

Alternative Stock Assessments

Patagonian Toothfish (*Dissostichus eleginoides*)



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Summary

In order to provide a comparison to the established stock assessment for Patagonian toothfish (*Dissostichus eleginoides*), we apply two data-poor stock assessment approaches to the available toothfish data, and compare the results to the CASAL stock assessment model. The two approaches tested are JABBA (Just Another Bayesian Biomass Assessment; Winker et al. 2018) and LBB (Length-based Bayesian Biomass estimation; Froese et al. 2018). JABBA uses only catch data from each fishing fleet, while LBB uses only length frequency data. Both are Bayesian-based approaches that differ substantially with the CASAL model in the data required and the underlying formulation of the model.

The outputs from the JABBA model were stable over different model parameterizations, and paralleled the findings of the CASAL stock assessment. It found that the toothfish stock biomass is currently close to the biomass at maximum sustainable yield (B_{MSY}), and that the MSY is between 1,300 and 1,500 t. If future catches of toothfish remain below 1,500 t per year, the JABBA model projects that the biomass would not get depleted over time. Interpreting the outputs of the LBB model was more difficult, as this model depends solely on length frequency data, and rests on the assumption that length is an accurate proxy for age. Therefore, the segment of the population that is targeted by the longline fishery is not properly modelled by LBB, and this method is mostly useful to get an understanding of the trawl-caught segment of the population, which are younger and grow continuously on the Patagonian shelf. The LBB model suggests that the toothfish bycatch in the trawl fisheries has driven down the population of toothfish. Given the insight these alternative models provide, we recommend that JABBA and LBB models be run every year in parallel with the primary CASAL stock assessment model.

Introduction

A commercial longline fishery targeting Patagonian toothfish has been operating in Falkland Islands waters since 1992, and specifically licensed since 1995 (des Clers et al. 1996, Laptikhovsky and Brickle 2005). Management of the fishery has relied on an aged-structured production model implemented using CASAL (Bull et al. 2012) since 2012. This model integrates many data sources and provides useful outputs for the management of the species. The current stock assessment of Falkland Islands toothfish calculated toothfish total biomass of 31,891 tonnes and spawning stock biomass of 11,293 tonnes in 2017. The ratio of SSB2017:SSB0 (current spawning stock biomass to unfished spawning stock biomass) was 0.482. Maximum sustainable yield (MSY) was estimated by the stock assessment model at 1,932 tonnes.

Important quantities of toothfish are also caught in two other Falklands fisheries: finfish trawl, of which toothfish is not a target but commercially valuable bycatch, and *Loligo calamari* (*Doryteuthis gahi*) squid trawl, of which toothfish is also bycatch, but individuals caught in this fishery are usually too small to be commercially valuable. The fisheries access different parts of the toothfish population in different areas: longlining occurs on the slope and in deep water, finfish trawling on the shelf primarily north and west of the Falkland Islands, and calamari trawling also on the shelf, east of the Falkland Islands (Figure 1).

CASAL has become the standard approach to determining the status of toothfish in the southern oceans (Hillary et al., 2006; Dunn and Hanchet, 2010). However, as has been recently pointed out during both the Marine Stewardship Council (MSC) recertification process (Acoura, 2018) and the external review of the toothfish fishery (Bergh, 2018), examining alternative approaches to stock assessment models is part of the best practices in resource management. Alternative model structures can provide a check on the assumptions

of the CASAL model, and increase confidence in the outputs of the primary stock assessment. On the other hand, drastically different results with alternative models can prompt managers to re-evaluate their model assumptions. In addition, the toothfish stock assessment model using CASAL is one of the most data-intensive models used by the Falkland Islands Fisheries Department (FIFD). Therefore, comparing this approach to more data-poor approaches for toothfish may provide insight into the usefulness of these data-poor approaches for other species/stocks managed by FIFD.

In this report, we apply two data-poor stock assessment approaches to the available toothfish data, and compare the results to the CASAL stock assessment model. The two approaches tested are JABBA (Just Another Bayesian Biomass Assessment; Winker et al. 2018) and LBB (Length-based Bayesian Biomass estimation; Froese et al. 2018). JABBA uses only catch data from each fishing fleet, while LBB uses only length frequency data. Both are Bayesian-based approaches that differ substantially with the CASAL model in the data required and the underlying formulation of the model. We hypothesize that the outputs of these two alternative approaches will show the same general status and historical trends as the CASAL model, although we expect these data-poor approaches to provide less sophisticated and nuanced results as the data requirements are substantially simpler.

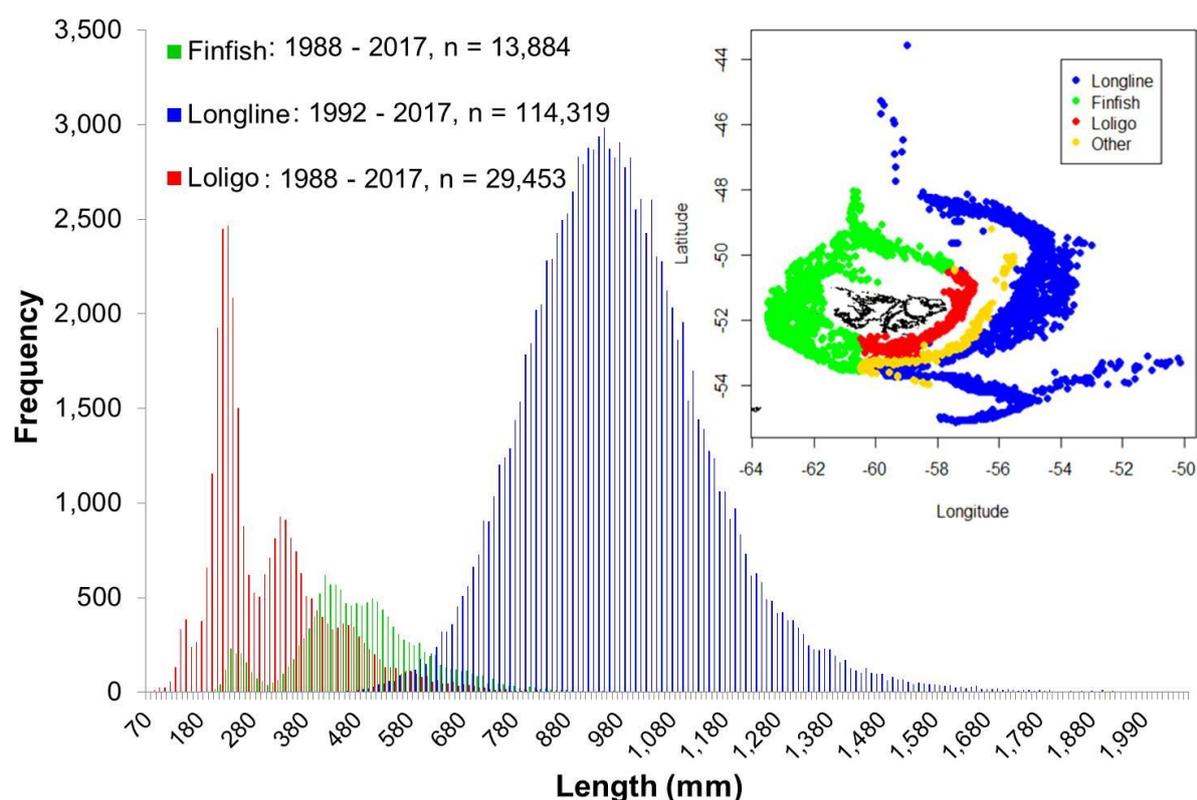


Figure 1. Length frequency of all toothfish measured from different fisheries. In the legend, years denote years for which length data was available, and sample size is the total number of individuals measured across those years. Inset map shows the geographic location of the length measurements, by fishery type.

Methods

The two alternative stock assessment models were constructed using subsets of the data on which the CASAL model is based. The JABBA and LBB model frameworks each employ different portions of the overall available data, as they represent two different approaches. Both are open-source, R-based, Bayesian frameworks, and are useful for data-poor situations.

As a surplus production model, JABBA uses state-space Bayesian modelling to estimate changes in biomass as a function of previous biomass and the removal of biomass through fishing. The data used included the overall annual catch of toothfish in the zone (1987 – 2018), catch per unit effort (CPUE) of toothfish in the finfish (FIN) and squid (LOL) trawl fisheries calculated as the toothfish catch divided by the number of vessel days (FIN: 1987 – 2018, LOL: 1989 – 2018), and the annual CPUE index for the longline fishery that was calculated by the CPUE standardization of the CASAL model (Farrugia and Winter, 2018) along with the standard errors associated with those indices (1996 – 2018). The longline fishery was further divided into the Spanish longline gear (LLH, 1996 – 2007 and 2013) and the umbrella gear (LLU, 2007 - 2018). Three runs of the JABBA model were produced: 1) including catch and CPUE data from all fisheries, 2) including catch and CPUE data from the longline fisheries only (LLH and LLU), and 3) including only longline fisheries with standard errors for the CPUE. For each run, the model was run with three different surplus production functions (Fox, Schaefer, and Pella-Tomlinson functions). These functions all use the same basic surplus production equation, but take different approaches to setting the shape parameter of the biomass depletion ratio (Winker et al., 2018). Therefore, in total there were 9 sets of outputs for the JABBA model (three runs with three production functions each). For further details on parameter specifications, see R script in Appendix.

On the other hand, LBB uses catch-at-length data to estimate mortality rates relative to somatic growth, and subsequently exploited biomass relative to unexploited biomass. For the LBB model, the only data used were the length frequencies of toothfish across all years (1987 – 2018) and fisheries (LLU, LLH, FIN, LOL). Because the different fisheries target different segments of the toothfish population (Figure 1), the model was run separately for the FIN, LOL and LLU/LLH fisheries. Years with very few length frequencies (less than 30), were not included in the analyses. In addition, because the longline gear changed substantially in 2007 (from a Spanish longline system to the umbrella system, Brown et al., 2010), the LBB model was run with data from all longline gear (LL), and with data from only the umbrella gear (LLU). For further details on parameter specifications, see R script in Appendix.

Outputs from both models were consolidated and compared to the outputs of the CASAL model. Specifically, metrics on the stock status (e.g. B/B_{msy} , F/F_{msy}) and sustainable fishing pressure (e.g. MSY , resilience) were compared when more than one modelling approach yielded estimates of the parameter of interest. Trends in estimated spawning stock biomass and fishing mortality were also compared across models.

Results

JABBA

The three different runs of the JABBA model yielded similar estimates for all model outputs (Table 1). Most notably, the estimates of maximum sustainable yield (MSY) ranged narrowly between 1,330 and 1,463 t. Given these similarities, we chose to present the results from the Pella-Tomlinson model from the third model run (which included CPUE data from longlines only, along with the standard error of the CPUE estimate). The outputs from the other model runs were very similar and would not lead to different conclusions.

The change in biomass estimated by the JABBA model shows that there has been an approximately 50% decrease in the stock biomass since the beginning of the fishery (Figure

2). Currently, the biomass is estimated to be slightly below the biomass at MSY (B_{MSY}), although the 95% confidence interval includes the B_{MSY} estimate. The largest biomass decrease happened in the 1990s, at the beginning of the fishery and when there was considerable illegal, unregulated and unreported (IUU) catch of toothfish in the southwest Atlantic. Since 2005, when the ITQ system began and a total allowable catch was imposed, the biomass trend has levelled.

Table 1. Summary of posterior estimates (medians) and 95% Bayesian credibility intervals of parameters for all three model runs, and for each production functions.

