fish from this experiment.

There are a number of known sources of bias inherent in tagging data that needed to be accounted for in the assessment (bias corrections were made either inside the model or as a data adjustment prior to model input).

4.5.1 Correcting for initial mortality

The tag release observations were corrected for initial mortality prior to input into the assessment models. Corrections were made following the approach given in McKenzie & Davies (1996) these being consistent with experimental findings from net holding experiments conducted in the early 1990s (Appendix 3).

4.5.2 Correcting for tag loss

The external dart tags used in the 1985 programme were prone to dropping out. The loss rate estimate of the primary (anterior) tag is given by the coefficient derived from a temporal logistic regression to double-tag recovery data (Figure 6; see also McKenzie & Davies (1996) for methods).

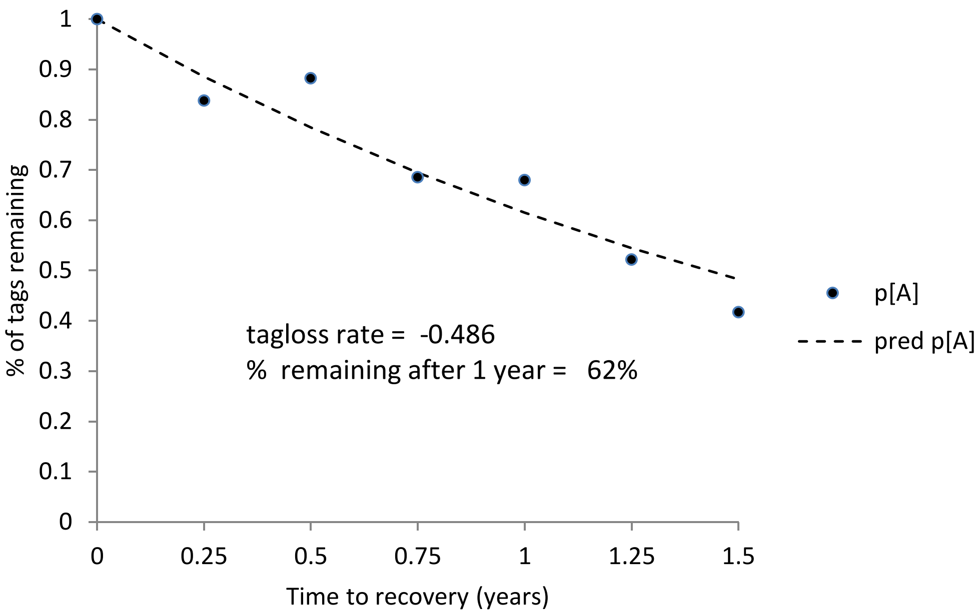

Figure 6: Fitted logistic curve to observed proportions of retained anterior tags from double tag recoveries (1985 programme data).

Given that only 10% of released fish in the 1985 programme were doubled tagged it was more feasible to remove all posterior-only tag recoveries from the total tag recovery dataset rather than to correct for the loss of both posterior and anterior tags for the double tag recoveries.

Internal coded wire tags were used in the 1994 programme; the loss rate of these tags was assumed to be close to zero (0.001). A quarter of the tag loss for each year was assumed to occur in time step 1.

4.5.3 Corrections for non-detection of tags (1985) and underreporting (1994).

CASAL's tag detection probability parameter was used to allow for tagged fish that were caught but not reported.

Tag recovery during the 1985 dart tagging programme was achieved through voluntary reporting by the commercial fishery. Tag recovery data used in the assessment spanned the thirteen month period from February 1985 through to February 1986. Recovered tags were assumed to relate to the total reported commercial catch from this period. Method catch totals were converted to length-frequencies prior to input to the CASAL model on the basis of length frequency data collected over the tag recovery period (Sullivan et al. 1988).

There are no empirical data from the 1985 tagging programme to estimate under-reporting. Sullivan et al. (1988) assumed that under-reporting in the 1985 programme was in the order of 10%, basing their assumption on anecdotal evidence from the Danish seine fishery. The Working Group felt that the Sullivan et al. estimate was too low, opting for a 0.15 under-reporting rate (i.e., a detection rate of 0.85) for the 2012 assessment model.

The 1994 tagging programme's use of internal coded-wire tags required the instigation of dedicated catch scanning at fish processing plants to recover tags. As scanning was not 100% successful there was the need to estimate an under-detection rate. A detection rate of 0.85 was derived by McKenzie & Davies (1996) from tag seeding trials, and this was also the rate applied in the 2012 assessment.

4.5.4 Correcting for trap shyness

Gilbert & McKenzie (1999) found evidence of same-method recapture bias or "trap shyness" for single-trawl and longline-caught fish in both tagging programs. That is, fish caught for tagging by either of these methods were less likely to be recaptured by the same method.

We corrected the tag-recapture data for trap shyness by reducing the numbers scanned as follows.

For a given tag release data set, year of recapture, and length bin, the expected number of recaptured fish is given by

$$N_{scan}\,[P_{OTH} + P_{LL}(p_{OTH} + p_{ST} + p_{LL}\,s_{LL}) + P_{ST}(p_{OTH} + p_{LL} + p_{ST}\,s_{ST})]\;td$$

where

N_{scan} = number of fish scanned (examined for tags)
t = tag rate (proportion of population tagged)
d = tag detection rate (set at 0.85 for all tag recapture data sets – see Section 4.5.3)
p_{METH} = proportion tagged by method METH (ST = single trawl, LL = longline, or OTH = other)
P_{METH} = proportion of scanned fish caught by method METH
s_{METH} = trap-shyness effect for method METH.

Note that without trap shyness (i.e., $s_{LL} = s_{TR} = 1$) the expected number of recaptures is simply $N_{scan}td$. Thus, to correct for trap shyness we simply multiplied the number scanned for each recapture data set by the correction factor f_{corr} given by

$$f_{corr} = P_{OTH} + P_{LL}(p_{OTH} + p_{ST} + p_{LL}\,s_{LL}) + P_{ST}(p_{OTH} + p_{LL} + p_{ST}\,s_{ST})$$

The scanned proportions P_{ST}, P_{LL}, and P_{OTH} (= 1 – P_{ST} – P_{LL}) were all known; but it was necessary to assume that the tagged proportions, p_{ST}, p_{LL}, and p_{OTH} (= 1 – p_{ST} – p_{LL}) were unaffected by growth and movement between areas. Gilbert & McKenzie (1999) estimated that the trap shyness effects, s_{ST} and s_{LL}, were 0.6–0.7.

Because the evidence for trap shyness seemed stronger for the longline method, we calculated two versions of f_{corr}: one correcting just for longlines (setting s_{ST} =1 and s_{LL} = 0.65); and the other correcting for both methods (setting $s_{ST} = s_{LL}$ = 0.65). Because both tagging and scanned proportions were usually much higher for longline than for single trawl (Table 8), there was often little difference between the two versions of f_{corr} (Figure 7).

Table 8: Mean scanned and tagging proportions (see text for definitions) used in correcting for trap shyness (both types of proportions varied by length; the values presented here are averaged across all length bins).

			Proportions scanned			Proportions tagged		
Year tagged	Area tagged	Year recaptured	P_{LL}	P_{ST}	P_{OTH}	p_{LL}	p_{ST}	p_{OTH}
1984	EN	1985	0.65	0.05	0.30	0.87	0.10	0.04
	HG	1985	0.33	0.24	0.43	0.54	0.39	0.07
	EN	1986	0.59	0.03	0.39	0.87	0.10	0.04
	HG	1986	0.52	0.15	0.33	0.54	0.39	0.07
1993	EN	1994	0.85	0.00	0.15	0.77	0.21	0.01
	HG	1994	0.52	0.13	0.35	0.73	0.14	0.13
	BP	1994	0.45	0.15	0.40	0.51	0.28	0.21
	EN	1995	0.88	0.00	0.12	0.77	0.21	0.01
	HG	1995	0.67	0.00	0.33	0.73	0.14	0.13
	BP	1995	0.42	0.24	0.34	0.51	0.28	0.21

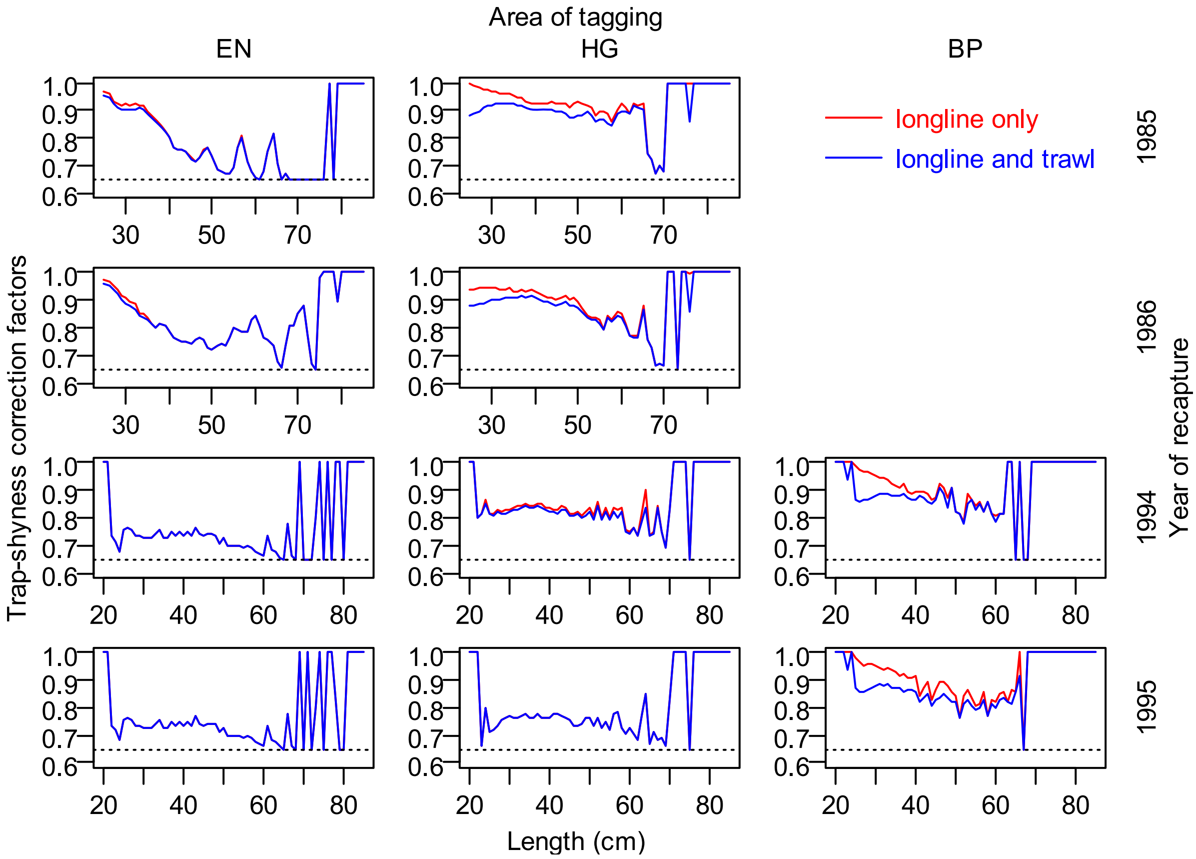

Figure 7: Estimated trap-shyness correction factors, f_{corr}, by fish length, area of tagging (columns) and year of recapture (rows). Two versions of f_{corr} are plotted: that correcting for longline only (red lines); and that correcting for both longline and single trawl (blue lines). The horizontal dotted line in each panel is at 0.65.

4.6 Observations for the single-stock models

All biomass and age or length composition observations in the spatial model are associated with just one of the three areas. Therefore, a one-stock model for a given area simply used those biomass and composition observations associated with that area. However, the construction of tag-associated data for the one-stock models was a bit more complicated. It involved decisions about both the tag release data (in the population.csl file) and the tag-recapture observations (in the estimation.csl file).

The approach taken for the tag release data is simple in concept, but a little complicated in technical detail (for which see Appendix 4). The concept is this: when providing the number and length composition of fish tagged in a given year (say 1994) for a one-stock model in a given area (say HG) we take

– all fish tagged in 1994 in HG,
– remove the proportion of those fish that are expected to move to another area (EN or BP),
– add the proportion of fish tagged in 1994 in EN that are expected to move to HG, and
– add the proportion of fish tagged in 1994 in BP that are expected to move to HG.

5 PRELIMINARY MODEL RUNS

In this section we describe the results, and conclusions, from a series of preliminary model runs that were used to decide on key aspects of the base model structure and assumptions. We provide labels for each of the preliminary runs that are presented, but, in the interests of brevity, we make no attempt to document all the ways in which these runs differed from the base run.

5.1 Data weighting

We used the approach proposed by Francis (2011) to weight the different data sets. The first step was to fit a series of Lowess splines of increasing smoothness through the CPUE data, calculate the CV of the residuals from each fit, and choose a CV that corresponded to the desired goodness of fit. After examining the fits in Figure 8, the Working Group agreed to use a CV of 0.15 for all the CPUE data.

Next, observation-error multinomial sample sizes were estimated for each age- and length-composition data set. The raw data were bootstrapped to estimate an observation-error CV for each proportion at age or length, these CVs were plotted against the proportions (in log-log space), and a non-linear regression was used to find the multinomial sample size, *N*, which predicted CVs that best matched the bootstrap CVs (see figure 3 of Crone & Sampson 1998 for an illustration of this regression procedure). The estimated sample sizes varied substantially, both within and between data sets, covering more than 2 orders of magnitude (from 42 to 18 000), and being typically higher for length than for age data (Figure 9).

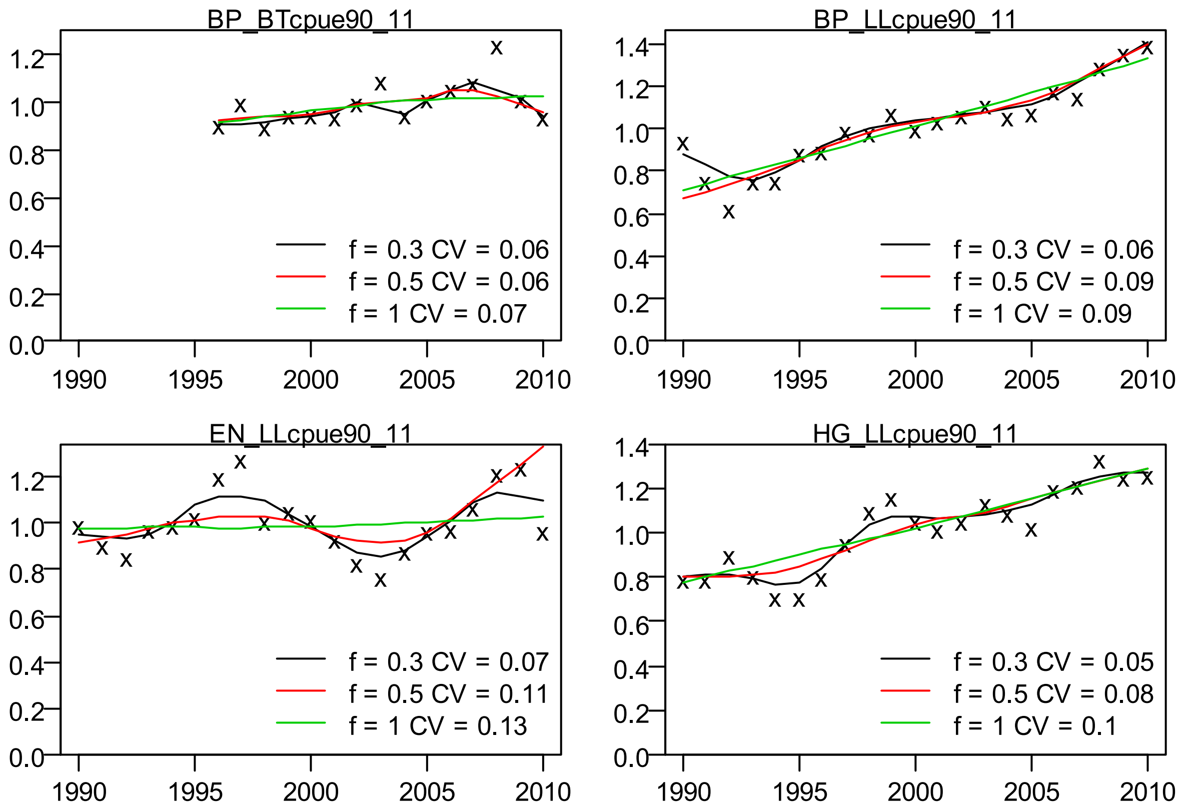

Figure 8: Plot used to decide on the weighting assigned to the CPUE observations. Each panel shows lowess lines with varying degrees of smoothness fitted to one of the four CPUE time series used in the base model. The legend in each panel shows, for each fitted line, the lowess smoothness parameter, *f*, and the CV of the residuals.