	Schaefer			Fox			Pella-Tomlinson			
	Median	2.5%	97.5%	Median	2.5%	97.5%	Median	2.5%	97.5%	
1 st Model Run	$K(t)$	24,664	14,750	50,591	22,952	14,844	42,560	22,341	14,411	41,712
	r	0.233	0.090	0.440	0.177	0.084	0.313	0.195	0.088	0.332
	ϕ	0.726	0.478	1.001	0.704	0.439	0.989	0.703	0.454	0.981
	σ	0.055	0.032	0.089	0.055	0.032	0.089	0.055	0.032	0.089
	F_{MSY}	0.116	0.045	0.220	0.177	0.084	0.313	0.164	0.074	0.280
	B_{MSY}	12,332	7,375	25,296	8,448	5,463	15,665	8,936	5,764	16,684
	$MSY(t)$	1,446	951	1,833	1,463	1,112	2,612	1,462	1,077	1,881
	B/B_{MSY}	0.809	0.495	1.300	0.953	0.540	2.098	0.911	0.559	1.532
	F/F_{MSY}	1.108	0.570	2.190	0.926	0.235	1.736	0.970	0.456	1.703
2 nd Model Run	$K(t)$	28,230	15,619	55,381	25,004	16,182	44,907	26,150	14,474	48,827
	r	0.186	0.072	0.405	0.147	0.067	0.256	0.152	0.063	0.322
	ϕ	0.850	0.614	1.023	0.888	0.664	1.027	0.826	0.589	1.022
	σ	0.055	0.032	0.089	0.055	0.032	0.089	0.055	0.032	0.089
	F_{MSY}	0.093	0.036	0.203	0.147	0.067	0.255	0.128	0.053	0.271
	B_{MSY}	14,115	7,810	27,690	9,203	5,956	16,529	10,459	5,789	19,530
	$MSY(t)$	1,330	846	1,714	1,355	966	1,740	1,344	903	1,746
	B/B_{MSY}	0.643	0.393	1.036	0.803	0.460	1.452	0.704	0.414	1.278
	F/F_{MSY}	1.506	0.792	2.954	1.189	0.529	2.235	1.364	0.603	2.611
3 rd Model Run	$K(t)$	31,071	17,696	61,618	24,785	15,804	45,084	25,398	16,505	48,611
	r	0.179	0.069	0.364	0.156	0.068	0.280	0.164	0.069	0.288
	ϕ	0.857	0.625	1.028	0.917	0.638	1.030	0.872	0.568	1.026
	σ	0.045	0.032	0.084	0.045	0.032	0.084	0.045	0.032	0.084
	F_{MSY}	0.089	0.035	0.182	0.156	0.068	0.280	0.138	0.058	0.242
	B_{MSY}	15,535	8,848	30,809	9,123	5,817	16,594	10,159	6,602	19,444
	$MSY(t)$	1,378	840	2,267	1,422	999	1,911	1,402	970	1,855
	B/B_{MSY}	0.844	0.491	1.538	0.992	0.569	1.633	0.914	0.547	1.497
	F/F_{MSY}	1.130	0.377	2.461	0.921	0.413	1.839	1.009	0.465	1.962

K: unfished biomass, r: resilience, ϕ : initial depletion (B_{1987}/K), σ : process variance

According to the outputs of the JABBA model, the early 2000s saw several years of overfishing (Figure 3), as the biomass was being drawn down. Currently, the stock seems to be very close to B_{MSY} , and surplus production close to its maximum. There is little evidence that the stock is currently undergoing overfishing (catch has been at or below MSY in recent years, Figure 3), and the model suggests that the stock has remained in the same general region of the surplus-production phase plot in the last 10 years (Figure 3).

Another way to examine the changes in the stock status over time is through a Kobe plot (Figure 4). In this case, the overfished (B/B_{MSY}) and overfishing (F/F_{MSY}) status of the stock through time shows that starting in the year 2000, the stock was undergoing overfishing, and by 2007, the stock was overfished. Since then, the stock has remained fairly stable, and overfishing does not seem to be a concern.

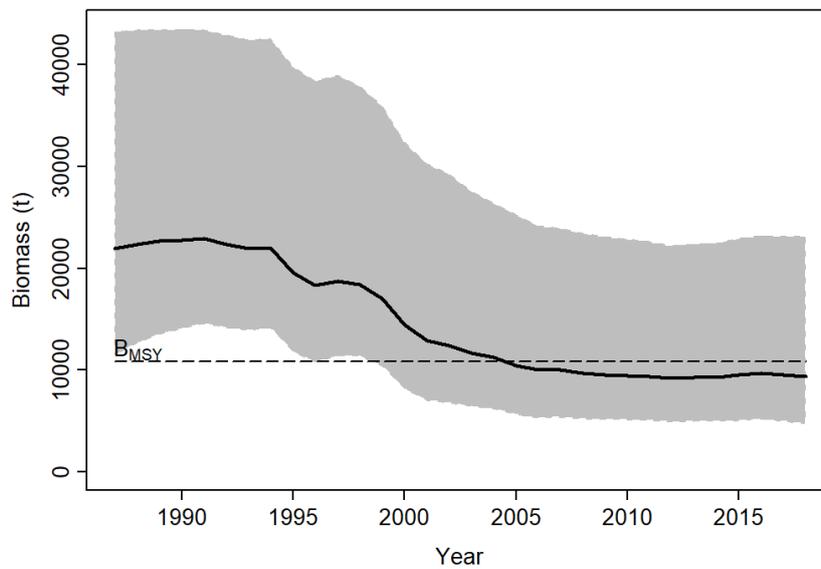


Figure 2. Estimated trajectory of the toothfish stock biomass (black line) with 95% confidence interval (grey shading). Horizontal dashed line represents the estimated B_{MSY} . This is the output for the Pella-Tomlinson model of the 3rd run.

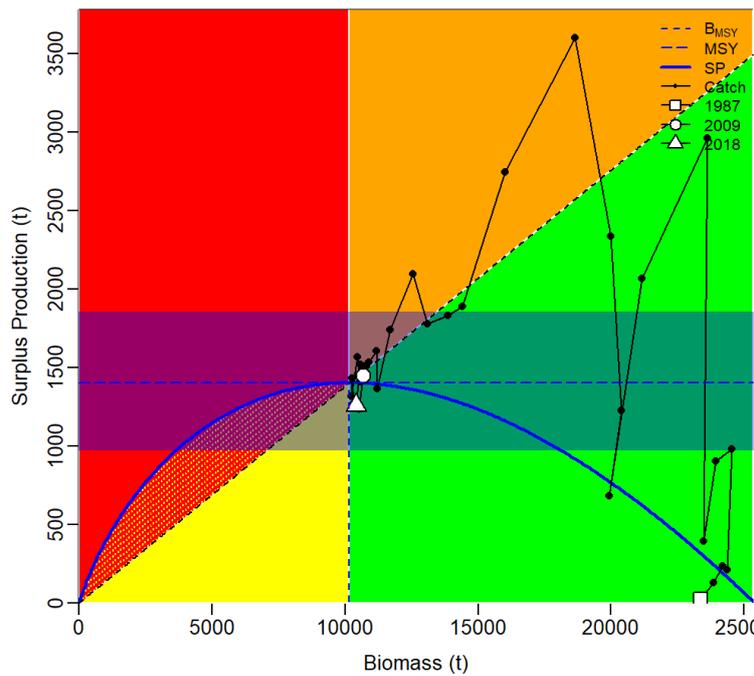


Figure 3. Surplus-production phase plot, showing estimated surplus production curve (blue line), catch/biomass trajectory (black line and dots). Background plot is divided by the vertical B_{MSY} line (short-dashed line) and horizontal MSY line (long-dashed line) with 95% credibility interval (shaded area). First year (1987), last year (2018) and ten year previous (2009) are marked with white symbols.

Finally, the model offers projection estimates of the future biomass of the stock under different catch scenarios (Figure 5). The projections show that total catches of 1,250 t or below seem to be sustainable for the next 20 years. In other words, with an annual catch of 1,250 t or below, the biomass (and therefore the biomass relative to the carrying capacity B/K) will increase. The lower the annual catch, the faster this increase will be. However,

catches of 1,500 t or above would lead to a decrease in biomass (Figure 5). The total catch of toothfish over the last 10 years has fluctuated between 1,233 and 1,564 t (mean = 1,395 t). Therefore, according to the JABBA model, the stock is being fully utilized and close monitoring should continue in order to ensure that overfishing does not take place.

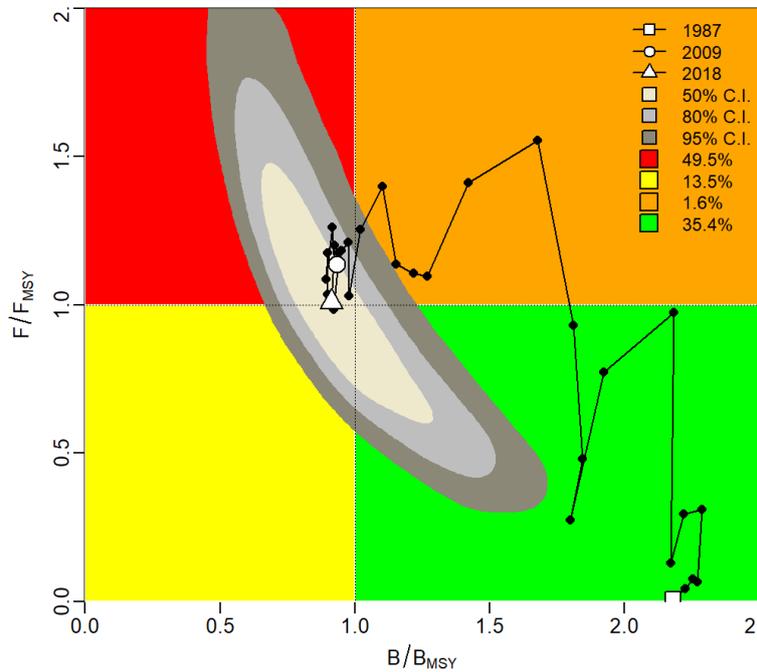


Figure 4. Kobe phase plot showing the estimated trajectory of B/B_{MSY} – F/F_{MSY} of the toothfish stock (black line). Grey shaded areas denote the 50, 80, and 95% credibility interval (from light to dark) for the last assessment year (2018). The probability of the last year falling within each quadrant is indicated with percentages.

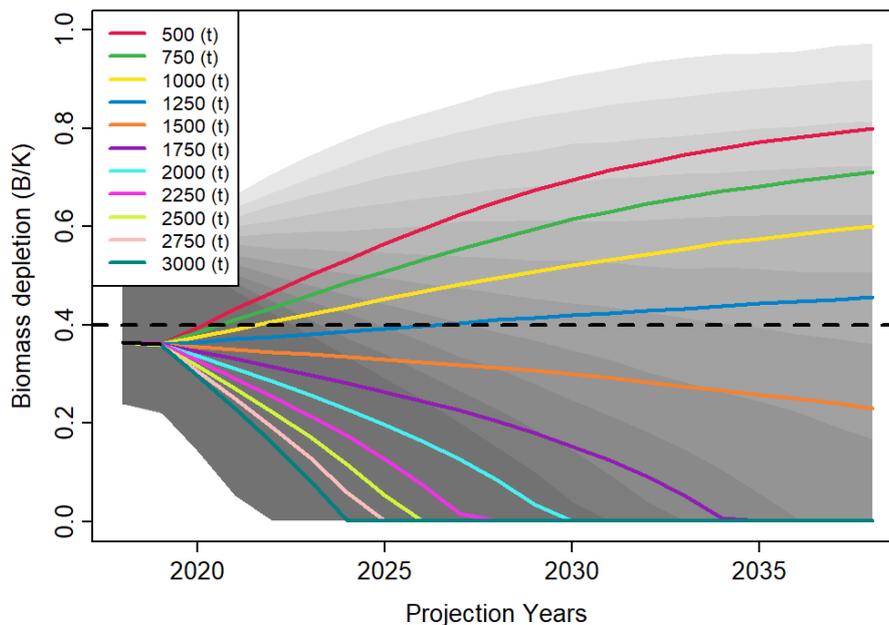


Figure 5. Projections of the toothfish biomass over a sequence of future catches (500 to 3,000 t a year) with 95% credible intervals. Credible intervals for each projection are denoted in increasingly darker shades of grey. Dashed line denotes B_{MSY} .

LBB

The LBB model was initially run on all available length frequency data simultaneously. However, it became apparent that because of the different fisheries targeting very different segments of the toothfish population (Figure 1), the model outputs were erratic and difficult to interpret. However, when the data was divided between the longline fishery, the finfish trawl fishery and the Loligo trawl fishery, more useful outputs were produced.

As expected, the three model runs using data from longline, finfish trawl, and Loligo trawl, respectively, produced markedly different outputs (Table 2). Asymptotic fish length, length at first capture, and the length at which unexploited cohort biomass is maximum was highest for the longline fishery, and smallest for toothfish caught in the Loligo trawl fishery. About 65% of the toothfish caught in the longline fishery were estimated to be mature by the model (based on length at maturity inputs), while none were mature in the two trawl fisheries. The relative index of yield-per-recruit (Y'/R) was highest in the longline fishery, and lowest in the Loligo trawl fishery, in line with the pattern of length frequencies encountered in these fisheries.

The most useful LBB parameter outputs for determining the status of the stock are the fishing mortality, biomass to virgin biomass ratio (B/B_0), and biomass to biomass at MSY ratio (B/B_{MSY}). The index for fishing mortality that is produced by the LBB model is a relative index to natural mortality (F/M). It is highest in the finfish trawl fishery, where the fishing mortality was estimated to be 3.69 times higher than the natural mortality. Fishing intensity was lowest in the Loligo trawl fishery (2.73), which could be explained by the high natural mortality experienced by very small toothfish typically caught in that fishery (around 29 cm). In the longline fishery, the LBB model estimated a rather high F/M ratio of 3.39, although this may not be surprising as this fishery targets large toothfish which are long-lived and have low natural mortality. For both biomass ratios (B/B_0 and B/B_{MSY}), the longline fishery had the highest estimated value (0.2 and 0.56, respectively), followed by the finfish trawl fishery (0.12 and 0.33, respectively), with the Loligo fishery at the lowest biomass level (0.081 and 0.21, respectively). This suggests that the longline fishery has had less effect on the oldest segment of the toothfish population than the finfish and Loligo fishery has had on the younger segment of the stock (Table 2).

Table 2. LBB model outputs (with 95% confidence limits) for the model runs on the three fisheries.

	Longline – Umbrella	Finfish Trawl	Loligo Trawl
Year range	2008 – 2018	1988 – 2018	2003 – 2018
Sample size	1,292	1,150	837
L_{inf} (cm)	214 (210 – 218)	125 (123 – 128)	97.2 (95.4 – 98.7)
L_c (cm)	93.2 (92.5 – 94.2)	34 (33.8 – 34.2)	29.3 (29.2 – 29.4)
L_{opt} (cm)	141	87	71
Percent Maturity	65%	0%	0%
Current Y'/R	0.032 (0.020 – 0.044)	0.021 (0.014 – 0.031)	0.011 (0.007 – 0.015)
F/M	3.39 (2.77 – 4.12)	3.69 (3.04 – 4.96)	2.73 (2.13 – 3.52)
Current B/B_0	0.2 (0.127 – 0.285)	0.12 (0.080 – 0.183)	0.081 (0.0557 – 0.109)
Current B/B_{MSY}	0.56 (0.349 – 0.782)	0.33 (0.215 – 0.49)	0.21 (0.145 – 0.284)

L_{inf} : asymptotic length, L_c : length at first capture, L_{opt} : length at which unexploited cohort biomass is maximum, Y'/R : relative yield per recruit (Beverton and Holt, 1966)

The toothfish caught in the longline fishery have a very narrow and constant length frequency distribution (Figure 6). The distribution is usually centred on 100 cm, and hasn't changed much between 2008 and 2018. Since 2008, the mean length at capture (L_{mean}) has

remained constant just above 100 cm, and is about 40 cm below the length of the unfished population, L_{opt} (Figure 6). Similarly, the length at first capture L_c has been almost 50 cm below the optimum selectivity length $L_{c,opt}$. This suggests that there may growth-overfishing taking place in this fishery (i.e. harvest happens at a size that is smaller than the size that would produce maximum yield per recruit; Diekert, 2012). Both the trendline of the F/M and B/B_0 ratios show that there has been overfishing and the stock was overfished in the past, but that the situation is improving (Figure 6).

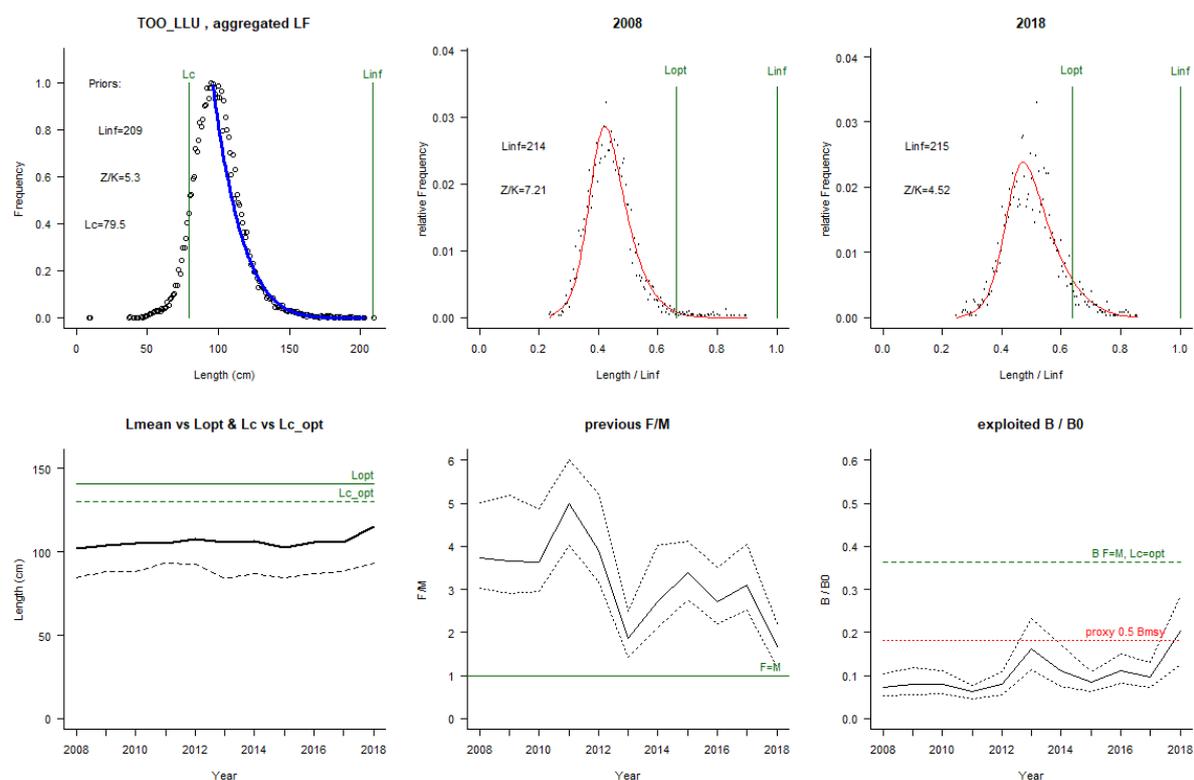


Figure 6. LBB model outputs for the umbrella longline fishery (LLU). The upper left panel shows the accumulated length frequency data used. The upper middle and right panels show the length frequency data for the first and last year in the time series, respectively. The lower left panel shows mean length in the exploited population, L_{mean} (bold curve) relative to the length in the unfished population, L_{opt} (solid green line) and the length at first capture, L_c (dashed curve) relative to the optimum selectivity length, $L_{c,opt}$ (dashed green line). The lower middle panel shows the relative fishing pressure (F/M) with 95% confidence limits. The lower right panel shows the relative biomass (B/B_0) with 95% confidence limits with a proxy for B_{MSY} (green dashed line) and a proxy for $0.5 B_{MSY}$ (red dotted line).

However, it is important to note that outputs from the LBB model using longline length frequency data should be analysed with caution. Two characteristics of the longline fishery for toothfish may limit the applicability of the LBB model to these length frequency data. First, longline gear is very selective, with a narrow size range being targeted based on the size of the hook. It is therefore possible that the length frequency of caught toothfish is not representative of the length composition of the exploited stock. Since all of the underlying fisheries equations used by the LBB model assume a representative sampling of the length composition, a very size-selective gear like longlines would lead to poor model performance (Froese et al., 2018). Secondly, the LBB model uses length as a proxy for age of the exploited

fish in the exploited stock (Froese et al., 2018). But in the areas targeted by the longline fishery, the exploited population is primarily composed of mature adult fish that will continue to age without growing in length (B. Lee, FIFD, pers. comm.). Therefore, in this segment of the population, length is not a proxy for age, and no estimate of length-dependent mortality can be obtained by the model. The authors of the LBB model note that in this situation, the model would only be applicable to the shallow-water phases of the species, where length of the fish does reflect the age (Froese et al., 2018).

As a consequence, LBB should be well suited for the young, shallow-water phase of the toothfish life cycle that is sampled by the finfish and Loligo trawl fisheries. In addition, these fisheries use much less size-selective gear, and therefore avoid the first pitfall mentioned above as well. The finfish trawl fishery captures toothfish of a fairly wide range, centred on an L_{mean} value of about 50 cm, which has decreased slowly between 1988 and 2018 (Figure 7). As in the longline fishery, there is evidence of growth overfishing in the finfish trawl fishery where the optimum selectivity length is 80 cm. There’s also evidence of past and current overfishing, and that the stock is currently in an overfished state, although in certain years (2006, 2014) it seems like the stock was not being overfished (Figure 7). However, over the majority of the time series, the biomass was estimated to be well below the level of $0.5B_{MSY}$, with occasionally also having very high fishing mortality (F/M) estimates (Figure 7).