Then, a two-stage weighting procedure was used to down-weight the composition data to allow for process error. That is, the model was run using the observation-error sample sizes for the composition data; the residuals from the fits to the composition data were used to calculate a weighting parameter, *w*, for each composition data set (using method TA1.8 of Francis 2011); and the original sample sizes were multiplied by the weighting parameters to down-weight these data. The weighting parameter was lowest for the length data (0.012), and ranged between 0.021 and 0.109 for the age data (Table 9).

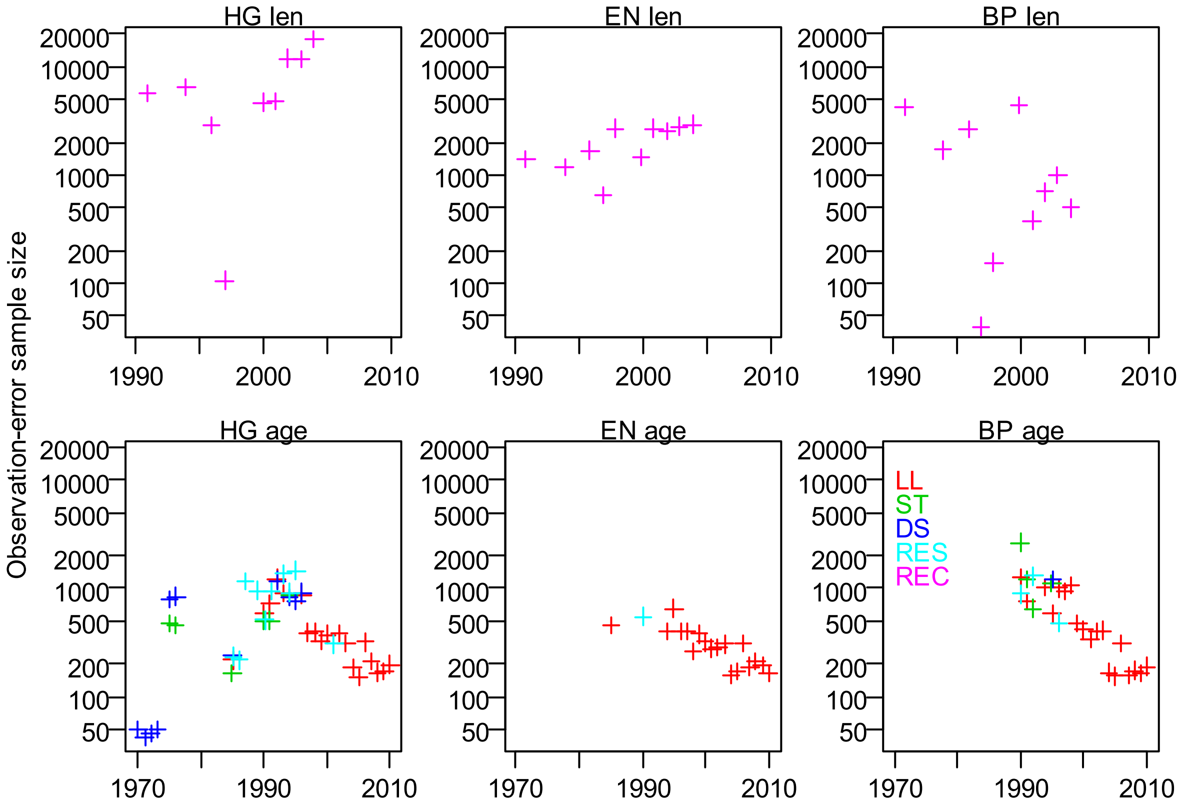

Figure 9: Inferred observation-error sample sizes for the length-composition (upper panels) and age-composition data sets. The colour of each plotting symbol identifies the source of the data (LL, ST, and DS refer to commercial catches by longline, single trawl, and Danish seine, respectively; RES = research survey; REC = recreational catch).

Table 9: Weighting parameters, *w*, used to down-weight the multinomial sample sizes in the two-stage weighting procedure. Sometimes, two or more data sets needed to be combined to obtain a large enough number of years' data to make the estimates of *w* robust. Thus, for example, all length composition data sets were combined, as were the single trawl data sets from all areas.

	Data set (or combination of data sets)						
	Length	ST.age	DS.age	BP.LL.age	EN.LL.age	HG.LL.age	RES.age
No. of years' data	29	10	12	19	18	22	14
w	0.012	0.021	0.042	0.037	0.098	0.109	0.026

The need to down-weight the composition data, and the substantial effect of this down-weighting, are shown clearly by plots comparing the fits to various data sets in two model runs, before and after down-weighting (runs v2 and v3, respectively). Fits to mean ages were very poor before down-weighting, and much better afterwards (Figure 10: note that the expected mean ages often lie outside the plotted confidence intervals in the upper panels, but not in the lower panels). An analogous plot for mean length (not shown) was very similar. The down-weighting also produced a dramatic improvement in the fits to the tag recapture data (Figure 11: the point to note is that many of the 'x's are outside the 95% confidence intervals, but this is true of far fewer of the 'X's), although the fits to the CPUE data were only slightly improved (Figure 12). Most importantly, the estimated spawning biomass trajectories are very different (Figure 13).

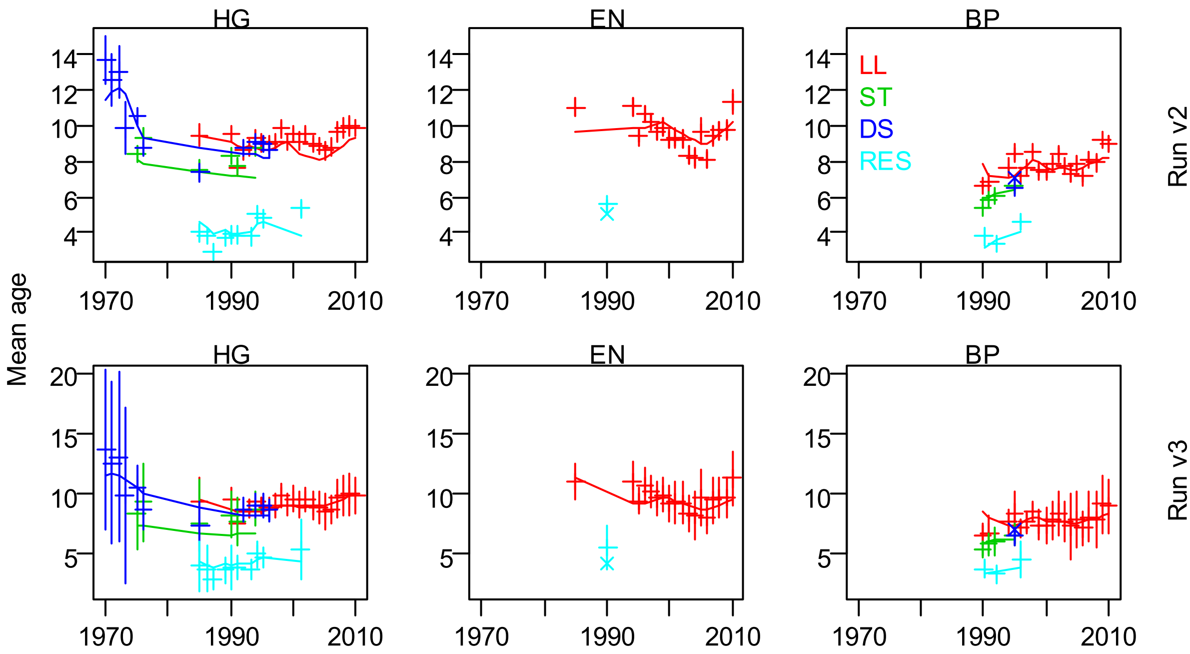

Figure 10: Fits to mean age in models runs before (upper panels) and after (lower panels) the composition data sets were down-weighted. The observed mean ages are plotted as short horizontal lines, with their 95% confidence intervals (which depend on the multinomial sample size) shown as a vertical line; the expected mean ages are plotted as a curved line (or, for data sets with only one year, as an 'x'). The data sources are identified by colour (LL = longline; ST = single trawl; DS = Danish seine; RES = research trawl).

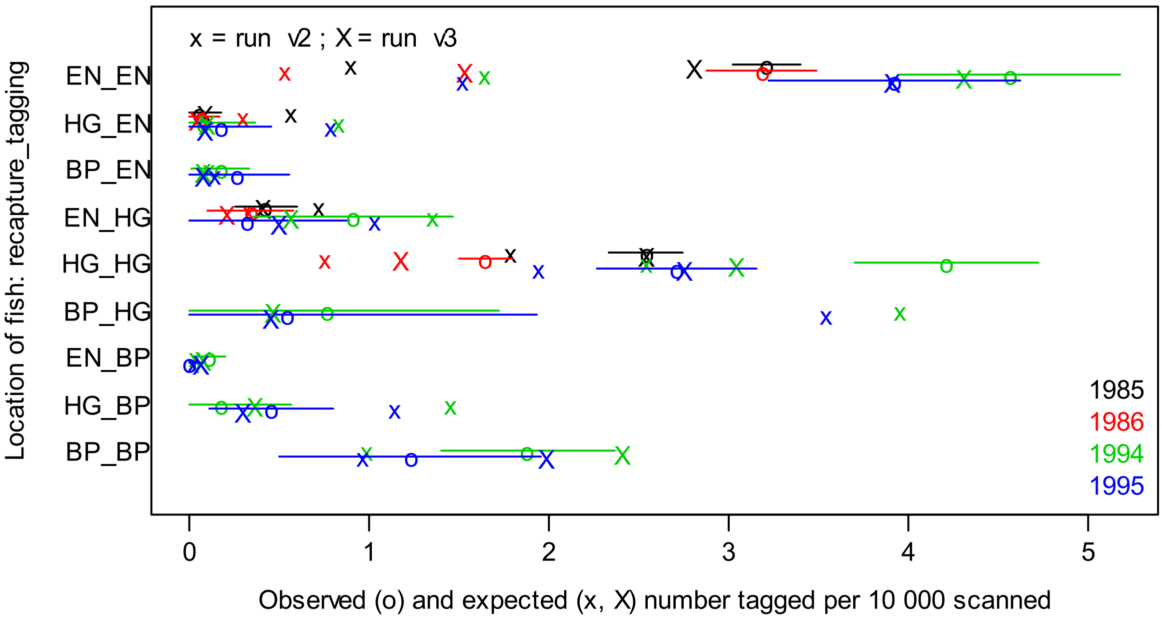

Figure 11: Fits to the tag recapture data in model runs before (run v2) and after (run v3) the composition data sets were down-weighted. A total of 26 observed values ('o', with 95% confidence intervals indicated by horizontal lines) are plotted: these are grouped vertically by their locations of recapture and tagging (with each group identified by the label on the vertical axis – e.g., BP_BP, HG_BP), with the year of recapture (1985, 1986, 1994, or 1995) indicated by the colour of the plotting symbol. Associated with each observed value are two expected values: one each for runs v2 ('x') and v3 ('X').

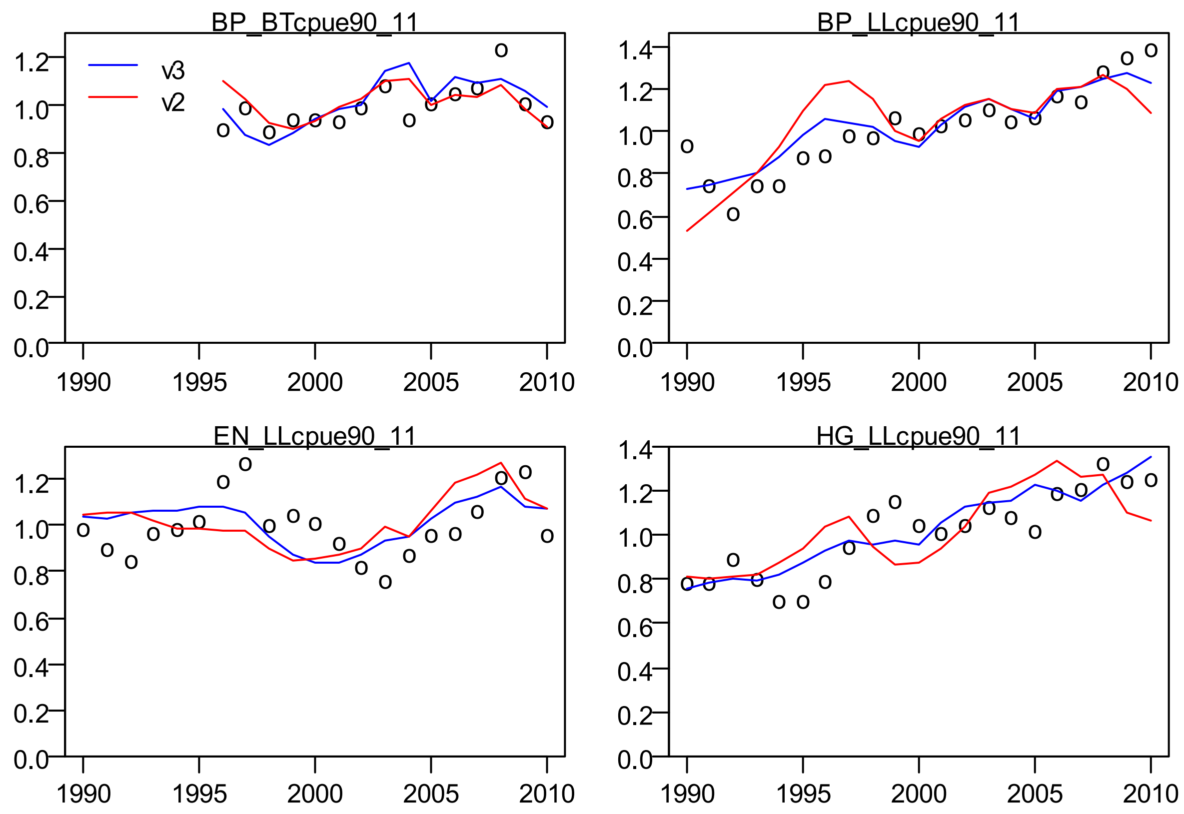

Figure 12: Fits to the CPUE data in model runs before (run v2) and after (run v3) the composition data sets were down-weighted. Observed values are shown as 'o', and expected values as coloured lines (red for v2, blue for v3).

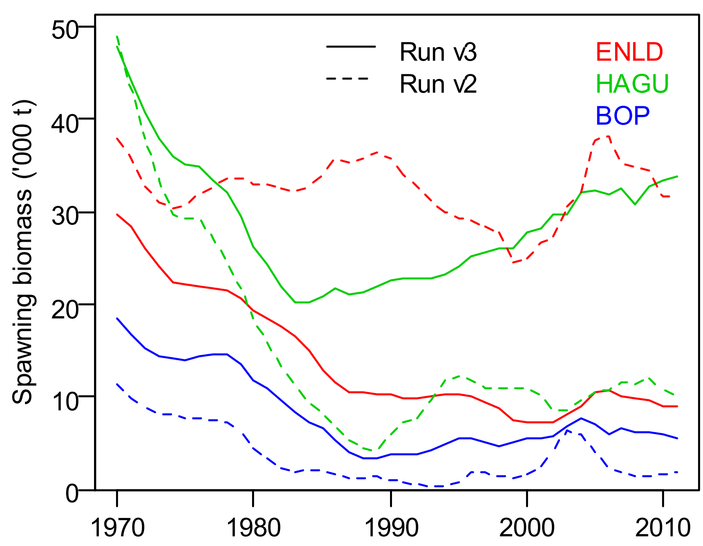

Figure 13: Estimated spawning biomass trajectories for the three stocks from model runs before (run v2, broken lines) and after (run v3, solid lines) the composition data sets were down-weighted.

There are three types of observations for which we have not yet discussed data weights. For the absolute biomass observation (from the 1983 BP tagging) no estimate of precision was available, so the Working Group arbitrarily assigned it a CV of 0.4 (although runs with a CV of 0.3 gave almost identical results). For the trawl survey biomass indices (which were not available at the time that runs v2 and v3 were done) we followed the advice of Francis et al. (2003), adding a process-error CV of 0.2 (to allow for year-to-year variation in catchability) to the observation-error CVs estimated from the survey data. For the tag-recapture data we simply used the observation-error sample sizes (i.e., the number of fish scanned in each length class). This almost certainly gave too much weight to these observations (because no allowance was made for process error), but we were not aware of any alternative weighting scheme (this type of observation was not considered by Francis 2011).

We investigated two ways of improving the fits to the tag recapture observations. Dropping the CPUE observations had little effect, so we concluded that the poor fit was not caused by conflict between these two types of observations. Iterating the two-stage weighting procedure for the composition observations (the weighting parameters, *w*, calculated from the fits in run v3 were much closer to 1 – between 0.4 and 1.1) also had little effect.

5.2 Growth and tag recapture data

Some concern was expressed by the Working Group that the fit to the tag recapture data may be compromised by a substantial mismatch between the observed and expected length frequencies of tagged fish. There were several reasons for this concern. First, recapture lengths were not available for most fish tagged in 1984, so the lengths used in the assessment model for these fish were actually the lengths at release. Second, there are grounds to believe that tagged fish grow more slowly than untagged fish. Third, each year's recaptures were treated as occurring at the same time, whereas they actually occurred throughout the year. Thus it was felt that the model may need some adjustment to deal with a mismatch between the observed and expected length frequencies. However, a plot of these length frequencies showed no substantial mismatch (Figure 14), so no adjustments were made.

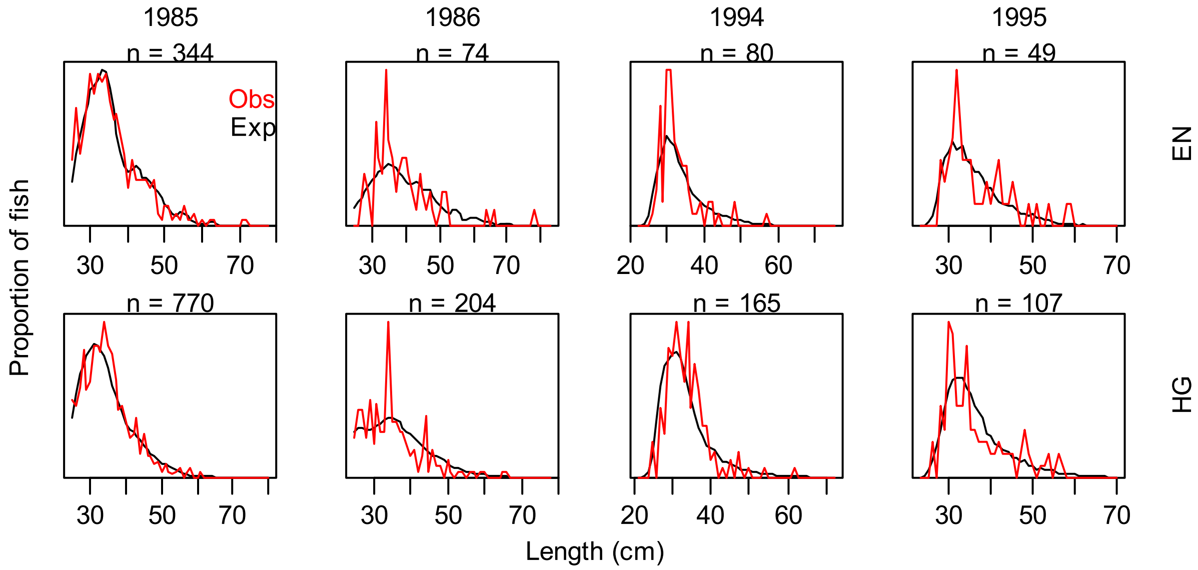

Figure 14: Observed (red lines) and expected (black lines) length frequencies of tagged fish by year of recapture and area of tagging and recapture (east Northland, EN upper panels, or Hauraki Gulf, HG, lower panels). The sample size (number of recaptures) is given above each panel. Data (which are from run v7) are plotted only for fish tagged and recaptured in these two areas because sample sizes for recaptures in areas other than the area of tagging, and for fish tagged in Bay of Plenty, were too low (0 to 40).

5.3 Corrections for trap shyness

The effect of the trap-shyness corrections was evaluated by comparing results from three runs: run v7, with no corrections; run v7a, with corrections for longline only; and run v7b, with corrections for longline and trawl. The corrections had clear effects on spawning biomass trajectories – producing trajectories that were lower for areas EN and HG, and slightly higher for BP – though there was very little difference between correcting for both methods and correcting for longline only (Figure 15). These corrections slightly degraded the model fits to most data sets, but plots comparing fits for runs v7 and v7b showed that this degradation was visually significant only for some of the tag recapture data (Figure 16; note difference in fits for 1994 and 1995 recaptures for EN_EN and HG_HG). The only substantial effect these corrections had on the migration matrix was to reduce the proportion of BOP fish migrating to HG (the proportions migrating to HG and BP, respectively, changed from 0.33 and 0.62 in run v7 to 0.30 and 0.65 in run v8b). The Working Group decided that trap-shyness corrections for both longline and single trawl would be applied in the base model.

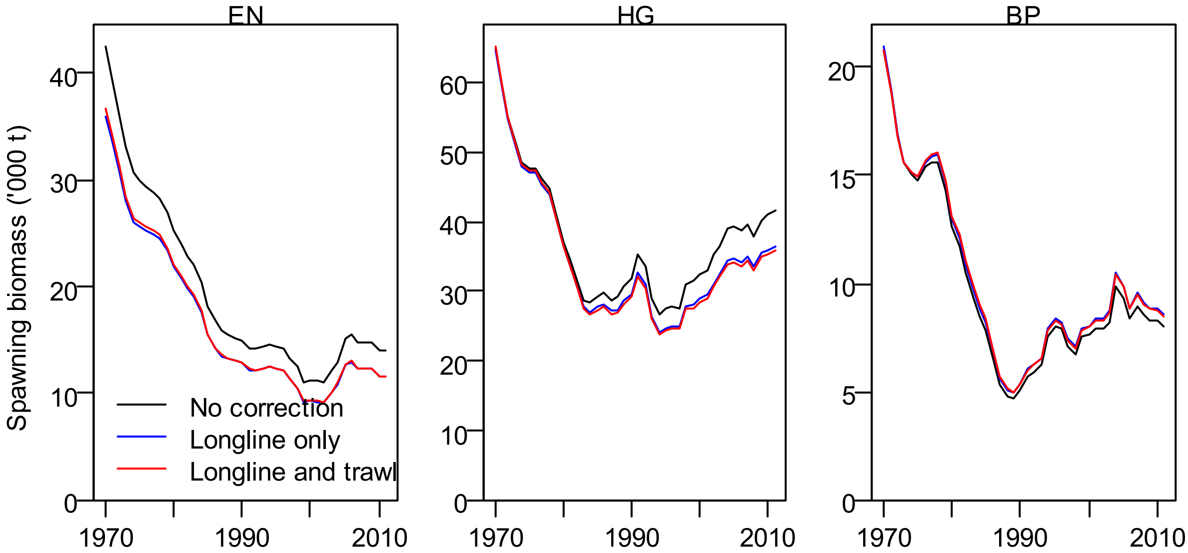

Figure 15: Effect of trap-shyness corrections on estimated spawning biomass (SSB) by area, showing SSB estimates from three model runs: run v7 (no correction, black lines); run v7a (correction for longline only, blue lines); and run v7b (corrections for longline and trawl, red lines).

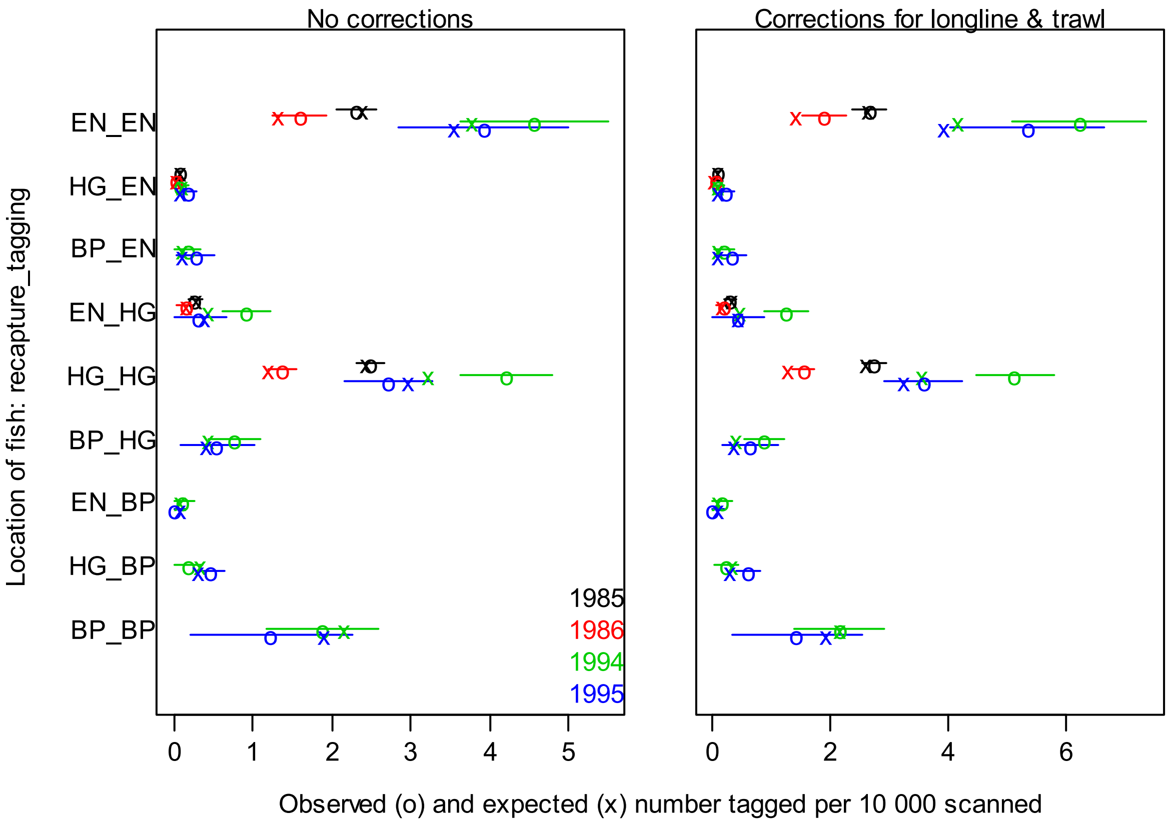

Figure 16: Effect of trap-shyness corrections on fits to tag recapture data: A, fits with no corrections (run v7); and B, fits with corrections for longline and trawl. Plotting conventions as in Figure 11.

5.4 Initializing the age structure

As mentioned above (see Section 3.1) the initial (1970) age structure of each stock in the base model was determined by just two parameters: R0 (the mean unfished recruitment) and Rinitial (where the recruitment in the years preceding 1970 was assumed to be Rinitial × R0). A less parsimonious parameterization, in which the assumption of a stable age distribution was dropped and Rinitial was replaced by Cinitial (a vector of numbers at age in 1970), was used in some preliminary runs. A comparison between run v7 (using Cinitial) and v7d (using Rinitial) showed marked differences in the estimated biomass trajectories (Figure 17) and the migration matrix (the estimated proportions of BOP fish migrating to HG and BP, respectively, changed from 0.33 and 0.62 to 0.29 and 0.68). The simpler parameterization (with Rinitial) was used in the base model because the additional 57 parameters needed when Cinitial was used made virtually no difference in goodness of fit to the observations (the objective function decreased by only 2). [There was also another complication: strong prior distributions were needed on Cinitial in order to obtain plausible shapes to the initial age structures, and there was insufficient time to investigate these priors.]

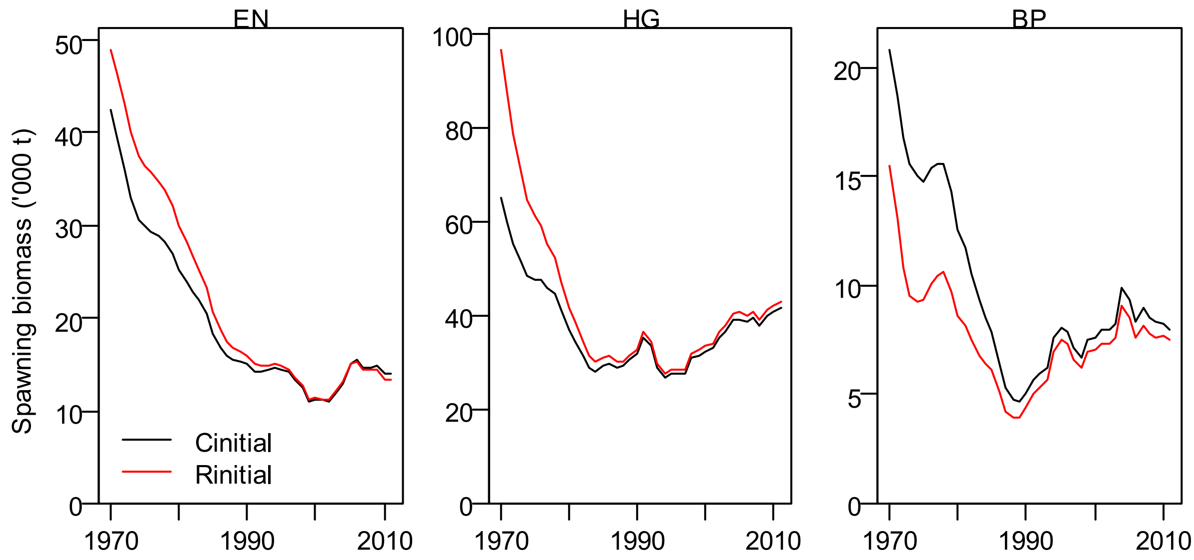

Figure 17: Effect on estimated spawning biomass by area (SSB) of changing the way age structures were initialized: using parameters Cinitial (run v7, black lines) or Rinitial (run v7d, red lines).

5.5 Fixed and time-varying B_0

The fact that SNA 1 growth (i.e., mean length at age) has varied with time (see Figure 5) presents a potential problem in interpreting stock assessment results. In New Zealand, many biological reference points (e.g., current biomass, and B_{MSY}) are expressed as percentages of the unfished spawning biomass, B_0. However, B_0 depends on growth, and so, strictly speaking, varies with time. Thus, in presenting results relative to B_0 for each stock we can either stick with the single ('fixed') B_0 output by CASAL (this is based on the mean growth over the assessment period) or use a time-varying B_0. After seeing a comparison of fixed and time-varying B_0s (Figure 18) the Working Group decided to use fixed B_0s.

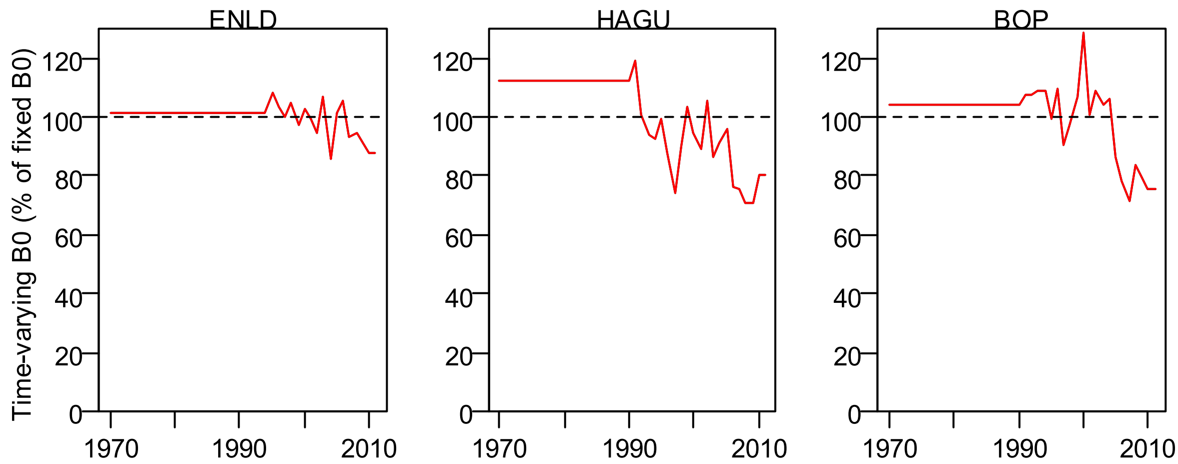

Figure 18: Time-varying B_0 plotted as a percentage of fixed B_0 (results from run v8b).