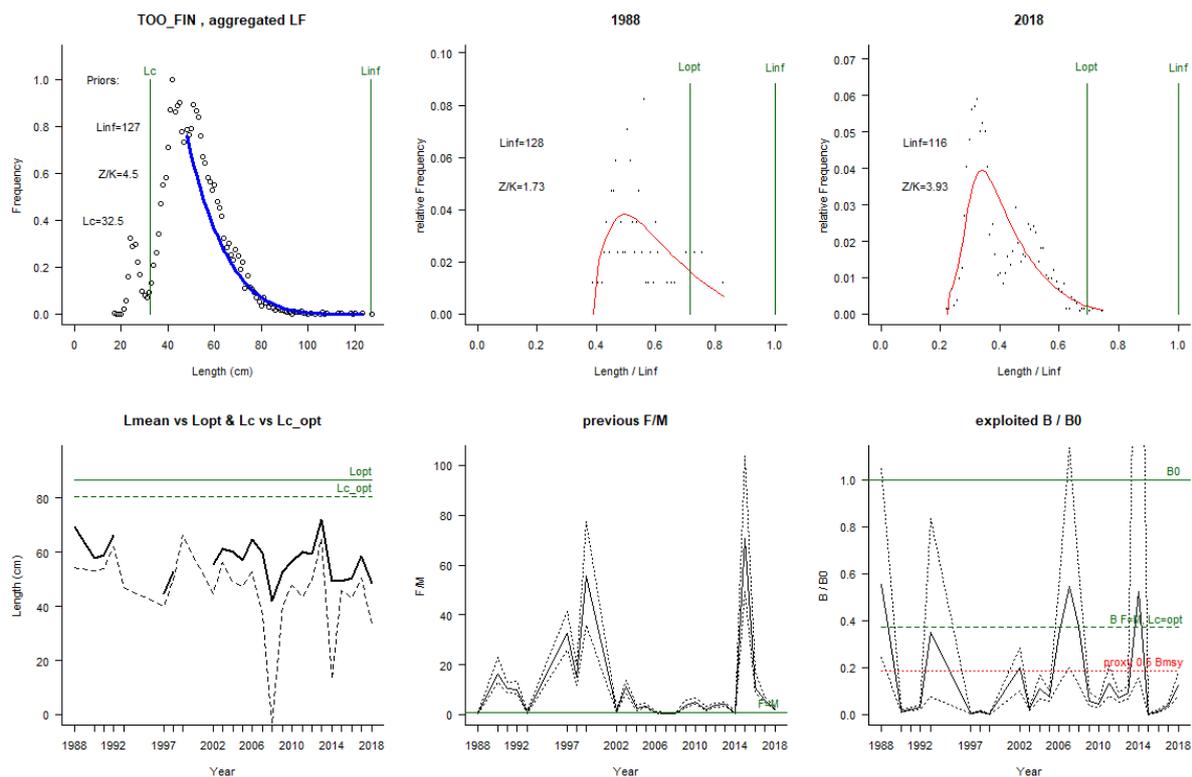


Figure 7. LBB model outputs for the finfish trawl fishery (FIN). Plot description as in Figure 6.

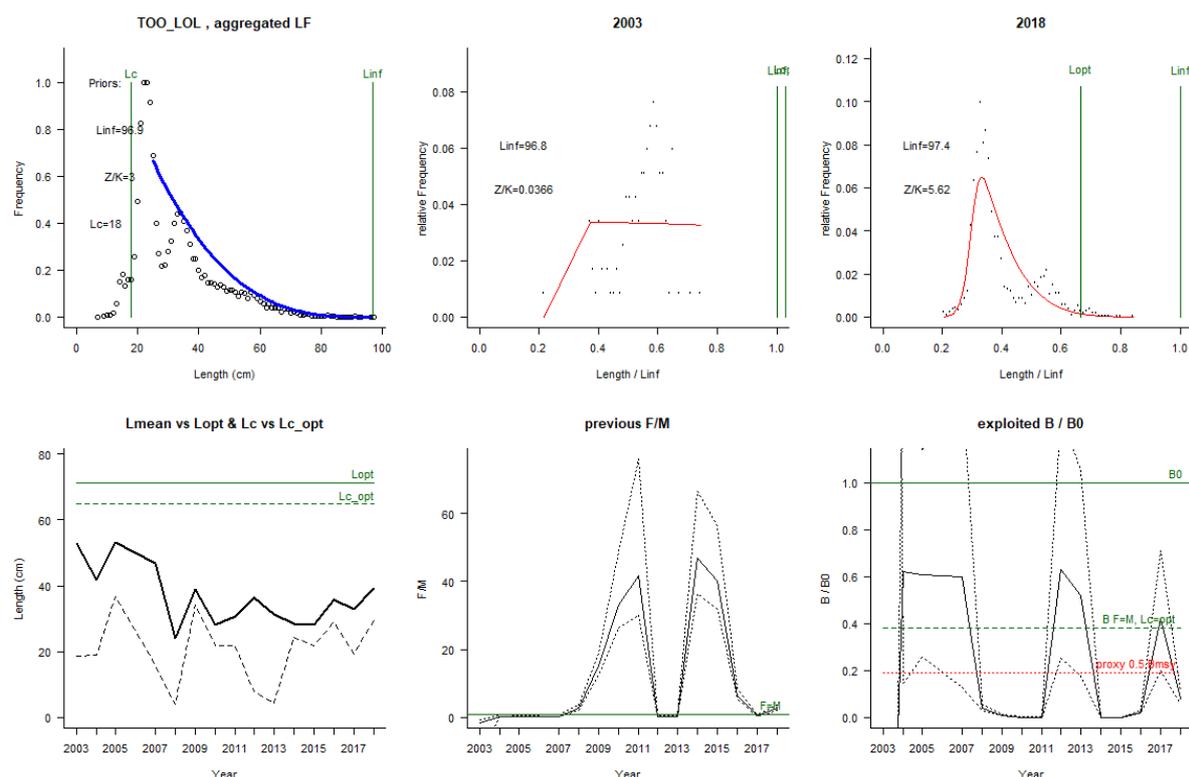


Figure 8. LBB model outputs for the Loligo trawl fishery (LOL). Plot description as in Figure 6.

Finally, the toothfish length frequency from the Loligo trawl fishery shows a similar pattern to the finfish trawl fishery. There is evidence that growth overfishing is taking place, with the mean length of the exploited population (40 – 50 cm) is well below the length of the unfished population (~70 cm), and the length at first capture (20 – 30 cm) below the optimum selectivity length (~65 cm). The capture length seems to be slowly decreasing in the Loligo trawl fishery (Figure 8). As in the finfish trawl fishery, the fishing mortality and biomass estimates are extremely variable over time, with some years showing high overfishing, and states of being overfished (2009 – 2011, 2014 – 2016).

Discussion and Recommendation

The alternative stock assessment approaches examined in this study provide some useful perspective to the assessment of the Falkland Islands toothfish stock. Interestingly, the two approaches, JABBA and LBB, seem to be appropriate for different segments of the toothfish stock. JABBA provides very comprehensive stock management outputs with less data than the CASAL model, but still requires estimates of catch and CPUE. Unfortunately, this information is only reliably available in the longline fishery at this time. Although bycatch is monitored to some degree in the trawl fisheries, there is still some doubt as to the accuracy of the toothfish catch data given the likelihood of missing small juvenile toothfish in trawls, and their similarity to juveniles of other species (rock cod *Patagonotothen sp.*, and icefish *Champscephalus esox*). Therefore, the JABBA outputs are likely to only mirror changes in the larger deep-water adult and sub-adult segment of the population, the one that is targeted by the longline fishery.

On the other hand, the LBB model is mostly appropriate for the young shallow-water segment of the population. As mentioned in the results section above, this is primarily due to

the gear selectivity of the longline and the much slower rate of somatic growth at older ages in adult toothfish. But given the small amount of data available for toothfish in trawl fisheries (consisting primarily of length frequency data collected by observers) LBB is valuable as it provides some information on that segment of the toothfish population. Overall, the JABBA and LBB approaches are most appropriate for different portions of the Falkland Islands toothfish stock, and taken together they can provide insight into the entire toothfish stock around the Falkland Islands.

The outputs of the age-structured production model run with CASAL on the toothfish stock of the Falkland Islands suggests that the toothfish fishery is currently sustainable (the stock is not overfished and not undergoing overfishing), with a MSY estimated at 1,932 t (Farrugia and Winter, 2018). The JABBA model produces slightly more conservative outputs, with an MSY of about 1,402 t. Additionally, the biomass time series produced by the JABBA and CASAL models are very similar. Based on the CASAL model, the total allowable catch of toothfish in the longline fishery was set at 1,040 t, which according to the JABBA model projections should lead to an increase in biomass. If toothfish catch in trawl fisheries is also considered, total catch of toothfish has ranged between 1,233 and 1,564 t in the last 10 years (average 1,395 t). Three of those years had total catch above 1,500 t, the level at which the JABBA model projects biomass will decrease.

The outputs of the LBB model are not directly comparable to the CASAL model because they focus on different parts of the population, but also because the LBB model produces relative parameter estimates rather than absolute ones as CASAL does. But the LBB outputs do provide some insight into the data-poor segment of the toothfish stock, and as such are valuable to examine. However, the time series produced by the LBB model show very high variability (Figures 7 and 8). This is likely an artefact of the variability of the data in the trawl fisheries and it makes drawing firm conclusions about the current status of the stock difficult. In addition, it should be noted that the LBB method has been criticized for being sensitive to the assumption that the system is in equilibrium conditions, and to the assumption that the largest observed size can approximate the asymptotic length (Hordyk et al., 2019). It is therefore important that the outputs of the LBB be examined critically, and only used to provide insight and not as the sole information on which to base management recommendations. As more data on the trawl-caught toothfish are collected, it may be possible in the future to switch from LBB to other approaches to describe the small, young shallow-water segment of the toothfish population.

Given the ease with which these models can be run, we recommend that an alternative toothfish stock assessment using JABBA and LBB be run every year in parallel with the primary CASAL stock assessment model. These alternative models can be used to 1) increase confidence in the overall results of the toothfish CASAL model (using the outputs from JABBA), and 2) complement the CASAL model by providing some insight into the juvenile segment of the population caught in trawl fisheries (using the outputs from LBB). Furthermore, we recommend that both of the JABBA and LBB approaches be tested on other commercial species in the Falkland Islands, especially ones for which other more data-intensive techniques are not possible.

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R code – LBB

```

# Length-based Bayesian Biomass estimator (LBB)
# Fits LBB model to length frequency data to estimate Linf, Lc, M/K, F/K
# and derived reference points F/M, Z/K, Lopt, Lc_opt, B/B0, B/Bmsy, Y/R
# Main code developed by Rainer Froese in May-June 2017, modified in April-May 2018
# Gianpaolo Coro and Henning Winker did the JAGS coding

rm(list=ls(all=TRUE)) # clear previous variables etc
options(digits=3) # displays all numbers with three significant digits as default
graphics.off() # close graphics windows from previous sessions
library(R2jags)
library(Hmisc)

# Select stock to be analysed, TOO, TOO_LL, TOO_TR, TOO_LLU, TOO_FIN, TOO_LOL, TOO_OTH
Stock <- "TOO_LL"

# Set working directory
setwd("C:/Work/Stock Assessment/LBB/TOO 2019")

# Select file with stock ID info
ID.File <- "Stock_ID.csv"

# Initialize some variables
n.sim <- 10 #ifelse(Stock %in% c("CodRedFSim"),1,10) # number of years to be created in simulations

#####
# Functions
#####
#-----
# Exploited B/B0 ratio from B&H equations, for variable F
#-----
# assuming that observed lengths are the lower bounds of length classes
# get lowest exploited (>= 0.01 F) length class and class width

BH <- function(AllLength,Linf,MK,FK,GausSel,selpar1,selpar2) {
  if(GausSel==F) {
    r.Lc <- selpar1
    r.alpha <- selpar2
    Lx <- AllLength[AllLength >= Linf*(r.Lc-4.59/r.alpha)][1]
  } else if(GausSel==T) {
    r.GLmean <- selpar1
    r.SD <- selpar2
    Lx <- AllLength[AllLength >= Linf*(r.GLmean-3*r.SD)][1]
  }
  class.width <- median(diff(sort(unique(AllLength))))
  FM <- FK/MK

# Linf=120;Lx=22.5;r.Lc=0.2917;r.alpha=60;MK=1.5385;FK=0.7692;FM=0.5;ZK=2.3077
# uncomment above row for comparison of Y/R= 0.0332, B/B0=0.467 with CodLightSim
r <- vector() # auxiliary reduction factor
G <- vector() # product of reduction factors
SL.bh <- vector() # selection at length
YR1.2 <- vector() # relative yield per recruit per length class
CPUER1.2 <- vector() # relative CPUE per recruit per length class
B1.2 <- vector() # relative unexploited biomass per recruit by length class
L.bh <- seq(from=Lx, to=Linf, by=class.width) # lengths to be considered
r.L.bh <- L.bh / Linf # standardized lengths

# calculate selection, Y/R and CPUE/R for every length class
for(o in 1 : length(r.L.bh)) {
  if(GausSel==F) {
    if(o<length(r.L.bh)) { SL.bh[o] <- mean(c(1/(1+exp(-r.alpha*(r.L.bh[o]-r.Lc))), # mean selection in length class
      1/(1+exp(-r.alpha*(r.L.bh[o+1]-r.Lc))))))
    } else SL.bh[o] <- 1/(1+exp(-r.alpha*(r.L.bh[o]-r.Lc)))
  } else if(GausSel==T) { # gill net selection
    if(o<length(r.L.bh)) { SL.bh[o] <- mean(c(exp(-((r.L.bh[o]-r.GLmean)^2/(2*r.SD^2))), # mean selection in length class
      exp(-((r.L.bh[o+1]-r.GLmean)^2/(2*r.SD^2))))))
    } else SL.bh[o] <- exp(-((r.L.bh[o]-r.GLmean)^2/(2*r.SD^2)))
  } # end of calculation of selectivity loop

  if(o<length(r.L.bh)) {
    r[o] <- (1-r.L.bh[o+1])^(FK*SL.bh[o])/(1-r.L.bh[o])^(FK*SL.bh[o])
    G[o] <- prod(r[1:o])
  }
  if(o==1) {
    YR1.2[o] <- (FM*SL.bh[o])/(1+FM*SL.bh[o])*(1-r.L.bh[o])^MK*(1-3*(1-r.L.bh[o]))/(1+1/

```

```

(MK+FK*SL.bh[o])+3*(1-r.L.bh[o])^2/(1+2/(MK+FK*SL.bh[o]))-
(1-r.L.bh[o])^3/(1+3/(MK+FK*SL.bh[o]))) -
(FM*SL.bh[o]/(1+FM*SL.bh[o]))*(1-r.L.bh[o+1])^MK*(1-3*(1-r.L.bh[o+1]))/(1+1/
(MK+FK*SL.bh[o])+3*(1-r.L.bh[o+1])^2/(1+2/(MK+FK*SL.bh[o]))-
(1-r.L.bh[o+1])^3/(1+3/(MK+FK*SL.bh[o]))) * G[o]
} else if(o==length(r.L.bh)) {
  YR1.2[o] <- (FM*SL.bh[o]/(1+FM*SL.bh[o]))*(1-r.L.bh[o])^MK*(1-3*(1-r.L.bh[o]))/(1+1/
(MK+FK*SL.bh[o])+3*(1-r.L.bh[o])^2/(1+2/(MK+FK*SL.bh[o]))-
(1-r.L.bh[o])^3/(1+3/(MK+FK*SL.bh[o]))) * G[o-1]
} else {
  YR1.2[o] <- (FM*SL.bh[o]/(1+FM*SL.bh[o]))*(1-r.L.bh[o])^MK*(1-3*(1-r.L.bh[o]))/(1+1/
(MK+FK*SL.bh[o])+3*(1-r.L.bh[o])^2/(1+2/(MK+FK*SL.bh[o]))-
(1-r.L.bh[o])^3/(1+3/(MK+FK*SL.bh[o]))) * G[o-1] -
(FM*SL.bh[o]/(1+FM*SL.bh[o]))*(1-r.L.bh[o+1])^MK*(1-3*(1-r.L.bh[o+1]))/(1+1/
(MK+FK*SL.bh[o])+3*(1-r.L.bh[o+1])^2/(1+2/(MK+FK*SL.bh[o]))-
(1-r.L.bh[o+1])^3/(1+3/(MK+FK*SL.bh[o]))) * G[o]
} # end of loop to calculate yield per length class

CPUER1.2[o] <- YR1.2[o] / FM # CPUE/R = Y/R divided by F/M

if(o<length(r.L.bh)) {
  B1.2[o] <- ((1-r.L.bh[o])^MK*(1-3*(1-r.L.bh[o]))/(1+1/MK)+3*(1-r.L.bh[o])^2/
(1+2/MK)-(1-r.L.bh[o])^3/(1+3/MK)) -
(1-r.L.bh[o+1])^MK*(1-3*(1-r.L.bh[o+1]))/(1+1/MK)+3*(1-r.L.bh[o+1])^2/
(1+2/MK)-(1-r.L.bh[o+1])^3/(1+3/MK)) * SL.bh[o]
} else {
  B1.2[o] <- ((1-r.L.bh[o])^MK*(1-3*(1-r.L.bh[o]))/(1+1/MK)+3*(1-r.L.bh[o])^2/
(1+2/MK)-(1-r.L.bh[o])^3/(1+3/MK)) * SL.bh[o]
}
} # end of B&H loop through length classes
BB0 <- sum(CPUER1.2)/sum(B1.2)
YR <- sum(YR1.2)
if(BB0 < 0.25) YR <- YR * BB0 / 0.25 # reduce YR if recruitment and thus productivity is reduced
return(list(BB0,YR))
} # end of BH function

#-----
# Function to aggregate data by year
#-----
AG <- function(dat) { # where dat contains dat$Year, dat$Length in cm, dat$CatchNo

# aggregate normalized annual LFs by weighing with square root of sample size
# get sum of frequencies per year
sum.Ny <- aggregate(Freq~Year,dat,sum)$Freq
# get the sqrt of the sum of frequencies for every year
sqrt.Ny <- sqrt(sum.Ny)
# get highest frequency in each year
max.Ny <- aggregate(Freq~Year,dat,max)$Freq
# get Number of Length bins in each year
binsN <- aggregate(Freq~Year,dat,length)$Freq
# create vectors for sqrt.Ni and sum.Ni to weigh LF data
sqrt.Ni = rep(sqrt.Ny,binsN)
sum.Ni = rep(sum.Ny,binsN)
#Do weighing
# Divide all years by sum.Ni and multiply by sqrt.Ni
LF.w = dat$Freq/sum.Ni*sqrt.Ni
# Aggregate
LF = aggregate(LF.w, by=list(dat$Length),FUN=sum)
# Add correct column names
colnames(LF) <- c("Length","Freq")
return(LF)
} #end of aggregate function

#-----
# Function to plot LBB-fit for a single year
#-----
# expects lengths relative to Linf (L/Linf)
plot.year <- function(r.L.y,r.Freq.y,r.Lopt, SL1, SL2, MK, FK, Linf) {
  SL <- vector(); SL[1] <- 0
  xN <- vector(); xN[1] <- 1
  for(p in 2:length(r.L.y)) {
    if(dat.ID$GausSel==T) {
      SL[p] <- exp(-((r.L.y[p]-SL1/Linf)^2/(2*(SL2/Linf)^2))) # selection at length r.L[i]
    } else {SL[p] <- 1/(1+exp(-SL2*(r.L.y[p]-SL1/Linf)))}
  }
}

```

```

  xN[p] <- xN[p-1]*exp((MK+FK*SL[p])*(log(1-r.L.y[p])-log(1-r.L.y[p-1])))
} # end of loop for length classes
# determine sum of squared residuals, store parameters if less then min of previous
Freq.pred <- xN*SL
sum.Freq.pred <- sum(Freq.pred)
r.Freq.pred <- Freq.pred / sum.Freq.pred
plot(x=r.L.y, y= r.Freq.pred,
     xlab="Length / Linf",ylab="relative Frequency",
     xlim=c(0,1),ylim = c(0,1.2*max(r.Freq.y)),
     col="red", type="l", bty="n",main=Year,las=1)
points(x=r.L.y,y=r.Freq.y, cex=0.5)
lines(x=c(1,1), y=c(0,1.07*max(r.Freq.y,na.rm=T)),col="darkgreen")
text(x=1,y=1.15*max(r.Freq.y,na.rm=T),"Linf",col="darkgreen")
lines(x=c(r.Lopt,r.Lopt), y=c(0,1.07*max(r.Freq.y,na.rm=T)),col="darkgreen")
text(x=r.Lopt,y=1.15*max(r.Freq.y,na.rm=T),"Lopt",col="darkgreen")
text(x=0.15,y=0.8*max(r.Freq.y,na.rm=T),paste("Linf=",format(Linf,digits=3),sep=""))
text(x=0.15,y=0.6*max(r.Freq.y,na.rm=T),paste("Z/K=",format(MK+FK,digits=3),sep=""))
}

#####
# read files with ID and with LF data to be analyzed
#####
# read ID data
dat.ID <- read.csv(ID.File, header=T, stringsAsFactors=F)

# restrict ID data to selected Stock
dat.ID <- dat.ID[dat.ID$Stock==Stock,]

# read LF data
dat.raw <- read.csv(dat.ID$File, header=T, stringsAsFactors=F)

# restrict LF data to selected stock
dat.raw <- dat.raw[dat.raw$Stock == Stock,]

# restrict analysis to one or more gears
if(is.na(dat.ID$Gears.user[1])==FALSE) dat.raw <- dat.raw[dat.raw$Gear %in% dat.ID$Gears.user,]

# make sure data are numeric
dat.raw$Length <- as.numeric(dat.raw$Length)
dat.raw$CatchNo <- as.numeric(dat.raw$CatchNo)
dat.raw$Year <- as.integer(dat.raw$Year)

# if StartYear is given, restrict data to >= StartYear
if(is.na(dat.ID$StartYear)==F) dat.raw <- dat.raw[dat.raw$Year>=dat.ID$StartYear,]

# if EndYear is given, restrict data to <= EndYear
if(is.na(dat.ID$EndYear)==F) dat.raw <- dat.raw[dat.raw$Year<=dat.ID$EndYear,]

# if Years.user are given, restrict data to these years
#modification by Gianpaolo 09 07 17
if(is.na(dat.ID$Years.user[[1]])==F) dat.raw <- dat.raw[dat.raw$Year %in% (strsplit(dat.ID$Years.user, ",")[[1]),]

# if Linf.user is given, restrict data to < Linf.user
if(is.na(dat.ID$Linf.user)==F) dat.raw <- dat.raw[dat.raw$Length<(dat.ID$Linf.user*ifelse(dat.ID$mm.user==TRUE,1,10)),]

# if Lcut.user is given, restrict data to >= Lcut.user
if(is.na(dat.ID$Lcut.user)==F) dat.raw <- dat.raw[dat.raw$Length>=(dat.ID$Lcut.user*ifelse(dat.ID$mm.user==TRUE,1,10)),]

# remove NA records
dat.raw <- dat.raw[which(is.na(dat.raw$CatchNo)==F),]

# sort data by year and length
dat.raw <- dat.raw[order(dat.raw$Year,dat.raw$Length),]

# Put data into vectors
StartYear <- min(dat.raw$Year)
EndYear <- max(dat.raw$Year)
AllYear <- dat.raw$Year
AllLength <- dat.raw$Length
if(dat.ID$mm.user==FALSE) AllLength <- AllLength/10
AllFreq <- dat.raw$CatchNo
Years <- sort(unique(AllYear))
nYears <- length(Years)

# if data are simulated, add noise and n.sim more years