6 BASE CASE MPDS

In this section we present results associated with the point, or MPD (mode of the posterior distribution), estimates for the base model (full Bayesian, or MCMC, results are presented in Section 8). Three sets of results are presented: key outputs and diagnostics from the base model; results from sensitivity runs; and comparisons with one-stock models.

In these results we present two types of spawning biomass (and thus also B_0), which we label 'by stock' and 'by area'. The first is the conventional one, calculated in time step 1, when all fish are in their home grounds; the second is calculated in time step 2 (after half of the natural and fishing mortality has occurred) and measures the spawning biomass of all fish (from whatever stock) in each of the three areas. Uncertainty about three key assumptions (see Table 3) is one reason for presenting the 'by area' estimates; another reason is that all our observations occur at time step 2. It is reassuring to note that the main conclusions from the assessment do not strongly depend on whether we focus on results by stock or by area.

6.1 Key outputs and diagnostics

All estimated spawning biomass trajectories show substantial reductions up to about 1990, and then either stable (for ENLD) or slightly increasing trends (for HAGU and BOP) thereafter (Figure 19, upper panels). In terms of current biomass, both the stock BOP and area BP are estimated to be considerably more depleted (4% B_0) than the other stocks and areas (12–17% B_0) (Table 10). Stock HAGU and area HG are estimated to contain a much greater tonnage of fish than the other stocks and areas, both over the period of the assessment (Figure 19, upper panels) and in their unfished state (Table 10). In contrast, although ENLD/EN were estimated to contain much greater tonnages of snapper than BOP/BP over the assessment period, the reverse is estimated to have been true in the unfished state, because the latter was estimated to be more depleted in 1970 (Rinitial = 0.12 or 0.11) than the former (Rinitial = 0.66 or 0.65) (see Table 10).

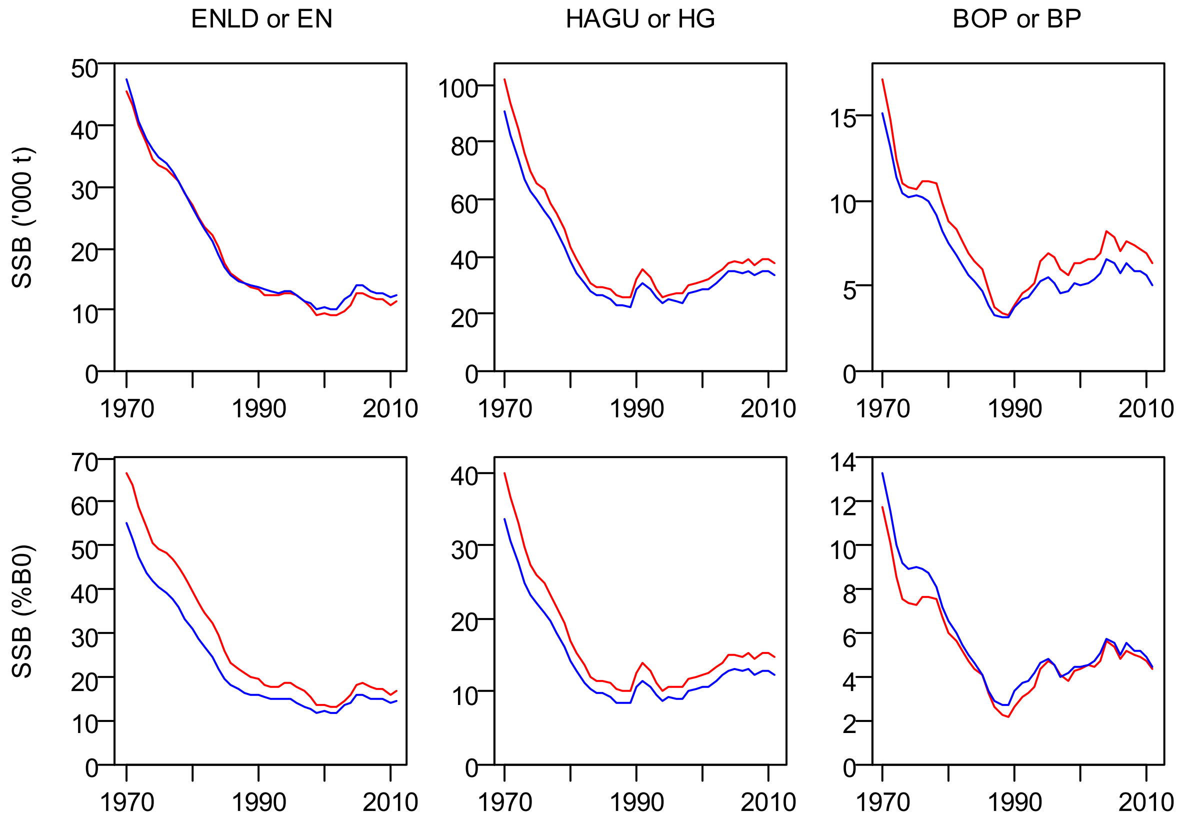

Figure 19: Base case estimates of spawning biomass (SSB) by stock (red lines, for stocks ENLD, HAGU, BOP) and by area (blue lines, for areas EN, HG, BP). These are presented in tonnes (upper panels) and relative to the corresponding unfished biomass, B_0 (lower panels).

Table 10: Base case estimates of unfished biomass, B_0, Rinitial, and current biomass by stock and area.

	B_0 ('000 t)		Rinitial		$B_{current}$ (% B_0)	
Stock/area	by stock	by area	by stock	by area	by stock	by area
ENLD/EN	68	86	0.66	0.65	17	15
HAGU/HG	255	270	0.40	0.41	15	12
BOP/BP	146	114	0.12	0.11	4	4

The majority of fish do not move away from their home grounds, with migration being most common for BOP fish, 27% of which migrate to area HG (Table 11).

Table 11: Base case migration matrix (showing proportions of each stock migrating to each area in time step 2).

	Area		
Stock	EN	HG	BP
ENLD	0.94	0.04	0.02
HAGU	0.07	0.89	0.04
BOP	0.03	0.27	0.70

Most estimated year-class strengths (YCSs) are between half and double the strength predicted by the stock-recruit relationship (Figure 20). Since there is a hypothesis that fish in HG and BP constitute a single spawning stock it was of interest to ask whether the estimated YCSs for HAGU and BOP were markedly more highly correlated with each other than with those for ENLD; this was not true (Figure 21).

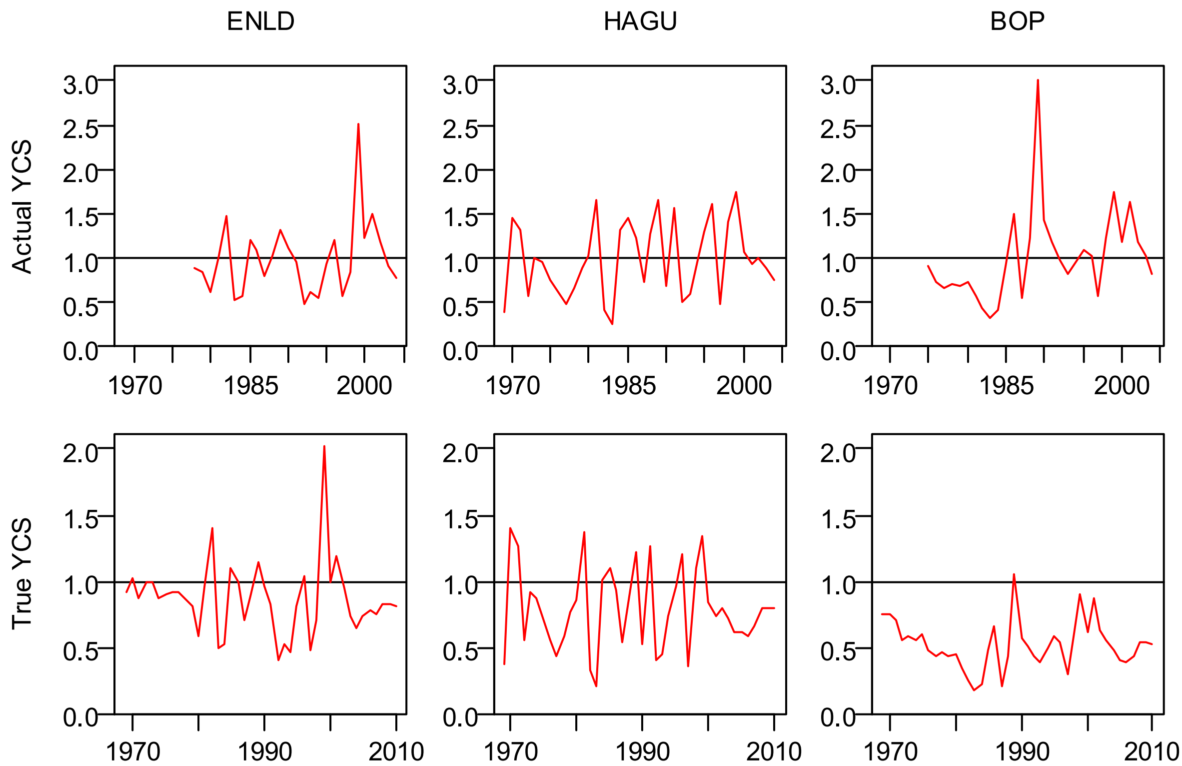

Figure 20: Base case estimates of year-class strengths (YCS) by stock, plotted both as 'actual' YCSs (upper panels, where a value of 1 corresponds to the recruitment predicted by the stock-recruit curve) and 'true' YCSs (lower panels, where a value of 1 corresponds to the mean unfished recruitment).

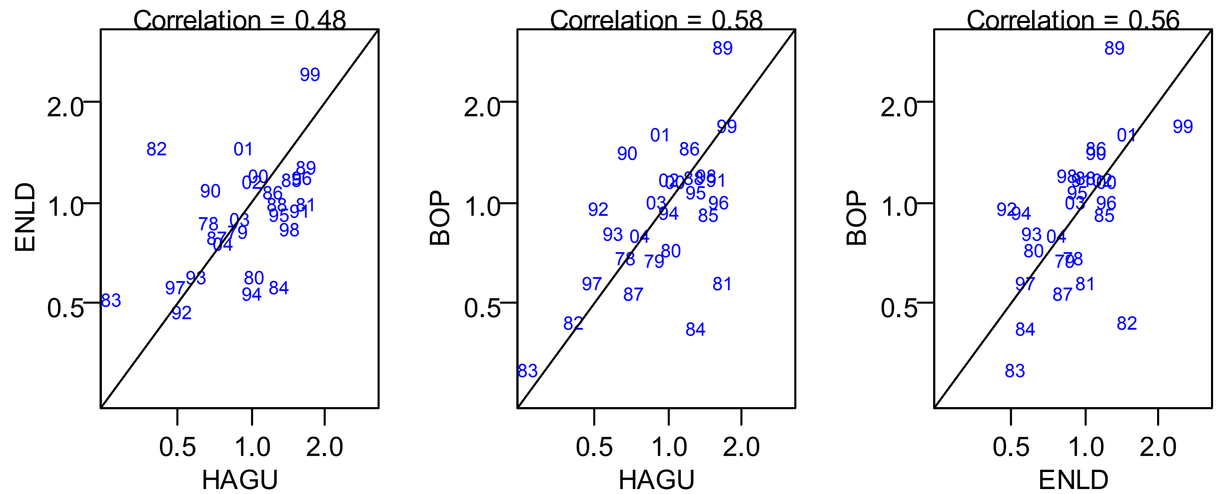

Figure 21: Between-stock comparisons of estimated (true) YCSs (Restricted to years 1978-2004). The plotting symbol for each point is the last two digits of the year (e.g., '89' relates to 1989).

The base model fitted all the relative and absolute biomass observations reasonably well (Figure 22) and fitted much, but not all, of the tag recapture data (Figure 23). Observed trends in mean length and age were reasonably matched by the model (Figure 24).

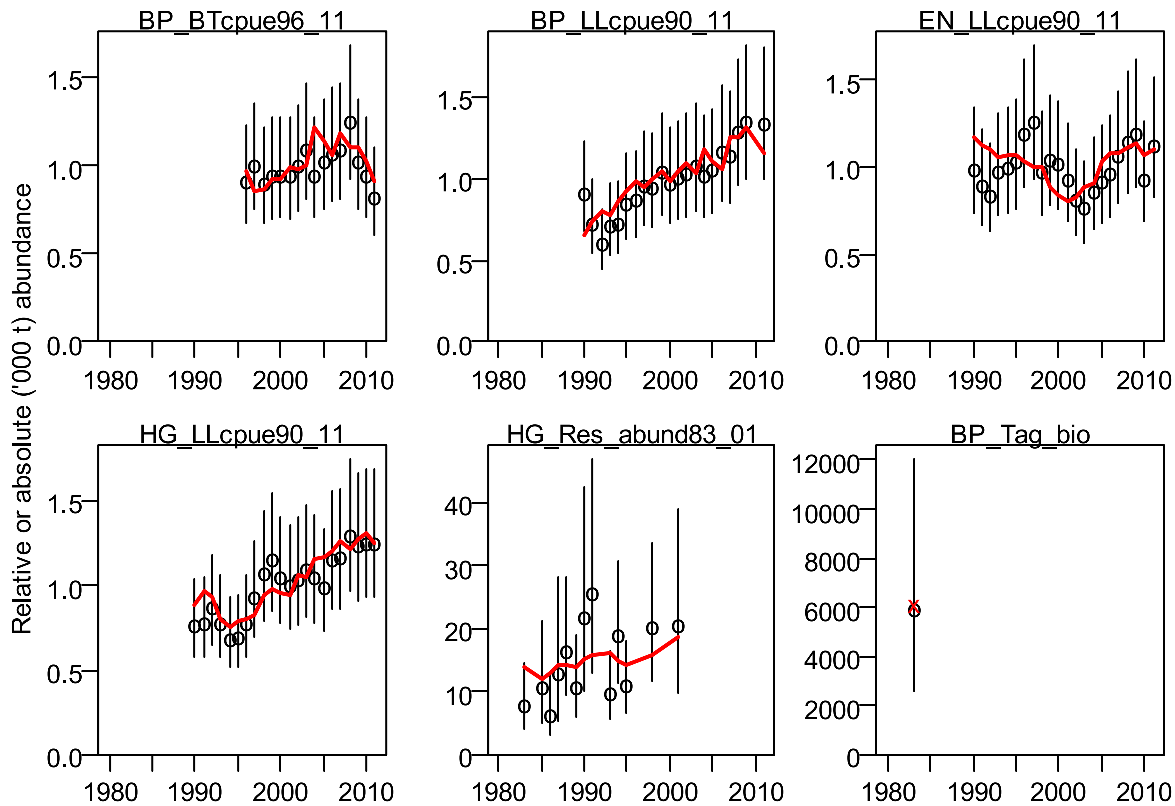

Figure 22: Base-case fits (red lines or 'x') to relative and absolute biomass observations ('o', with 95% confidence intervals as vertical lines).

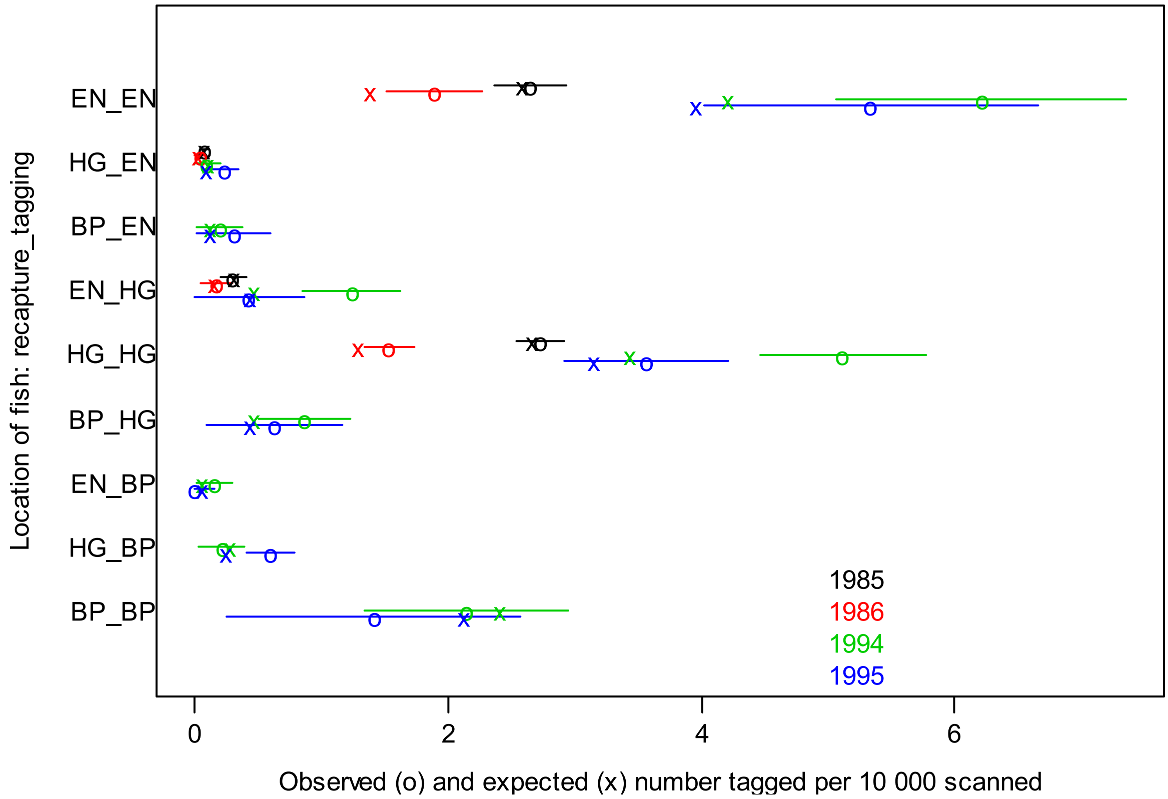

Figure 23: Base-case fits to tag recapture observations. Plotting conventions as in Figure 11.

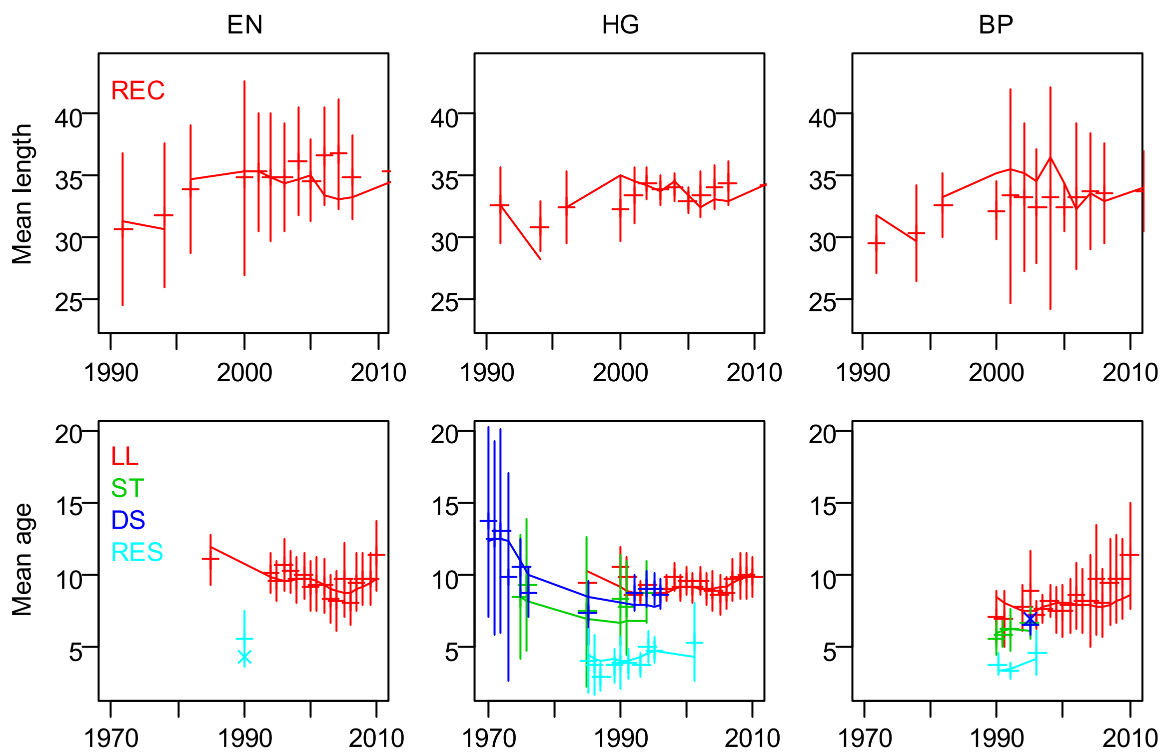

Figure 24: Base-case fits to mean length (upper panels) and age (lower panels) from the composition observations. The observed means are plotted as short horizontal lines, with their 95% confidence intervals shown as a vertical line; the expected means are plotted as a curved line (or, for data sets with only one year, as an 'x'). The data sources are identified by colour (REC = recreational; LL = longline; ST = single trawl; DS = Danish seine; RES = research trawl).

Estimated exploitation rates varied widely by fishery and were highest in area BP (Figure 25). The estimated selectivities suggested that research trawl caught the smallest fish and longlines caught the largest (Figure 26).

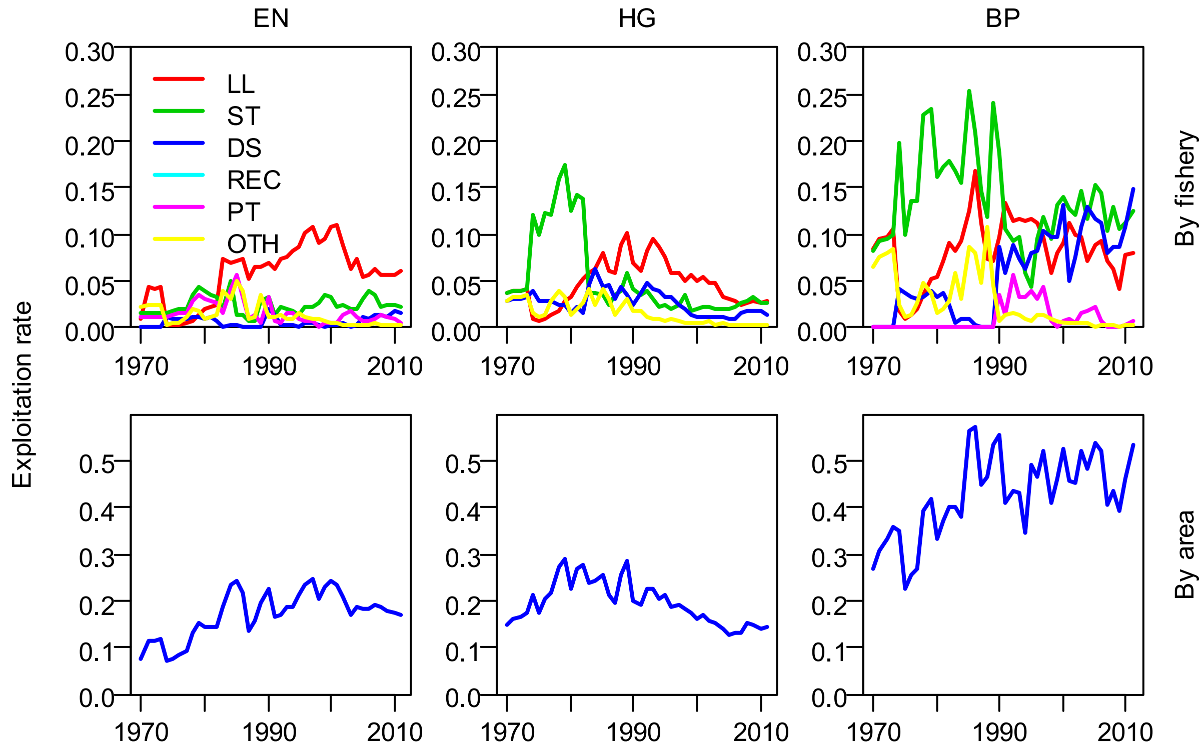

Figure 25: Base case estimates of exploitation rates by fishery (upper panels) and by area (lower panels).

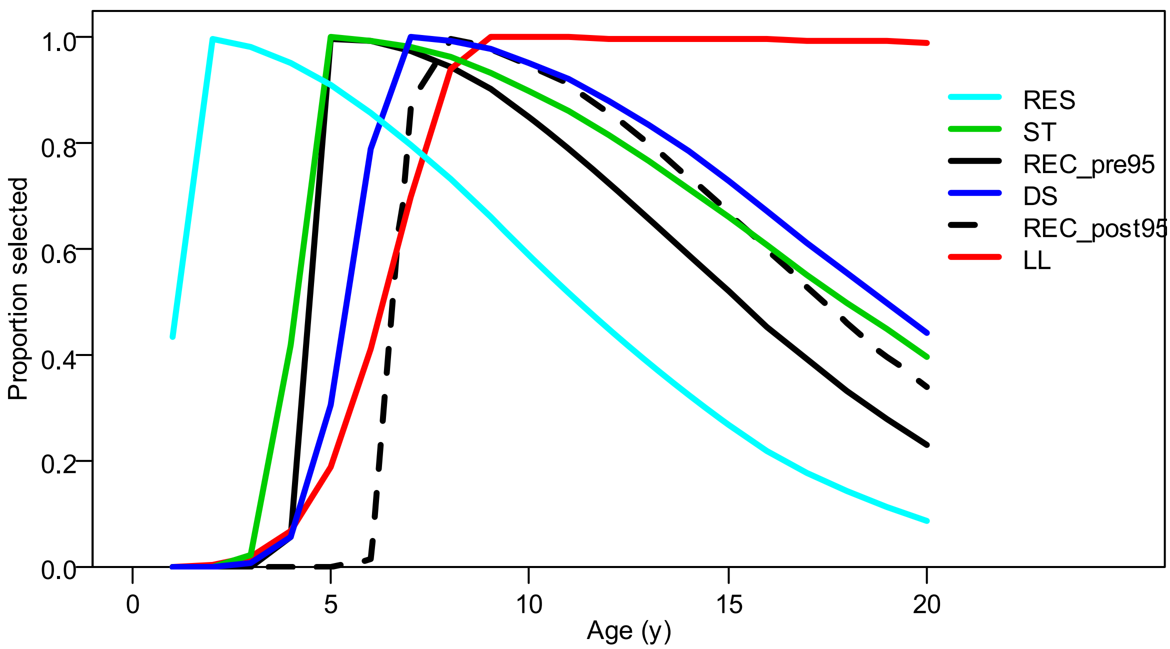

Figure 26: Selectivities estimated in the base model.

6.2 Sensitivity runs

The Working Group requested five sensitivity runs: two with alternative values of M (0.065 and 0.085; runs Mlo and Mhi); two with alternative values of steepness, h, (0.8, 0.9; runs hlo and hhi); and one with recreational catches increased by 25% (run RECh).

Results from the first four sensitivities are straightforward: an increase (or decrease) in either M or h implies an increase (or decrease) in the productivity of each stock, so the stocks are estimated as being less (or more) depleted by the observed catch histories (Figure 27; analogous plots of SSBs by area look very similar).

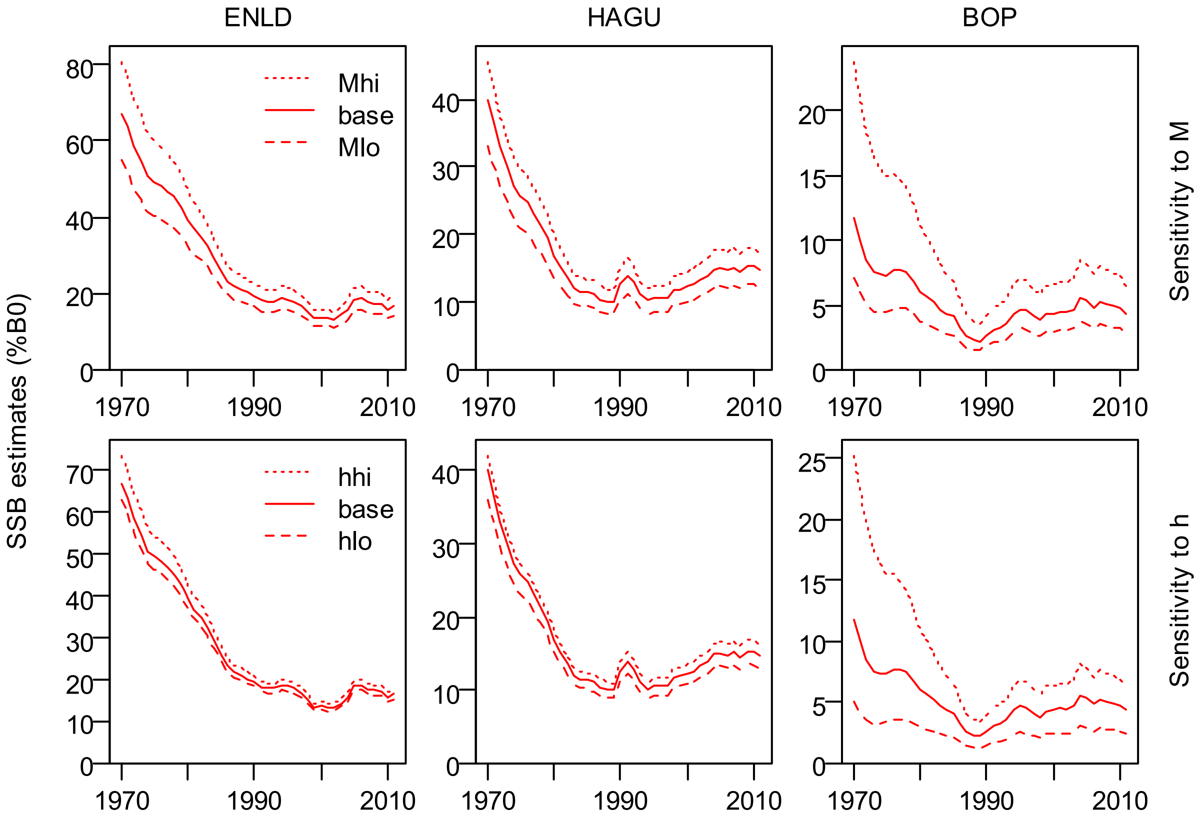

Figure 27: Effect on spawning biomass trajectories by stock (plotted as %B_0) of varying natural mortality, M (upper panels) or steepness, h (lower panels).

The sensitivity RECh is less straightforward. First, increasing the recreational catch substantially degraded the fit to all types of observation, whereas changes in M and h had relatively small effects on goodness of fit (Table 12). Second, the effect of the change in recreational catch on spawning biomass differed depending on which stock or area the biomass applied to (Figure 28). One reason for this is that the migration matrix for this run differs substantially from that of the base run (Table 13), which was not the case for the other sensitivities. Run RECh is implausible because Rinitial was estimated at its upper bound (1) for stocks ENLD and HAGU.

Table 12: Gains in fit (relative to the baserun) for each sensitivity run, to each type of observation. Positive (or negative) numbers indicate a better (or worse) fit.