```

```

if(substr(Stock,start=nchar(Stock)-2,stop=nchar(Stock))=="Sim") {
  n.L.sim <- length(AllLength)
  AllYearSim <- AllYear
  AllLengthSim <- AllLength
  AllFreqSim <- rlnorm(n=n.L.sim,mean=log(AllFreq),sd=0.1)
  if(!((Stock %in% c("CodFSim","CodRecSim")))) { # CodFSim and CodRecSim are simulations that should run for only one
  year
  for(i in 1 : (n.sim-1)) {
    AllYearSim <- append(AllYearSim,AllYear+i)
    AllLengthSim <- append(AllLengthSim,AllLength)
    AllFreqSim <- append(AllFreqSim,rlnorm(n=n.L.sim,mean=log(AllFreq),sd=0.1))
  }
  AllYear <- AllYearSim
  AllLength <- AllLengthSim
  AllFreq <- AllFreqSim
  Years <- sort(unique(AllYear))
  nYears <- length(Years)
  EndYear <- Years[nYears] }
} # end of simulation loop

#-----
# plot LF for all years to detect potential problems
#-----
for(z in 1:ceiling(nYears/6)) {
  #modification by Gianpaolo 09 07 17
  if(grepl("win",tolower(Sys.info()[sysname]))) {windows(12,8)
  } else if(grepl("linux",tolower(Sys.info()[sysname]))) {X11(12,8)
  } else {quartz(12,8)}
  par(mfrow=c(2,3))
  for(v in 1 : 6) {
    w <- v+(z-1)*6
    if(w > nYears) break()
    df.p <-
data.frame(AllYear[AllYear==Years[w]&AllFreq>0],AllLength[AllYear==Years[w]&AllFreq>0],AllFreq[AllYear==Years[w]&AllFreq
>0])
    names(df.p) <- c("Year","Length","Freq")
    LF.p <- AG(dat=df.p) # function to aggregate data in case bins are not unique
    plot(x=LF.p$Length,y=LF.p$Freq,xlab="",ylab="Freq",bty="l",main=Years[w],cex=0.5)
  }
}

#-----
# Create matrix to store annual estimates
#-----
Ldat <- data.frame(Stock=rep(Stock,nYears),Year=rep(NA,nYears),
  Linf=rep(NA,nYears),
  Linf.lcl=rep(NA,nYears),
  Linf.ucl=rep(NA,nYears),
  Lc=rep(NA,nYears), # for trawl selection
  Lc.lcl=rep(NA,nYears),
  Lc.ucl=rep(NA,nYears),
  Lmean=rep(NA,nYears),
  r.alpha=rep(NA,nYears),
  r.alpha.lcl=rep(NA,nYears),
  r.alpha.ucl=rep(NA,nYears),
  r.GLmean=rep(NA,nYears),r.SD=rep(NA,nYears), # for gill net selection
  MK=rep(NA,nYears),
  MK.lcl=rep(NA,nYears),
  MK.ucl=rep(NA,nYears),
  FK=rep(NA,nYears),
  FK.lcl=rep(NA,nYears),
  FK.ucl=rep(NA,nYears),
  ZK=rep(NA,nYears),
  ZK.lcl=rep(NA,nYears),
  ZK.ucl=rep(NA,nYears),
  FM=rep(NA,nYears),
  FM.lcl=rep(NA,nYears),
  FM.ucl=rep(NA,nYears),
  r.Lopt=rep(NA,nYears),
  BB0=rep(NA,nYears),
  BB0.lcl=rep(NA,nYears),
  BB0.ucl=rep(NA,nYears),
  YR=rep(NA,nYears),
  YR.lcl=rep(NA,nYears),
  YR.ucl=rep(NA,nYears),

```

```

perc.mat=rep(NA,nYears),
L95=rep(NA,nYears))

#-----
# Use aggregated LF data for estimation of Linf (and overall Z/K)
#-----
df <- data.frame(AllYear,AllLength,AllFreq)
names(df) <- c("Year","Length","Freq")

LF.all <- AG(dat=df) # function to aggregate data by year and across years

# standardize to max Freq
LF.all$Freq = LF.all$Freq/max(LF.all$Freq)
# remove leading empty records
LF.all <- LF.all[which(LF.all$Freq>0)[1] : length(LF.all$Length),]
# remove trailing empty records
LF.all <- LF.all[1 : which(LF.all$Length==max(LF.all$Length[LF.all$Freq>0])),]

# get number of records in LF.all
n.LF.all <- length(LF.all$Length)
# use largest fish as Lmax
Lmax <- LF.all$Length[n.LF.all]
# use median of largest fish per year as Lmax.med
Lmax.med <- median(as.numeric(by(dat.raw$Length[dat.raw$CatchNo>0],dat.raw$Year[dat.raw$CatchNo>0],max)))/10

# If no Linf is provided by the user (preferred), determine Linf from fully selected LF:
# Freq=Nstart*exp(ZK*(log(1-L/Linf)-log(1-Lstart/Linf)))
# Nstart is canceled out when dividing both sides by their sums
# -----
# determine start values of selection ogive to find first fully selected length class Lstart
L10 <- LF.all$Length[which(LF.all$Freq>0.1)[1]] # use length at 10% of peak frequency as proxy for L10
L90 <- LF.all$Length[which(LF.all$Freq>0.9)[1]] # use length at 90% of peak frequency as proxy for L90
Lc.st <- ifelse(is.na(dat.ID$Lc.user)==TRUE,(L10 + L90)/2,dat.ID$Lc.user) # use mean of L10 and L90 as proxy for Lc,
else user input
alpha.st <- -log(1/LF.all$Freq[which(LF.all$Freq>0.1)[1]])/(L10-Lc.st) # use rearranged logistic curve to estimate slope alpha

# determine start values for Linf and Z/K
Linf.st <- max(LF.all$Length) # use Lmax as proxy for Linf
Lmean.st <- sum(LF.all$Length[LF.all$Length>=Lc.st]*LF.all$Freq[LF.all$Length>=Lc.st])/
sum(LF.all$Freq[LF.all$Length>=Lc.st])
MK.st <- ifelse(is.na(dat.ID$MK.user)==TRUE, 1.5,dat.ID$MK.user) # default 1.5
ZK.st <- (Linf.st-Lmean.st)/(Lmean.st-Lc.st) # the Holt equation
FK.st <- ifelse((ZK.st-MK.st)>0,ZK.st-MK.st,0.3) # prevent M/K being larger than Z/K

# get vectors with fully selected length classes for Linf estimation
if(is.na(dat.ID$Lstart.user)==FALSE) {Lstart <- dat.ID$Lstart.user} else {
  Lstart <- (alpha.st*Lc.st-log(1/0.95-1))/alpha.st # Length where selection probability is 0.95
  # test if there are enough (>=4) length classes for estimation of aggregated Linf and ZK
  Lstart.i <- which(LF.all>=Lstart)[1]
  Lmax.i <- length(LF.all$Length)
  peak.i <- which.max(LF.all$Freq)
  if(Lstart.i<(peak.i+1)) Lstart <- LF.all$Length[peak.i+1] # make sure fully selected length starts after peak
  if((Lmax.i-Lstart.i)<4) Lstart <- LF.all$Length[Lstart.i-1] # make sure enough length classes are available
}
# do not include Lmax to allow Linf < Lmax and to avoid error in nls when Linf-L becomes negative
L.L <- LF.all$Length[LF.all$Length >= Lstart & LF.all$Length < Linf.st]
L.Freq <- LF.all$Freq[LF.all$Length>=L.L[1]& LF.all$Length < Linf.st]

if(length(L.L)<4) {
  #modification by Gianpaolo 09 07 17
  if(grepl("win",tolower(Sys.info()['sysname']))) {windows(6,4)
  } else if(grepl("linux",tolower(Sys.info()['sysname']))) {X11(6,4)
  } else {quartz(6,4)}

  plot(x=LF.all$Length,y=LF.all$Freq, bty="l",main=Stock)
  lines(x=c(Lstart,Lstart),y=c(0,0.9*max(LF.all$Freq)),lty="dashed")
  text(x=Lstart,y=max(LF.all$Freq),"Lstart")
  lines(x=c(Linf.st,Linf.st),y=c(0,0.9*max(LF.all$Freq)),lty="dashed")
  text(x=Linf.st,y=max(LF.all$Freq),"Lmax")
  stop("Too few fully selected data points: set Lstart.user\n")
}

# standardize frequencies by dividing by sum of observed frequencies, needed to drop NLstart from equation
sum.L.Freq <- sum(L.Freq)
L.Freq <- L.Freq/sum.L.Freq

```

```

# use nls() to find Linf-ZK combination with least residuals
if(is.na(dat.ID$Linf.user)==TRUE) {
  Linf.mod <- nls(L.Freq ~ ((Linf-L.L)/(Linf-L.start))^ZK /
    sum(((Linf-L.L)/(Linf-L.start))^ZK),
    start=list(ZK=ZK.st,Linf=Linf.st),
    lower=c(0.5*ZK.st,0.999*Linf.st),
    upper=c(1.5*ZK.st,1.2*Linf.st),
    algorithm = "port")

  ZK.nls <- as.numeric(coef(Linf.mod)[1])
  ZK.nls.sd <- as.numeric(coef(summary(Linf.mod))[2][1])
  ZK.nls.lcl <- ZK.nls-1.96*ZK.nls.sd
  ZK.nls.ucl <- ZK.nls+1.96*ZK.nls.sd
  Linf.nls <- as.numeric(coef(Linf.mod)[2])
  Linf.nls.sd <- as.numeric(coef(summary(Linf.mod))[2][2])
  Linf.lcl <- Linf.nls-1.96*Linf.nls.sd
  Linf.ucl <- Linf.nls+1.96*Linf.nls.sd
} else { # end of loop to determine Linf and ZK.L
  # use given Linf and determine ZK.L
  # use Linf provided by user if given
  Linf.nls <- dat.ID$Linf.user
  Linf.nls.sd <- 0.01*dat.ID$Linf.user
  ZK.mod <- nls(L.Freq ~ exp(ZK*(log(1-L.L/Linf.nls)-log(1-L.L[1]/Linf.nls)))/
    sum(exp(ZK*(log(1-L.L/Linf.nls)-log(1-L.L[1]/Linf.nls))))),
    start=list(ZK=ZK.st),
    lower=c(0.7*ZK.st),
    upper=c(1.3*ZK.st),
    algorithm = "port")

  ZK.nls <- as.numeric(coef(ZK.mod)[1])
  ZK.nls.sd <- as.numeric(coef(summary(ZK.mod))[2][1])
  ZK.nls.lcl <- ZK.nls-1.96*ZK.nls.sd
  ZK.nls.ucl <- ZK.nls+1.96*ZK.nls.sd
} # end of loop if Linf is given by user

#-----
# Plot aggregated results
#-----
# plot aggregated histogram with fit to fully selected part
#modification by Gianpaolo 09 07 17
if(grepl("win",tolower(Sys.info()[ "sysname" ]))) {windows(12,8)
} else if(grepl("linux",tolower(Sys.info()[ "sysname" ]))) {X11(12,8)
} else {quartz(12,8)}

par(mfrow=c(2,3),las=1)
plot(x=LF.all$Length,y=LF.all$Freq, bty="n",xlim=c(0,max(max(LF.all$Length),Linf.nls)),
  ylim=c(0,1.1*max(LF.all$Freq)),
  main=paste(Stock," aggregated LF"),xlab=ifelse(dat.ID$mm.user==F,"Length (cm)","Length (mm)"),ylab="Frequency")

Lstart.i <- which(LF.all$Length>=Lstart)[1]
Lstart.Freq <- mean(c(LF.all$Freq[(Lstart.i-1):(Lstart.i+1)]))
if(dat.ID$GausSel==F) {
  lines(x=L.L,y=Lstart.Freq*exp(ZK.nls*(log(1-L.L/Linf.nls)-log(1-L.L[1]/Linf.nls))), col="blue", lwd=3)
  lines(x=c(Lc.st,Lc.st), y=c(0,1), col="darkgreen")
  text(x=Lc.st,y=1, "Lc", col="darkgreen", adj=c(0.5,-0.5))
}
lines(x=c(Linf.nls,Linf.nls), y=c(0,1), col="darkgreen")
text(x=Linf.nls,y=1, "Linf", col="darkgreen", adj=c(0.5,-0.5))
text(x=0.1*Linf.nls,y=1,"Priors:")
text(x=0.15*Linf.nls,y=0.8,paste("Linf=",format(Linf.nls,digits=3),sep=""))
if(dat.ID$GausSel==F) text(x=0.15*Linf.nls,y=0.6,paste("Z/K=",format(ZK.nls,digits=2),sep=""))
text(x=0.1*Linf.nls,y=0.4,paste("Lc=",format(Lc.st,digits=3),sep=""))

# get vector of all lengths <= prior Linf to avoid error in equation
AllFreq <- AllFreq[AllLength <= Linf.nls]
AllYear <- AllYear[AllLength <= Linf.nls]
AllLength <- AllLength[AllLength <= Linf.nls]

#-----
# Start LF analysis by year
#-----
cat("Running Jags model to fit SL and N distributions for",dat.ID$Species,"in", Years,"...\n")
i = 0 # start counter
for(Year in Years) {