	Sensitivity run				
Type of observation	Mlo	Mhi	hlo	hhi	RECh
Biomass	-1	1	0	0	-10
Comps	3	-4	-1	1	-28
Tag	6	-6	0	0	-5
All	8	-9	-1	1	-43

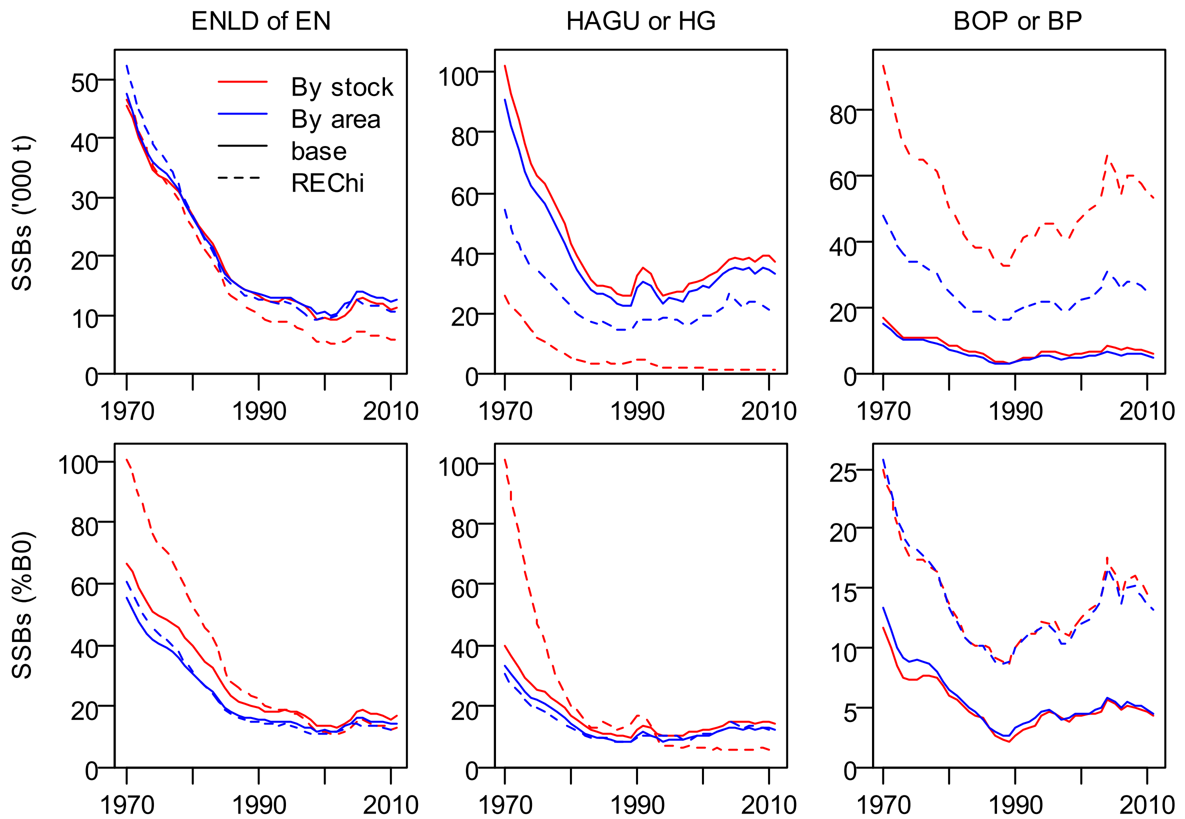

Figure 28: Comparison of spawning biomass (SSB) trajectories (in '000 t in the upper panels, and as %B_0 in the lower panels) from the base run (solid lines) and RECHi (broken lines). SSBs are plotted both by stock (red lines) and by area (blue lines).

Table 13: Comparison of migrations matrices estimated for the base and RECHi runs

	base			RECHi		
	EN	HG	BP	EN	HG	BP
ENLD	0.94	0.04	0.02	0.92	0.04	0.05
HAGU	0.07	0.89	0.04	0.07	0.79	0.14
BOP	0.03	0.27	0.70	0.11	0.41	0.48

6.3 Comparisons with one-stock models

The biomass trajectories estimated from the one-stock models were quite similar to those from the base model (Figure 29), particularly when we focus on the years for which biomass indices were available and consider the trends in biomass, rather than their absolute values (Figure 30). The one-stock models fitted the biomass indices slightly worse than did the base model (Figure 31).

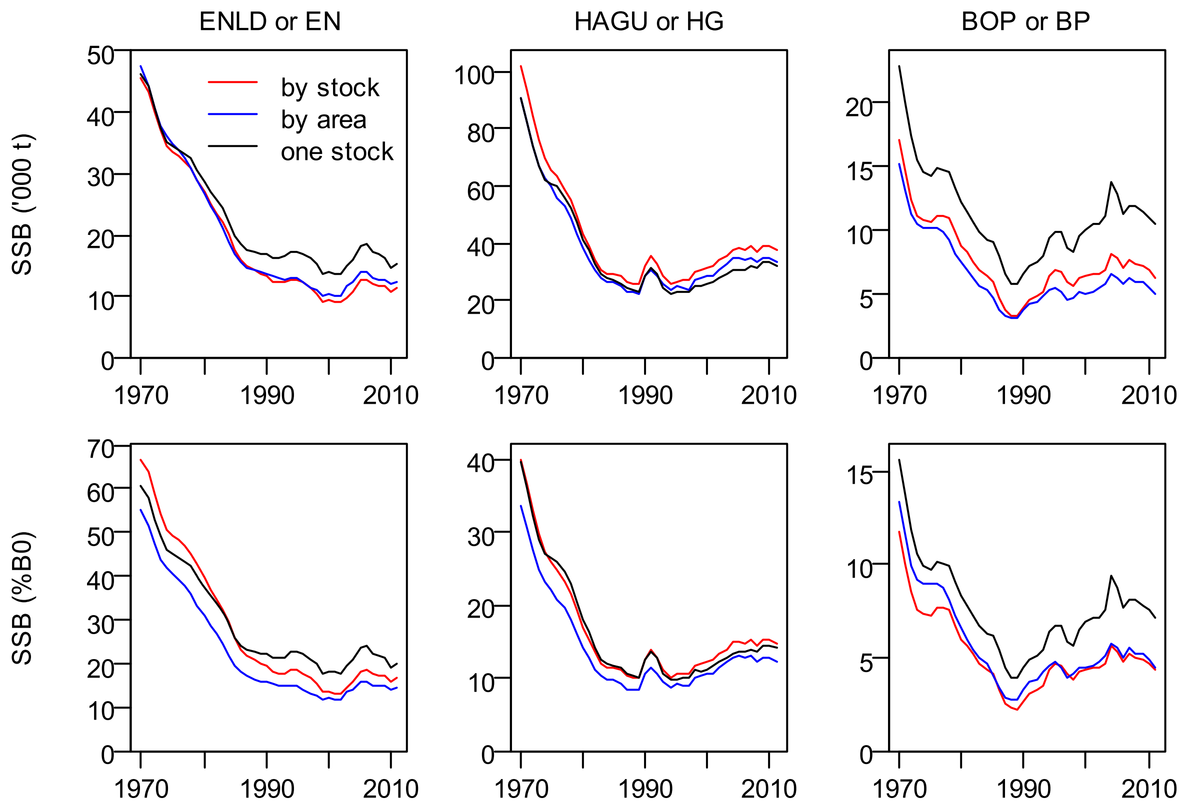

Figure 29: Comparison of spawning biomass (SSB) trajectories from the base model (red line, by stock; and blue lines, by area) with those for the corresponding one-stock models (black lines).

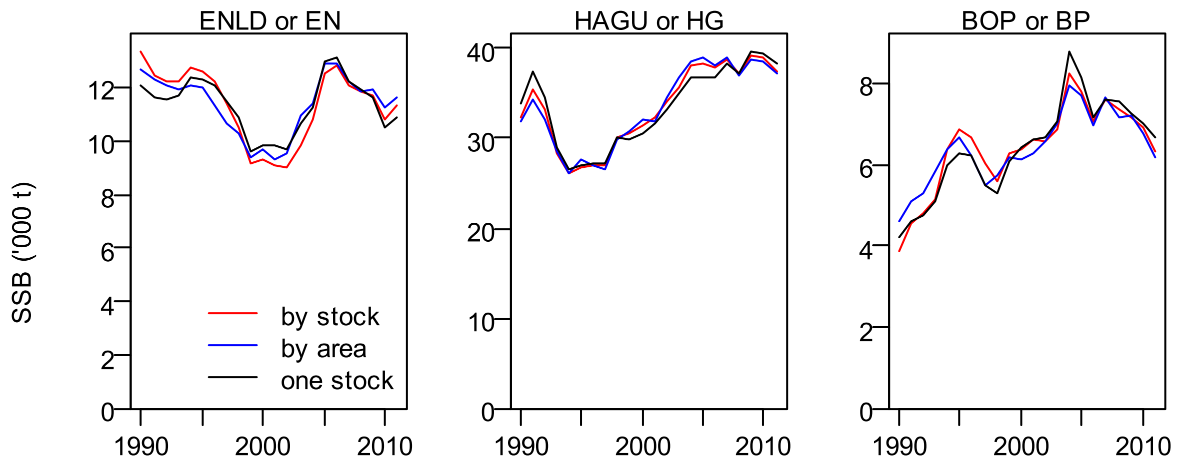

Figure 30: Comparison like that in the upper panels of Figure 29 but (a) restricted to the years where there are biomass indices, and (b) with the blue and black lines in each panel scaled to have the same mean as the red line (so as to facilitate the comparison of trend, rather than absolute value).

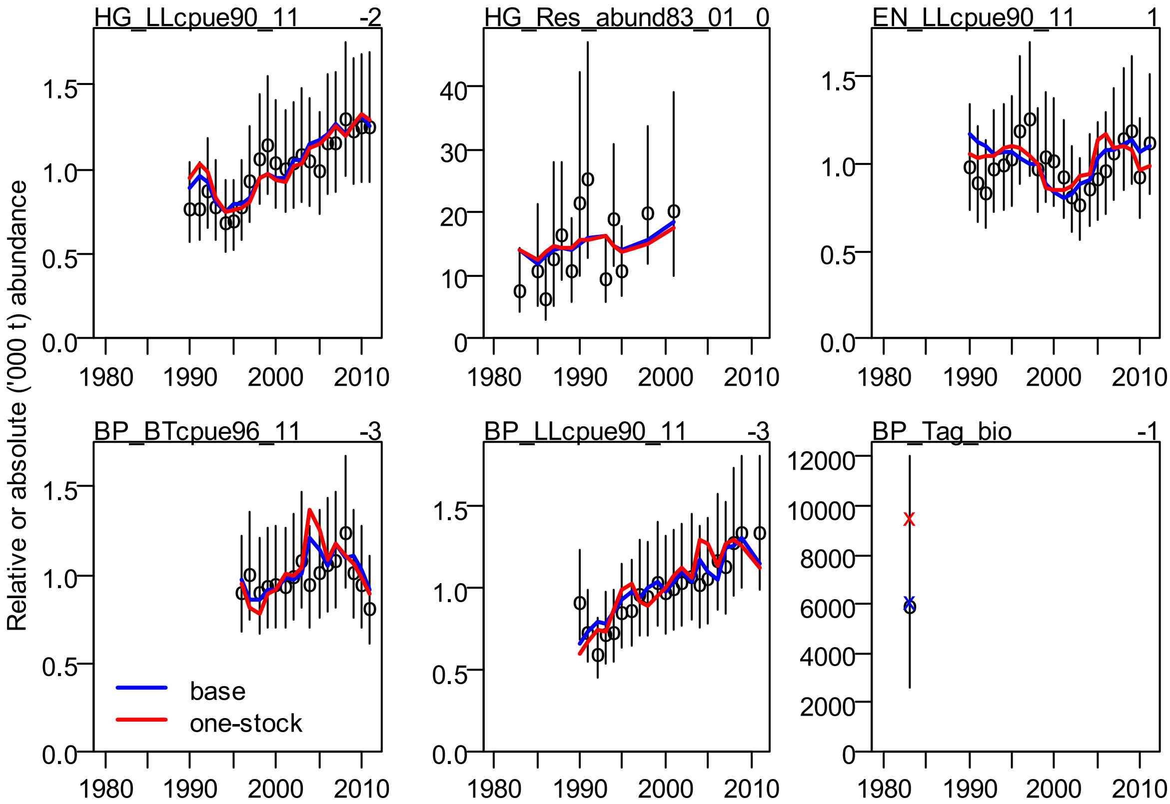

Figure 31: Comparison of the fits to the biomass indices from the base model (blue lines) and the corresponding one-stock model (red line). The observations are plotted as 'o', with the 95% confidence interval shown as a vertical line. The number shown above each panel on the right is the gain in fit (a negative number means that the one-stock model fitted worse than the base model).

7 FURTHER EXPLORATIONS

7.1 Profiles on Rinitial

One striking aspect of the base model was the very different levels of initial depletion estimated for the three stocks, with Rinitial varying from 0.12 for BOP to 0.66 for ENLD (Table 10). A posterior profile was constructed on Rinitial for each stock to explore how well these parameters were determined, and which observations contributed most to their estimates.

Approximate 95% confidence intervals from the profiles showed that Rinitial was much better determined for HAGU (where the width of the interval was 0.15) than for ENLD and BOP (with interval widths 0.36 and 0.25, respectively) (upper panels, Figure 32). The observations that should be most informative about Rinitial are the age and length compositions, but it was only for HAGU that these data drove the estimate of Rinitial (lower panels, Figure 32). Further, as might be expected, the most influential objective-function component for this stock was the earliest composition data set, HG_DS_age (Table 14). For ENLD, no single type of observation drove the estimate of Rinitial, with the lower bound being determined mostly by the tag recapture observations (primarily 1985HAGU_HAGU_Tags), and the upper bound by biomass observation (mostly EN_LLcpue90_11). For BOP, none of the observations appeared to contain much information about Rinitial, which was determined mostly by the prior distributions on YCSs.

[Technical note concerning Table 14. For the purposes of this table we defined the most influential component of the objective function at one end (lower or upper) of a posterior profile as the one whose removal most reduced the contrast at that end, where the contrast is the difference between the values of the objective function at that end and at the minimum.]

Table 14: The individual objective-function components that are most influential in determining lower and upper bounds for the parameter Rinitial in each of the three stocks.

	ENLD	HAGU	BOP
Lower	1985HAGU_HAGU_Tags	HG_DS_age	prior on HAGU YCS
Upper	EN_LLcpue90_11	HG_DS_age	prior on BOP YCS

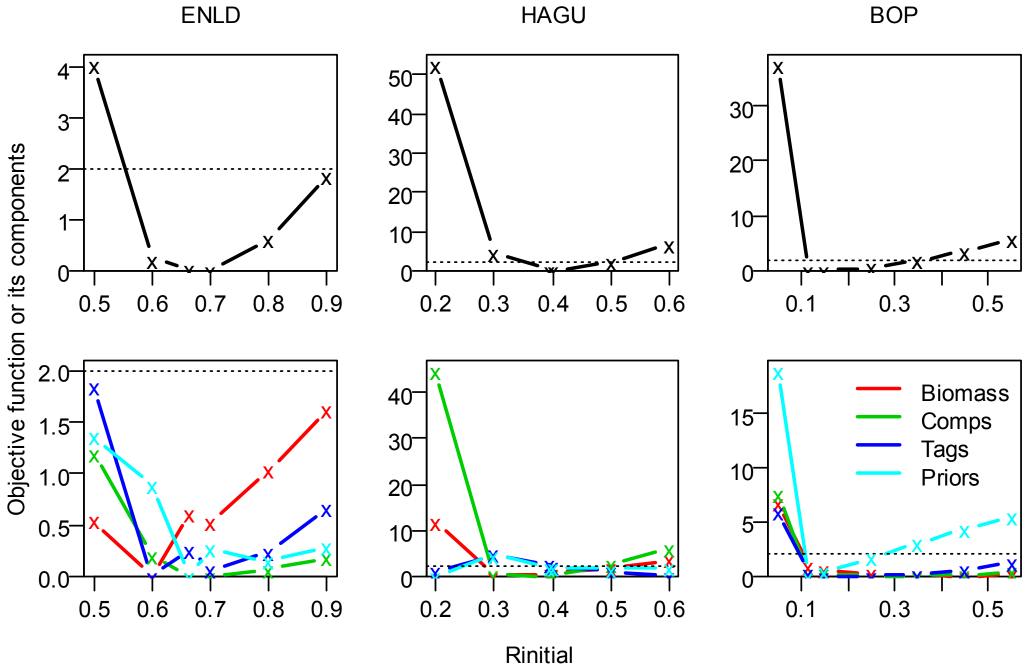

Figure 32: Results of posterior profiles on the parameter Rinitial for each stock: the upper panel shows the total objective function values for each profile; the lower panels shows the contributions to the objective function from three groups of observations (Biomass, (age and length) Compositions, and Tag recapture) and also from prior distributions. In all panels the objective function lines have all been zero-adjusted (i.e., shifted vertically to have minimum value zero). Where the horizontal dotted line (at *y* = 2) intersects the other line in the upper panels indicates an approximate 95% confidence interval for each Rinitial.

For given catch histories, we might expect that the estimated current status of each stock (i.e., the current spawning biomass as a percentage of B_0) would be determined by the combination of the unfished size of the stock (B_0) and its initial depletion (Rinitial). The posterior profiles showed that the latter parameter, by itself, had little effect on current status (Figure 33).