```

```

i = i+1
# if MergeLF==TRUE and if this is the second or heigher year and no simulation, aggregate LF with previous year LF
if(i>1 & dat.ID$MergeLF==TRUE & substr(Stock,start=nchar(Stock)-2,stop=nchar(Stock))!="Sim") {
  AG.yr <- c(Years[i-1],Year) } else AG.yr <- Year

# aggregate data within the year (sometimes there are more than one sample per year)
df <- data.frame(AllYear%in%AG.yr,AllLength[AllYear%in%AG.yr],AllFreq[AllYear%in%AG.yr])
names(df) <- c("Year","Length","Freq")
LF.y <- AG(dat=df) # function to aggregate data by year and across years
LF.y$Freq <- LF.y$Freq/sum(LF.y$Freq) # standardize frequencies

# remove empty leading and trailing records
LF.y <- LF.y[which(LF.y$Freq>0)[1] : length(LF.y$Length),]
LF.y <- LF.y[1 : which.max(LF.y$Length[LF.y$Freq>0]),]
# get vectors
L.y <- LF.y$Length
r.Freq.y <- LF.y$Freq

# fill remaining zero frequencies with very small number, to avoid error
r.Freq.y[r.Freq.y==0] <- min(r.Freq.y[r.Freq.y>0],na.rm=T)/100
# enter data for this year into data frame
Ldat$Year[i] <- Year

#-----
# Estimate annual parameters Lc, alpha, M/K, F/K from LF curve with trawl-type selection
#-----
# determine priors
n.L <- length(L.y)
Linf.pr <- Linf.nls
Linf.sd.pr <- ifelse(Linf.nls.sd/Linf.nls<0.01,Linf.nls.sd,0.01*Linf.nls) # restrict prior CV of Linf to < 0.01
MK.pr <- MK.st
MK.sd.pr <- ifelse(is.na(dat.ID$MK.user)==TRUE,0.15,0.075)

if(dat.ID$GausSel==FALSE){ # apply trawl-like selection
Lc.pr <- ifelse(is.na(dat.ID$Lc.user)==TRUE,1.02*Lc.st,dat.ID$Lc.user) # with 1.02 multiplier to account for systematic
small underestimation
Lc.sd.pr <- ifelse(is.na(dat.ID$Lc.user)==TRUE,0.1*Lc.pr,0.05*Lc.pr) # assume narrower SD if Lc is given by user
r.max.Freq <- max(r.Freq.y,na.rm=T)
r.alpha.pr <- -log(r.max.Freq/r.Freq.y[which(r.Freq.y>(0.1*r.max.Freq))]1)]/(L10/Linf.nls-Lc.st/Linf.nls) # relative alpha for
standardized data
r.alpha.sd.pr<- 0.025*r.alpha.pr
FK.pr <- ifelse((ZK.nls-MK.st) > 0,ZK.nls-MK.st,0.3) # if Z/K <= M/K assume low F/K = 0.3

# list of data to pass to JAGS plus list of parameters to estimate
jags.data <- list
("r.Freq.y","L.y","n.L","Linf.pr","Linf.sd.pr","Lc.pr","Lc.sd.pr","r.alpha.pr","r.alpha.sd.pr","MK.pr","MK.sd.pr","FK.pr")
jags.params <- c("r.alpha.d","Lc.d","SL","xN","FK.d","MK.d","Linf.d")

#-----
# LBB JAGS model
#-----
sink("SLNMod.jags")
cat("
model {
  r.alpha.d_tau <- pow(r.alpha.sd.pr, -2)
  r.alpha.d ~ dnorm(r.alpha.pr,r.alpha.d_tau)

  Lc.d_tau <- pow(Lc.sd.pr,-2)
  Lc.d ~ dnorm(Lc.pr,Lc.d_tau) #

  MK.d_tau <-pow(MK.sd.pr, -2) # strong prior on M/K
  MK.d ~ dnorm(MK.pr, MK.d_tau)

  Linf.tau <- pow(Linf.sd.pr,-2)
  Linf.d ~ dnorm(Linf.pr,Linf.tau)

  FK.d ~ dlnorm(log(FK.pr),4) # wide prior range for F/K

  SL[1] ~ dlogis(0,1000)
  Freq.pred[1]<-0
  xN[1] <-1

  for(j in 2:n.L) {
    SL[j]<- 1/(1+exp(-r.alpha.d*(L.y[j]/Linf.d-Lc.d/Linf.d))) # selection at length L[j]
  }
}

```

```

xN[j] <- xN[j-1]*((Linf.d-L.y[j])/(Linf.d-L.y[j-1]))^(MK.d+FK.d*SL[j])

      Freq.pred[j]<-xN[j]*SL[j]

# normalize frequencies by dividing by sum of frequencies; multiply with 10 to avoid small numbers and with 1000 for
effective sample size
  r.Freq.pred[j]<- Freq.pred[j]/sum(Freq.pred)*10*1000
}

#><> LIKELIHOOD FUNCTION
#><> Fit observed to predicted LF data using a Dirichlet distribution (more robust in JAGS)
r.Freq.y[2:n.L] ~ ddirch(r.Freq.pred[2:n.L])

} # END OF MODEL
",fill = TRUE)
sink()

MODEL = "SLNMod.jags"
jagsfitSLN <- jags.parallel(data=jags.data, working.directory=NULL, inits=NULL,
  parameters.to.save=jags.params,
  model.file=paste(MODEL),
  n.burnin=300, n.thin=10, n.iter=600, n.chains=3)

# use median and percentiles
Ldat$Lc[i] <- median(jagsfitSLN$BUGSoutput$sims.list$Lc.d)
Ldat$Lc.lcl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$Lc.d,0.025)
Ldat$Lc.ucl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$Lc.d,0.975)
Ldat$Lmean[i] <- sum(L.y[L.y>=Ldat$Lc[i]]*r.Freq.y[L.y>=Ldat$Lc[i]])/sum(r.Freq.y[L.y>=Ldat$Lc[i]])
Ldat$r.alpha[i] <- median(jagsfitSLN$BUGSoutput$sims.list$r.alpha.d)
Ldat$r.alpha.lcl[i]<- quantile(jagsfitSLN$BUGSoutput$sims.list$r.alpha.d,0.025)
Ldat$r.alpha.ucl[i]<- quantile(jagsfitSLN$BUGSoutput$sims.list$r.alpha.d,0.975)
Ldat$MK[i] <- median(jagsfitSLN$BUGSoutput$sims.list$MK.d)
Ldat$MK.lcl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$MK.d,0.025)
Ldat$MK.ucl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$MK.d,0.975)
Ldat$FK[i] <- median(jagsfitSLN$BUGSoutput$sims.list$FK.d)
Ldat$FK.lcl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$FK.d,0.025)
Ldat$FK.ucl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$FK.d,0.975)
FMi <- jagsfitSLN$BUGSoutput$sims.list$FK.d/jagsfitSLN$BUGSoutput$sims.list$MK.d
Ldat$FM[i] <- median(FMi)
Ldat$FM.lcl[i] <- quantile(FMi,0.025)
Ldat$FM.ucl[i] <- quantile(FMi,0.975)
ZKi <- jagsfitSLN$BUGSoutput$sims.list$MK.d + jagsfitSLN$BUGSoutput$sims.list$FK.d
Ldat$ZK[i] <- median(ZKi)
Ldat$ZK.lcl[i] <- quantile(ZKi,0.025)
Ldat$ZK.ucl[i] <- quantile(ZKi,0.975)
Ldat$r.Lopt[i] <- 3/(3+Ldat$MK[i])
Ldat$Linf[i] <- median((jagsfitSLN$BUGSoutput$sims.list$Linf.d))
Ldat$Linf.lcl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$Linf.d,0.025)
Ldat$Linf.ucl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$Linf.d,0.975)

} # end of trawl-like selection

#-----
# Estimate parameters GLmean, SD, F/K, M/K if selection is gillnet-like
#-----
if(dat.ID$GausSel==TRUE) {
  # determine priors
  # assume length at peak Freq as mean and distance to length at 80% of peak as SD of mean
  GLmean.st <- L.y[which.max(r.Freq.y)]
  # assume SD of Gaussian selection as distance between length at peak and length at 50% of peak
  Lc.pr <- L.y[which(r.Freq.y >= (0.5*max(r.Freq.y)))] [1]
  SD.st <- max(GLmean.st-Lc.pr,0.25*GLmean.st)

  cat("Running Jags model to fit SL and N distributions\n")

  n.L <- length(L.y)

  jags.data <- list ("n.L","GLmean.st","L.y","SD.st","ZK.nls","r.Freq.y","Linf.pr","Linf.sd.pr","MK.pr")
  jags.params <- c("GLmean.d","SD.d","SL","xN","FK.d","MK.d","Linf.d")

  #-----
  # JAGS model L-based with integral
  #-----
  sink("SLNMod.jags")
  cat("