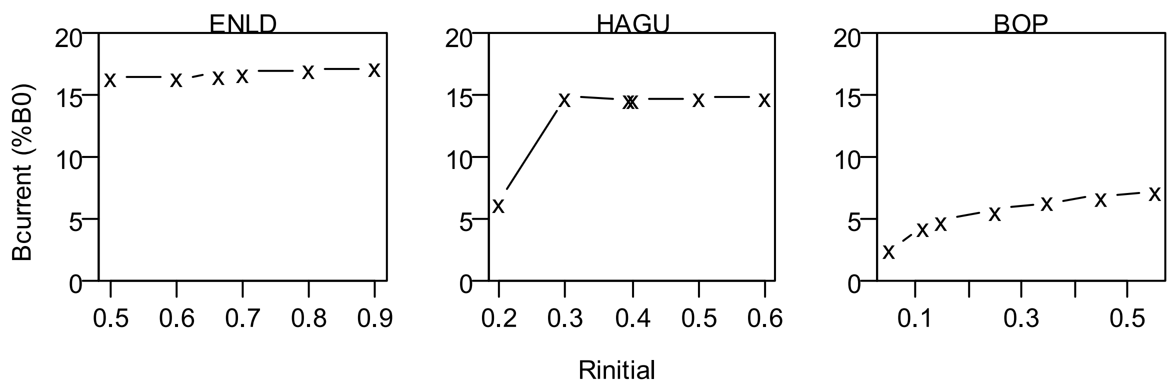

Figure 33: Relationship, from the posterior profile on Rinitial for each stock, between Rinitial and current biomass (as %B_0).

8 BASE CASE MCMC

For the base case model we calculated fully Bayesian estimates by generating an MCMC chain of length 1 million, starting at the MPD and retaining every 1000th sample. Following Francis (2005), four parameters (all for selectivities) that were estimated at a bound in the MPD were fixed in the MCMC in an attempt to improve performance.

The performance of the MCMC was very poor. Traces for key model outputs showed poor mixing (Figure 34), indicating that medians and 95% confidence intervals for these quantities would be unreliable. Because the MCMC ran very slowly (it took 106.5 hours) there was not time to investigate and correct this poor performance.

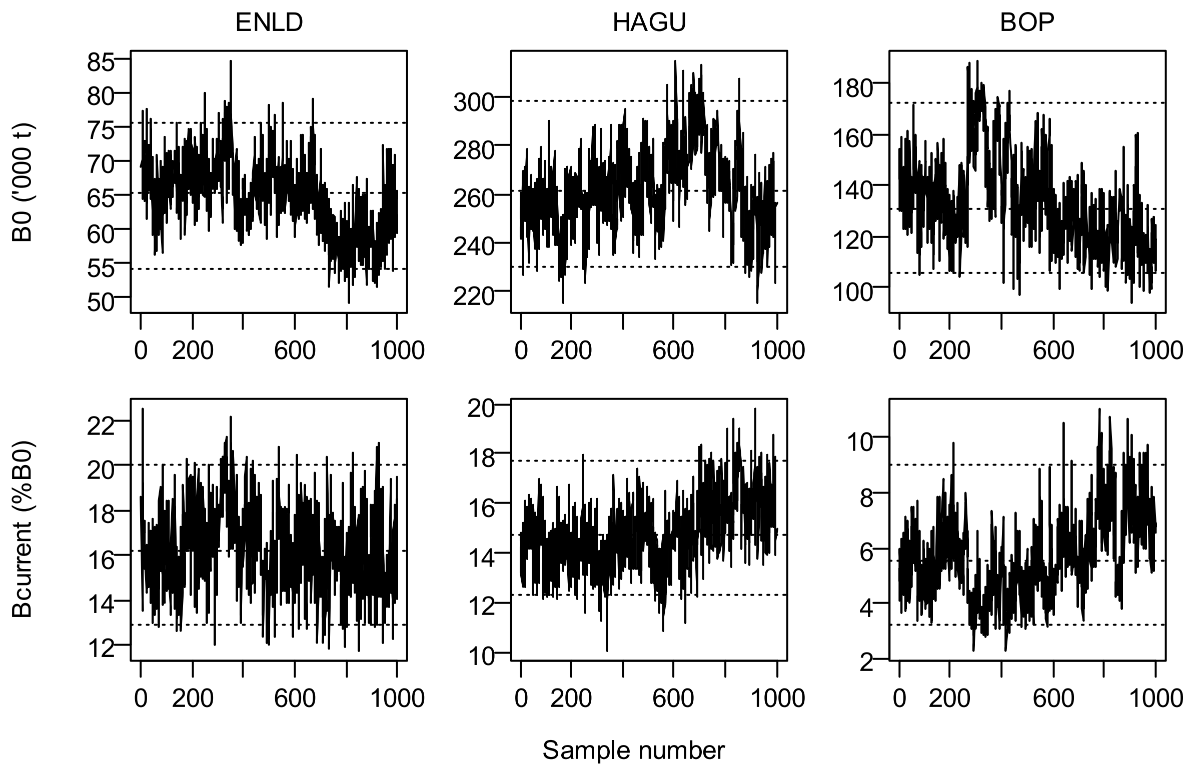

Figure 34: MCMC traces for key model outputs: B_0 (upper panels) and $B_{current}$ (%B_0) (lower panels), by stock. Dotted lines show the medians and 95% confidence intervals derived from these traces.

9 PROJECTIONS

At the request of the Working Group, five-year projections were used to assess the likely effect of current catches on the spawning biomass. The annual catches used in these projections were those from 2011, for commercial fisheries, and the average for 2009 – 2011 for recreational fisheries. Projections were done using both the deterministic (i.e., MPD) and stochastic (MCMC) versions of the base model. In both cases, year-class strengths for future years were selected at random from those estimated for years 1995 – 2004.

All projections suggested that, with current catch levels, biomass is likely to decline slightly for east Northland and Hauraki Gulf, or more rapidly for Bay of Plenty (Figure 35). The Working Group had little confidence in the projection results because of the poor performance in the MCMC fitting process.

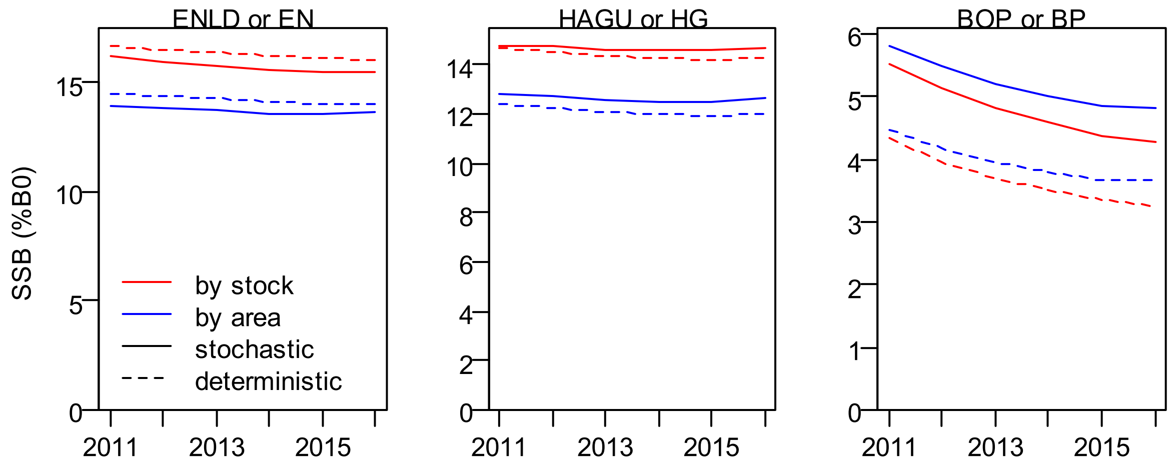

Figure 35: Projected median spawning-stock biomass (SSB), by stock and by area, assuming status quo catches, as estimated from both stochastic (MCMC, solid lines) and deterministic (MPD, broken) models.

10 DETERMINISTIC B_{MSY}

The standard method for calculating deterministic B_{MSY} – defined for a single-stock, single-fishery model – must be generalised for use with a model with multiple stocks, fisheries and areas. We used an approach similar to that developed for hoki by McKenzie & Francis (2009). This approach defines a harvest strategy in which the exploitation rate for fishery f is $U_{\text{mult}}U_{f,2011}$, where $U_{f,2011}$ is the estimated 2011 exploitation rate for that fishery, and U_{mult} is some multiplier (the same for all fisheries). For each of a series of values of U_{mult}, simulations were carried out with this harvest strategy and deterministic recruitment, with each simulation continuing until the population reached equilibrium. For each stock (or area), the value of the multiplier, U_{mult}, was found that maximised the equilibrium catch from that stock (or area). B_{MSY} for that stock (or area) run was then defined as the equilibrium spawning biomass (expressed as $\%B_0$) at that value of U_{mult} (as illustrated in Figure 36). Estimates of B_{MSY} were very similar for all stocks and areas, lying between 26% B_0 and 27% B_0 (Table 15).

There are two reasons why a management target for the SNA 1 fishery should be higher than the values of B_{MSY} presented here. First, the above calculation of B_{MSY} assumed a harvest strategy that is unrealistic in that it requires perfect knowledge (of both current biomass – in order to calculate the target catch – and key biological parameters, such as natural mortality and stock-recruit steepness), annual changes in TACC (which are unlikely to happen in New Zealand and not desirable for most stakeholders), and a constant relationship between the exploitation rates in the different fisheries. It is difficult to model more realistic assumptions (involving imperfect knowledge and control of the fishery) but it is clear that such assumptions would lead to higher values of B_{MSY}. A second reason to believe that 26–27% B_0 is too low a target is that it would be very difficult with such a target to avoid the biomass occasionally falling below 20% B_0, the default soft limit according to the Harvest Strategy Standard (Ministry of Fisheries 2008).

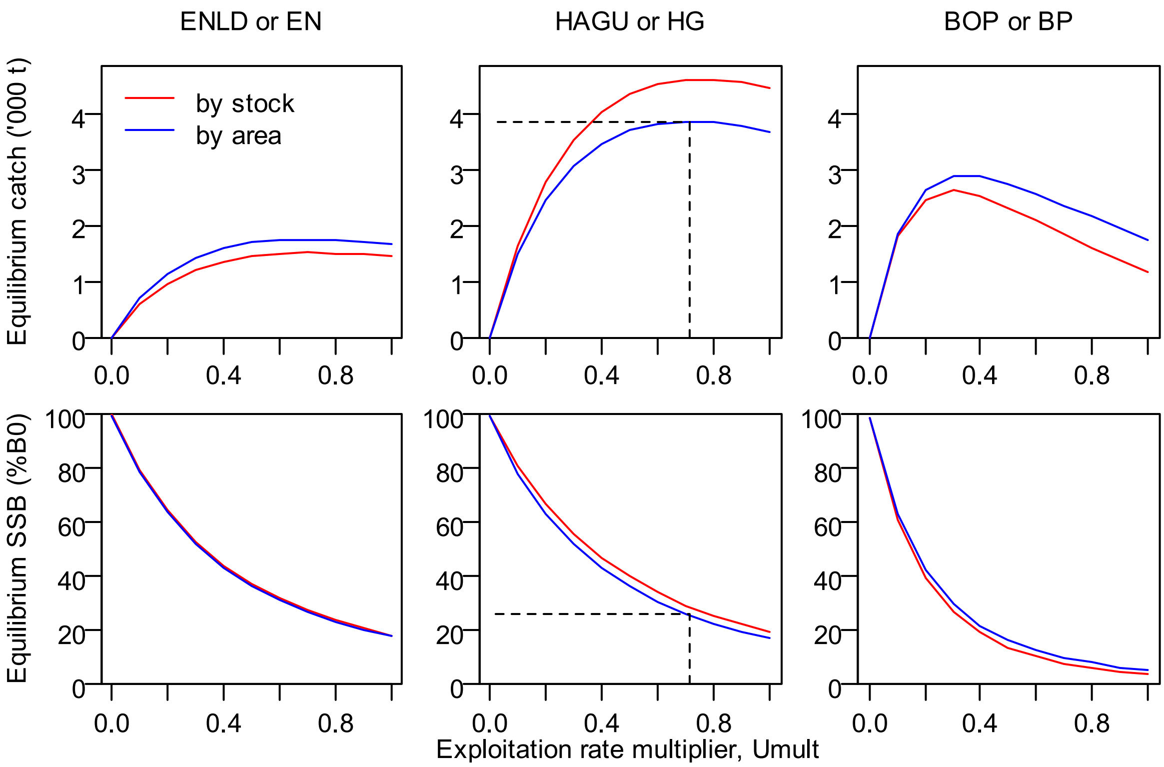

Figure 36: Illustration of the method for estimating deterministic B_{MSY} by stock (red lines) and by area (blue lines). The broken lines show how B_{MSY} is determined from these plots: for area HG these lines in the upper panel show that equilibrium catch is maximised at U_{mult} = 0.71; in the lower panel they show that the equilibrium SSB for this value of U_{mult} is 26% B_0.

Table 15: Estimates of deterministic B_{MSY} (%B_0) by stock (ENLD, HAGU, or BOP) and by area (EN, HG, or BP).

	ENLD/EN	HAGU/HG	BOP/BP
By stock	27	27	26
By area	27	26	26

11 DISCUSSION

The analyses and results presented here constitute another useful step towards the development of a model that describes the complex spatio-temporal interactions that occur in the SNA 1 stock. They have substantially refined the three-stock model proposed by McKenzie (2012) (by, *inter alia*, making the partition more efficient, improving the data weighting and initial age structure, and adding adjustments for trap shyness) and more fully explored its strengths and weaknesses.

The main structural differences between the previous (Gilbert et al. 2000) and the 2012 SNA 1 assessments are:

- Separation of Bay of Plenty and Hauraki Gulf sub-stocks;
- Incorporation of a Beverton & Holt stock recruitment relationship (h = 0.85; note: no stock recruit relationship was assumed in the 1999 SNA 1 assessment).

Deterministic B_{MSY} from the 2012 assessment was 26–27% B0 for all stocks and areas compared to 20% B0 in the 1999 assessment; the inclusion of a stock recruit dynamic is likely to have been a strong contributing factor to the difference in the B_{MSY}/B0 ratios between the two assessments (Hilborn & Stokes 2010; McKenzie 2012).

However, model development was not completed in 2012. Two major weaknesses of the 2012 model were the estimation of initial depletion (Rinitial) and very slow MCMC runs with poor diagnostics.

Work was undertaken in 2013 (under an extension to the SNA201101 project) to address these weaknesses (as well as a series of more minor issues), with the aim of producing a model that was sufficiently robust to produce results useful for management (see Francis & McKenzie 2015).

12 ACKNOWLEDGEMENTS

This work was contracted and funded by the Ministry for Primary Industries under research project SNA201101. Bruce Hartill undertook the majority of the analytical work which led to the recreational harvest estimates with John Holdsworth also providing significant input in developing recreational catch histories. Darren Parsons revised and updated the CPUE data series and undertook much of the revised CPUE analyses. Acknowledgement is also due to the Northern Inshore Working Group; the review and recommendations this group provided were critical to the final assessment outcome. Marc Griffiths, the Working Group convenor and chair, is due special recognition for keeping the assessment process on track. Finally, the authors would like to thank Andy McKenzie and Marc Griffiths for manuscript review and Marianne Vignaux for the final editorial.

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14 APPENDICES

Appendix 1: Model catch history (tonnes) by area and fishery

East Northland

Year	LL	ST	PT	DS	OTH	REC
1970	486	419	487	0	332	442
1971	1898	408	475	0	324	451
1972	1693	364	424	0	289	461
1973	1598	343	400	0	272	470
1974	83	314	368	224	40	480
1975	95	354	412	202	46	489
1976	107	421	491	204	52	498
1977	142	418	485	202	118	508
1978	239	683	797	218	218	517
1979	402	798	929	227	192	527
1980	496	660	767	168	104	536
1981	506	564	656	186	107	546
1982	536	494	575	114	132	555
1983	1446	281	328	23	358	565
1984	1223	673	781	35	258	574
1985	1111	164	929	34	389	584
1986	1021	153	491	13	282	593
1987	641	76	139	0	76	603
1988	791	85	201	0	95	612
1989	784	300	72	0	264	621
1990	800	363	420	197	86	631
1991	694	157	106	138	85	575
1992	780	235	79	34	101	539
1993	792	213	198	20	75	621
1994	865	199	189	33	80	630
1995	900	138	128	17	127	651
1996	1043	240	94	52	99	691
1997	1089	231	98	58	86	737
1998	893	261	15	31	77	580
1999	831	308	43	11	52	607
2000	904	284	44	20	41	588
2001	873	200	53	21	33	539
2002	722	224	136	36	25	476
2003	546	191	200	11	22	445
2004	646	223	136	30	23	509
2005	541	383	108	133	34	557
2006	603	507	110	108	39	562
2007	669	419	133	142	45	616
2008	625	264	183	144	31	700
2009	615	283	156	120	29	716
2010	593	268	107	184	35	559
2011	658	237	74	154	25	559

Appendix 1 cont: Model catch history (tonnes) by area and fishery

Hauraki Gulf

Year	LL	ST	DS	OTH	REC
1970	3365	1912	1607	764	799
1971	3283	1865	1567	746	817
1972	2927	1663	1397	665	834
1973	2762	1570	1319	628	851
1974	520	4260	1403	248	868
1975	428	3446	906	206	885
1976	503	4315	965	245	902
1977	640	4073	911	532	919
1978	836	5191	767	768	937
1979	1207	5191	679	576	954
1980	1146	3302	389	242	971
1981	1438	3468	530	302	988
1982	1498	2986	320	368	1005
1983	1451	760	869	532	1022
1984	1439	743	1115	314	1039
1985	1679	704	762	546	1056
1986	1191	520	780	418	1074
1987	1131	688	553	204	1091
1988	1750	752	767	331	1108
1989	1878	1112	570	427	1125
1990	1460	1014	486	319	1142
1991	1414	927	881	370	1153
1992	1854	1030	1091	266	1300
1993	1850	677	788	175	1172
1994	1555	479	699	174	1028
1995	1448	541	646	143	1035
1996	1129	460	627	176	1053
1997	1141	548	495	149	1255
1998	1157	865	443	102	1444
1999	1312	447	326	100	1526
2000	1142	496	250	103	1383
2001	1228	556	273	129	1344
2002	1199	587	266	146	1385
2003	1180	581	307	80	1488
2004	911	625	304	142	1436
2005	832	605	282	95	1345
2006	778	692	257	70	1578
2007	703	803	469	66	1597
2008	769	828	513	86	1754
2009	871	1005	503	103	1647
2010	833	747	486	64	1664
2011	875	757	394	57	1664

Appendix 1 cont: Model catch history (tonnes) by area and fishery

Bay of Plenty

Year	LL	ST	PT	DS	OTH	REC
1970	1324	0	752	0	301	346
1971	1291	0	733	0	293	354
1972	1151	0	654	0	262	361
1973	1086	0	618	0	247	368
1974	152	0	1250	224	73	376
1975	82	0	656	202	40	383
1976	115	0	989	204	56	391
1977	158	0	1007	202	131	398
1978	272	0	1693	218	251	405
1979	368	0	1583	227	175	413
1980	342	0	988	168	72	420
1981	415	0	1000	186	88	428
1982	479	0	955	114	118	435
1983	389	0	834	23	217	443
1984	394	0	730	35	108	450
1985	494	0	1150	34	287	457
1986	551	0	802	13	229	465
1987	316	0	473	0	122	472
1988	197	0	347	0	252	480
1989	174	0	691	0	100	487
1990	243	125	662	216	18	494
1991	356	58	444	177	42	398
1992	332	248	400	308	53	329
1993	333	143	422	232	47	395
1994	343	164	300	217	33	397
1995	395	215	246	338	35	464
1996	409	172	512	365	58	428
1997	351	223	587	439	58	474
1998	213	31	455	395	35	470
1999	308	0	670	416	29	513
2000	338	39	723	543	24	480
2001	429	55	692	219	21	495
2002	404	33	656	354	20	511
2003	388	85	836	479	26	531
2004	315	121	776	641	23	504
2005	377	139	982	590	7	516
2006	370	48	862	532	14	565
2007	320	11	661	419	12	550
2008	292	12	784	457	17	619
2009	196	10	640	457	10	647
2010	367	14	647	551	15	664
2011	355	37	662	695	11	664

Appendix 2: Relative and absolute abundance model input values. Assumed model CVs are in brackets.

Year	BP_Tag_bio	BP_Btcpue	BP_Llcpue	EN_Llcpue	HG_Llcpue	HG_Res_abund
1983	6000 (0.4)	–	–	–	–	8150580 (0.25)
1985	–	–	–	–	–	11197900 (0.31)
1986	–	–	–	–	–	6751430 (0.32)
1987	–	–	–	–	–	13300900 (0.39)
1988	–	–	–	–	–	16899000 (0.2)
1989	–	–	–	–	–	11102600 (0.22)
1990	–	–	0.92 (0.15)	1.00 (0.15)	0.78 (0.15)	22093300 (0.31)
1991	–	–	0.74 (0.15)	0.91 (0.15)	0.79 (0.15)	25976000 (0.26)
1992	–	–	0.61 (0.15)	0.85 (0.15)	0.89 (0.15)	–
1993	–	–	0.73 (0.15)	0.98 (0.15)	0.80 (0.15)	10011900 (0.18)
1994	–	–	0.74 (0.15)	1.00 (0.15)	0.70 (0.15)	19437200 (0.15)
1995	–	–	0.86 (0.15)	1.04 (0.15)	0.71 (0.15)	11360600 (0.15)
1996	–	0.92 (0.15)	0.88 (0.15)	1.21 (0.15)	0.79 (0.15)	–
1997	–	1.02 (0.15)	0.97 (0.15)	1.27 (0.15)	0.95 (0.15)	–
1998	–	0.91 (0.15)	0.96 (0.15)	0.99 (0.15)	1.08 (0.15)	20586000 (0.18)
1999	–	0.95 (0.15)	1.05 (0.15)	1.06 (0.15)	1.16 (0.15)	–
2000	–	0.96 (0.15)	0.99 (0.15)	1.03 (0.15)	1.06 (0.15)	–
2001	–	0.95 (0.15)	1.02 (0.15)	0.94 (0.15)	1.02 (0.15)	20866200 (0.29)
2002	–	1.01 (0.15)	1.05 (0.15)	0.83 (0.15)	1.05 (0.15)	–
2003	–	1.10 (0.15)	1.09 (0.15)	0.78 (0.15)	1.11 (0.15)	–
2004	–	0.96 (0.15)	1.04 (0.15)	0.87 (0.15)	1.07 (0.15)	–
2005	–	1.03 (0.15)	1.07 (0.15)	0.93 (0.15)	1.00 (0.15)	–
2006	–	1.08 (0.15)	1.18 (0.15)	0.97 (0.15)	1.17 (0.15)	–
2007	–	1.10 (0.15)	1.15 (0.15)	1.07 (0.15)	1.18 (0.15)	–
2008	–	1.26 (0.15)	1.30 (0.15)	1.16 (0.15)	1.31 (0.15)	–
2009	–	1.03 (0.15)	1.36 (0.15)	1.21 (0.15)	1.25 (0.15)	–
2010	–	0.96 (0.15)	1.40 (0.15)	0.94 (0.15)	1.26 (0.15)	–
2011	–	0.83 (0.15)	1.36 (0.15)	1.13 (0.15)	1.27 (0.15)	–

Appendix 3: Adjustment of 1995 and 1994 tagging programme releases for initial mortality

Estimates of tag-release mortality were derived using two logistic regression predictors (logits); one each for trawl and longline capture-release methods. Logit parameter values were derived as maximum likelihood fits to the combined data from three mortality experiments (NIWA unpublished data; Gilbert & McKenzie 1999).

The fitted logit function for trawl released fish was:

$$logit_{trawl} = 1.6979 + 0.00126C - 0.0842L$$

Where C is the total catch weight (kg) of the trawl capture shot and L is the length of the fish in centimetres. Because C was not available for the 1985 data, it was replaced by 400, an approximation at the weighted mean catch size based on the 1994 trawl tag catch weights. The formula was applied to release fish individually, using individual values for C and L.

The logit function for longline released fish was:

$$logit_{longline} = -4.6423 + 0.0548D$$

where D is the depth (m) at which the fish was captured for tagging.

The release mortality probability p[M] of a tagged snapper from an individual shot or set is:

$$p[M] = \frac{logit}{(1 + logit)}$$

The total number of effective (live) fish released was derived by summing the individual fish predicted survival probabilities.

Appendix 4: Movement adjustment of the tag release and recovery data for input to the single area models

Let N_i be the number of fish tagged in area i; let p_{il} be the proportion of those fish that were in the lth length class; and let **P** be the matrix describing the subsequent movement between areas (so that P_{ij} is the proportion of fish tagged in area i that move to area j). Then the tag release data used in the model for area j should be a mixture of the data from the releases in the three areas, with mixing proportions P_{1j}, P_{2j}, and P_{3j}. That is, the number released should be $M_j = P_{1j}N_1 + P_{2j}N_2 + P_{3j}N_3$, and the proportion of these that were in the lth length class should be $(p_{1l}P_{1j}N_1 + p_{2l}P_{2j}N_2 + p_{3l}P_{3j}N_3)/M_j$. The recapture data for this model should comprise all fish recaptured in area j, regardless of area of release.

There are two ways to get the movement matrix **P** needed to implement this approach: we can either use the matrix estimated in the spatial model, or estimate a matrix outside the model using a simplifying assumption. The former matrix is technically superior, but it was decided to use the latter so that the one-stock models were independent of the spatial model. The required simplifying assumption is that some tagged fish move immediately after tagging, but there is no subsequent movement. With this assumption it is straightforward to construct a maximum-likelihood estimate of **P**. The likelihood to be maximised is $\prod_{ij}\left(E_{ij}^{n_{ij}}\right)$, where n_{ij} is the number of fish that were tagged in area i and recaptured in area j (given in the above table), and $E_{ij} = P_{ij}N_i/M_j$ is the expected proportion of fish recaptured in area j that were tagged in area i.

Using the 1994 tag release/recapture data (TableAppendix 1) the maximum-likelihood estimate of **P** is given in TableAppendix 2. Using this matrix the assumed number of tagged fish in the HAGU single-stock model, for example, would be:

$$0.821 \times 13466 + 0.046 \times 8190 + 0.259 \times 3630 = 12\ 372.$$

TableAppendix 1: Number tagged and recaptured by area 1994 programme.

Tagging area	N tagged	No. recaptured by area HG	EN	BP	All
HG	13 466	272	20	17	309
EN	8 190	10	129	5	144
BP	3 630	25	2	41	68
All	25 286	307	151	63	521

TableAppendix 2: Maximum-likelihood estimate of P.

	HG	EN	BP
HG	0.821	0.093	0.086
EN	0.046	0.916	0.038
BP	0.259	0.032	0.709

Appendix 5: base model population.csl file

This appendix contains the CASAL population.csl file which, together with the CASAL User Manual (Bull et al. 2012) completely specifies the structure of the base model. To save space, inessential details, or material given elsewhere (e.g., annual catches for each fishery) are omitted, as signalled by comments in *italics*.

```
#POPULATION INITIAL STATE
@Rinitial_is_deviate T
@initialization   ENLD
    R0  8000000
    Rinitial 0.8
```

and similar command blocks for stocks HAGU and BOP

```
# PARTITION
@min_age      1
@max_age      20
@plus_group   True
@sex_partition False
@n_areas        3
@area_names     F_EN F_HG F_BP
@n_stocks       3
@stock_names    ENLD HAGU BOP
@exclusions_char1     stock          stock          stock          stock          stock
       stock          stock          stock          stock          stock
@exclusions_val1      ENLD           BOP            HAGU           BOP            HAGU
       ENLD           ENLD           BOP            HAGU           BOP
@exclusions_char2     tag            tag            tag            tag            tag
       tag            tag            tag            tag            tag
@exclusions_val2      1994HAGU_Tags  1994HAGU_Tags  1994ENLD_Tags  1994ENLD_Tags  1994BOP_Tags
       1994BOP_Tags   1985HAGU_Tags  1985HAGU_Tags  1985ENLD_Tags  1985ENLD_Tags

# TIME SEQUENCE
@initial    1970
@current    2011
@final      2016
@annual_cycle
    time_steps       2
    recruitment_time 1
    recruitment_areas F_EN F_HG F_BP
    spawning_time    1
    spawning_part_mort   0.0
    spawning_areas      F_EN F_HG F_BP
    spawning_p      1
    spawning_use_total_B
    aging_time    1
    growth_props  0.0 0.0
    M_props       0.0 1.0
    fishery_names      BP_LLINE       BP_PTRAWL      BP_STRAWL      BP_DSEINE      BP_OTHER
       BP_RECR_pre95          BP_RECR_post95         EN_LLINE       EN_STRAWL      EN_PTRAWL
       EN_DSEINE      EN_OTHER       EN_RECR_pre95          EN_RECR_post95 HG_LLINE
       HG_STRAWL      HG_DSEINE      HG_OTHER       HG_RECR_pre95          HG_RECR_post95

    fishery_times             2              2              2              2              2
             2                     2                     2              2              2
             2              2              2                     2              2
       2              2              2              2                     2

    fishery_areas      F_BP           F_BP           F_BP           F_BP           F_BP
       F_BP                  F_BP                  F_EN           F_EN           F_EN
       F_EN           F_EN           F_EN                  F_EN           F_HG           F_HG
              F_HG           F_HG           F_HG                  F_HG
    n_migrations        12
    migration_names     EN_HG_2 EN_BP_2   HG_EN_2   HG_BP_2  BP_HG_2  BP_EN_2   EN_HG_1    EN_BP_1
HG_EN_1  HG_BP_1  BP_EN_1 BP_HG_1
    migration_times      2     2       2       2       2       2        1       1          1
1       1       1           migrate_from         F_EN    F_HG     F_HG     F_EN    F_BP    F_HG
F_EN      F_EN     F_HG     F_HG     F_BP    F_BP
    migrate_to             F_HG     F_BP      F_EN      F_BP     F_HG     F_EN      F_HG       F_BP
F_EN     F_BP     F_EN    F_HG
@n_tags 5
@tag_names 1985ENLD_Tags 1994ENLD_Tags 1985HAGU_Tags 1994HAGU_Tags 1994BOP_Tags
@tag_shedding_rate 0.486 0.0001  0.486 0.0001  0.0001
@tag_loss_props    0.25 0.75
```

```
# RECRUITMENT
@standardise_YCS  True
@y_enter           1
@recruitment   ENLD
       YCS_years      1969    1970    … 2010
       YCS            1       1       …       1
    SR         BH
    steepness  0.85
    first_free   1969
    last_free    2007
    year_range   1995 2004
```
and similar command blocks for BOP and HAGU, with the following difference: first_free was 1971 for BOP
```
@randomisation_method   empirical
@first_random_year   2012

#SIZE WEIGHT
@size_weight
    a 4.467e-08
    b 2.793

# GROWTH {SIZE AT AGE}
@size_at_age_type     data
@size_at_age_step  1
@size_at_age_dist lognormal
@size_at_age_years 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003
2004 2005 2006 2007 2008 2009 2010 2011
@size_at_age_miss interp
```
followed by one @size_at_age command block for each stock giving the mean sizes at age for each year as shown in Figure 5
```
#MATURITY AND NATURAL MORTALITY
@maturity_props
all allvalues_bounded 3 8 0.00 0.5 1.00 1.00 1.00 1.00
@natural_mortality
    all      0.075

#   MIGRATION
@migration EN_HG_2
    stock ENLD
    migrators              all
    prop                   0.078
```
and similar command blocks for each of the 11 other migrations; for those occurring at time step 1, the subcommand prop always had value 1
```
# FISHING MORTALITY
@fishery EN_LLINE
years                 1970    1971    … 2011
catches               486     1898    … 658
future_years          2012    2013    2014    2015    2016

future_catches   632   632     632     632     632
selectivity Sel_LLINE
U_max 0.7
```
followed by a similar command block for each of the other 19 fisheries defined above, with historic catches as given in Appendix 1 and future catches
```
#TAGGING DETAILS
@tag 1985ENLD_Tags
       tag_name 1985ENLD_Tags
       area F_EN
       stock ENLD
       release_type deterministic
       year 1985
       step 1
       mature_only False
       number 6782
       plus_group False
       class_mins     20             21      …       81
       props_all      0.000236586    0.000106942    … 0
       mortality 0.0
```
followed by a similar command block for each of the other four tag release episodes
```
#SELECTIVITIES
@selectivity_names  Sel_LLINE  Sel_STRAWL  Sel_PTRAWL    Sel_DSEINE    Sel_OTHER  Sel_RECR_pre95
Sel_RECR_post95  Tag-bio_sel Sel_RESTRAWL
@selectivity Sel_LLINE
    all double_normal 7.809513  1.861128 100
```

```
@selectivity Sel_STRAWL
    all double_normal 5.155023 0.835889  17.21431
@selectivity Sel_DSEINE
    all double_normal 6.648807 1.35788 34.94152
@selectivity Sel_RESTRAWL
    all double_normal 4.543643 2.346748 2.55016
@selectivity Sel_RECR_pre95
    all double_normal 4.550965 0.5  10.24395
@selectivity Sel_RECR_post95
    all double_normal 5.29985 0.500005 10.39953
@selectivity Sel_PTRAWL
    all double_normal   6   1.5   30
@selectivity Sel_OTHER
    all double_normal   7    2   6.5
@selectivity Tag-bio_sel
    all size_based knife_edge  25
```