```

```

model {
  GLmean.tau <- pow(0.1*GLmean.st,-2)
  GLmean.d ~ dnorm(GLmean.st,GLmean.tau)

  SD.tau <- pow(0.2*SD.st,-2)
  SD.d ~ dnorm(SD.st,SD.tau)

  MK.d_tau <-pow(0.15,-2)
  MK.d ~ dnorm(MK.pr,MK.d_tau)

  Linf.tau <- pow(Linf.sd.pr,-2)
  Linf.d ~ dnorm(Linf.pr,Linf.tau)

  FK <- (ZK.nls-1.5) # ZK overestimated in gillnet selection, used as upper range
  FK.d ~ dunif(0,FK)

  SL[1]~ dlogis(0,1000)
  Freq.pred[1]<-0
  xN[1]<-1

  for(j in 2:n.L) {
    SL[j]<- exp(-((L.y[j]-GLmean.d)^2/(2*SD.d^2)))

    xN[j]<-xN[j-1]*exp((MK.d+FK.d*SL[j])*(log(1-L.y[j]/Linf.d)-log(1-L.y[j-1]/Linf.d)))

    Freq.pred[j]<-xN[j]*SL[j]

    #><> add effective sample size (try 100 typical for LF data)
    r.Freq.pred[j]<- Freq.pred[j]/sum(Freq.pred)*10000
  }

  #><> LIKELIHOOD FUNCTION
  #><> Fit observed to predicted LF data using a Dirichlet distribution (more robust in JAGS)
  r.Freq.y[2:n.L]~ddirch(r.Freq.pred[2:n.L])

} # END OF MODEL
",fill = TRUE)
sink()

MODEL = "SLNMod.jags"
#jagsfitSLN <- jags(jags.data, inits=NULL, jags.params, paste(MODEL), n.chains = Nchains , n.thin =Nthin , n.iter =Niter ,
n.burnin = Nburnin)

jagsfitSLN <- jags.parallel(data=jags.data, working.directory=NULL, inits=NULL,
parameters.to.save=jags.params,
model.file=paste(MODEL),
n.burnin=300, n.thin=10, n.iter=1000, n.chains=3)

# use median and percentiles
Ldat$GLmean[i] <- median(jagsfitSLN$BUGSoutput$sims.list$GLmean.d)
Ldat$GLmean.lcl[i]<- quantile(jagsfitSLN$BUGSoutput$sims.list$GLmean.d,0.025)
Ldat$GLmean.ucl[i]<- quantile(jagsfitSLN$BUGSoutput$sims.list$GLmean.d,0.975)
Ldat$SD[i] <- median(jagsfitSLN$BUGSoutput$sims.list$SD.d)
Ldat$SD.lcl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$SD.d,0.025)
Ldat$SD.ucl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$SD.d,0.975)
Ldat$MK[i] <- median(jagsfitSLN$BUGSoutput$sims.list$MK.d)
Ldat$MK.lcl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$MK.d,0.025)
Ldat$MK.ucl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$MK.d,0.975)
Ldat$FK[i] <- median(jagsfitSLN$BUGSoutput$sims.list$FK.d)
Ldat$FK.lcl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$FK.d,0.025)
Ldat$FK.ucl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$FK.d,0.975)
FMi <- jagsfitSLN$BUGSoutput$sims.list$FK.d/jagsfitSLN$BUGSoutput$sims.list$MK.d
Ldat$FM[i] <- median(FMi)
Ldat$FM.lcl[i] <- quantile(FMi,0.025)
Ldat$FM.ucl[i] <- quantile(FMi,0.975)
ZKi <- jagsfitSLN$BUGSoutput$sims.list$MK.d + jagsfitSLN$BUGSoutput$sims.list$FK.d
Ldat$ZK[i] <- median(ZKi)
Ldat$ZK.lcl[i] <- quantile(ZKi,0.025)
Ldat$ZK.ucl[i] <- quantile(ZKi,0.975)
Ldat$r.Lopt[i] <- 3/(3+Ldat$MK[i])
Ldat$Linf[i] <- median((jagsfitSLN$BUGSoutput$sims.list$Linf.d))
Ldat$Linf.lcl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$Linf.d,0.025)
Ldat$Linf.ucl[i] <- quantile(jagsfitSLN$BUGSoutput$sims.list$Linf.d,0.975)

} # end of gillnet loop

```

```

# call BH function to estimate B/B0 and YR for the given year [i]
BH.list <-
BH(AllLength=unique(AllLength[AllYear==Year]),Linf=Ldat$Linf[i],MK=Ldat$MK[i],FK=Ldat$FK[i],GausSel=dat.ID$GausSel,
  selpar1=ifelse(dat.ID$GausSel==T,Ldat$GLmean[i]/Ldat$Linf[i],Ldat$Lc[i]/Ldat$Linf[i]),
  selpar2=ifelse(dat.ID$GausSel==T,Ldat$SD[i]/Ldat$Linf[i],Ldat$r.alpha[i])
  Ldat$BB0[i] <- as.numeric(BH.list[1])
  Ldat$YR[i] <- as.numeric(BH.list[2])

# Error propagation, assuming that fractional uncertainties add in quadrature
rel.lcl <- sqrt(((Ldat$FM[i]-Ldat$FM.lcl[i])/Ldat$FM[i])^2+((Ldat$MK[i]-Ldat$MK.lcl[i])/Ldat$MK[i])^2+((Ldat$FK[i]-
Ldat$FK.lcl[i])/Ldat$FK[i])^2+((Ldat$Linf[i]-Ldat$Linf.lcl[i])/Ldat$Linf[i])^2)
rel.ucl <- sqrt(((Ldat$FM.ucl[i]-Ldat$FM[i])/Ldat$FM[i])^2+((Ldat$MK.ucl[i]-Ldat$MK[i])/Ldat$MK[i])^2+((Ldat$FK.ucl[i]-
Ldat$FK[i])/Ldat$FK[i])^2+((Ldat$Linf.ucl[i]-Ldat$Linf[i])/Ldat$Linf[i])^2)
Ldat$BB0.lcl[i] <- Ldat$BB0[i]-Ldat$BB0[i]*rel.lcl
Ldat$BB0.ucl[i] <- Ldat$BB0[i]+Ldat$BB0[i]*rel.ucl
Ldat$YR.lcl[i] <- Ldat$YR[i]-Ldat$YR[i]*rel.lcl
Ldat$YR.ucl[i] <- Ldat$YR[i]+Ldat$YR[i]*rel.ucl

# get MSFD D3.3 indicators
Ldat$L95[i] <- wtd.quantile(x=L.y,weights=r.Freq.y,probs=c(0.95))
Ldat$perc.mat[i] <- ifelse(is.na(dat.ID$Lm50)==F,sum(r.Freq.y[L.y>dat.ID$Lm50])/sum(r.Freq.y),NA)

# plot first and last year
if(which(Years==Year)==1 | which(Years==Year)==length(Years)) {
  r.L.y <- L.y[L.y < Ldat$Linf[i]] / Ldat$Linf[i]
  r.Freq.y <- r.Freq.y[L.y < Ldat$Linf[i]]
  plot.year(r.L.y=r.L.y, r.Freq.y=r.Freq.y,r.Lopty=Ldat$r.Lopty[i],
    SL1=ifelse(dat.ID$GausSel==T,Ldat$GLmean[i],Ldat$Lc[i]),
    SL2=ifelse(dat.ID$GausSel==T,Ldat$SD[i],Ldat$r.alpha[i]),
    MK=Ldat$MK[i],FK=Ldat$FK[i],Linf=Ldat$Linf[i])
}
} # end of annual loop

# get some reference points as median of time series
Linf.med <- median(Ldat$Linf)
Linf.lcl <- median(Ldat$Linf.lcl)
Linf.ucl <- median(Ldat$Linf.ucl)
if(dat.ID$GausSel==F) {
  Lc.med <- median(Ldat$Lc)
  r.alpha.med <- median(Ldat$r.alpha) } else {
  GLmean.med <- median(Ldat$GLmean)
  SD.med <- median(Ldat$SD) }
MK.med <- median(Ldat$MK)
MK.lcl <- median(Ldat$MK.lcl)
MK.ucl <- median(Ldat$MK.ucl)
FK.med <- median(Ldat$FK)
FK.lcl <- median(Ldat$FK.lcl)
FK.ucl <- median(Ldat$FK.ucl)
FM.med <- median(Ldat$FM)
FM.lcl <- median(Ldat$FM.lcl)
FM.ucl <- median(Ldat$FM.ucl)
ZK.med <- median(Ldat$ZK)
ZK.lcl <- median(Ldat$ZK.lcl)
ZK.ucl <- median(Ldat$ZK.ucl)
r.Lopty.med <- median(Ldat$r.Lopty)
Lopty.med <- r.Lopty.med*Linf.med
Lc_opt.med <- Linf.med*(2+3*FM.med)/((1+FM.med)*(3+MK.med))
BB0.med <- median(Ldat$BB0)
BB0.lcl <- median(Ldat$BB0.lcl)
BB0.ucl <- median(Ldat$BB0.ucl)
YR.med <- median(Ldat$YR)
YR.lcl <- median(Ldat$YR.lcl)
YR.ucl <- median(Ldat$YR.ucl)

BFM1B0.list <- BH(AllLength=unique(AllLength),Linf=Linf.med,MK=MK.med,FK=MK.med,GausSel=dat.ID$GausSel,
  selpar1=ifelse(dat.ID$GausSel==T,r.Lopty.med,5/(2*(3+MK.med))),
  selpar2=ifelse(dat.ID$GausSel==T,SD.med/Linf.med,r.alpha.med))

BFM1B0 <- as.numeric(BFM1B0.list[1])
YRFM1 <- as.numeric(BFM1B0.list[2])

cat("\n-----\n")

```

```

cat("Results for ",dat.ID$Species," , stock",Stock," , StartYear,"-",EndYear,ifelse(dat.ID$GausSel==T," , Gaussian selection",""),
"\n")
cat("(95% confidence limits in parentheses) File:",dat.ID$File,"\n")
cat("-----\n")
cat("Linf prior =",Linf.pr," , SD =",Linf.sd.pr,"(cm)",ifelse(is.na(dat.ID$Linf.user)==TRUE,"","(user-defined)"),"\n")
cat("Z/K prior =",ZK.nls," , SD =", ZK.nls.sd," , M/K prior =", MK.pr," , SD
=",MK.sd.pr,ifelse(is.na(dat.ID$MK.user)==TRUE,"","(user-defined)"),"\n")
if(dat.ID$GausSel==F) {
  cat("F/K prior =", FK.pr," (wide range with tau=4 in log-normal distribution)\n")
  cat("Lc prior =",Lc.pr," , SD =",Lc.sd.pr,"(cm)",ifelse(is.na(dat.ID$Lc.user)==TRUE,"","(user-defined)"),
  ", alpha prior=",r.alpha.pr," , SD =",0.1*r.alpha.pr,"\n\n")
}

cat("General reference points [median across years]: \n")
cat("Linf      =",Linf.med,paste("(",format(Linf.lcl,digits=3),"-",format(Linf.ucl,digits=3),
  ifelse(dat.ID$mm.user==F,"") cm",") mm)", sep=""), "\n")
cat("Lopt      =",format(Lopt.med,digits=2),paste(ifelse(dat.ID$mm.user==F,"cm","mm"),"Lopt/Linf
="),format(r.Lopt.med,digits=2),"\n")
cat("Lc_opt    =",format(Lc_opt.med,digits=2),paste(ifelse(dat.ID$mm.user==F,"cm","mm"),"Lc_opt/Linf
="),format(Lc_opt.med/Linf.med,digits=2),"\n")
cat("M/K      =",MK.med,paste("(",format(MK.lcl,digits=3),"-",format(MK.ucl,digits=3),
  ")"),sep=""),"\n")
cat("F/K      =",FK.med,paste("(",format(FK.lcl,digits=3),"-",format(FK.ucl,digits=3),
  ")"),sep=""),"\n")
cat("Z/K      =",ZK.med,paste("(",format(ZK.lcl,digits=3),"-",format(ZK.ucl,digits=3),
  ")"),sep=""),"\n")
cat("F/M      =",FM.med,paste("(",format(FM.lcl,digits=3),"-",format(FM.ucl,digits=3),
  ")"),sep=""),"\n")
cat(ifelse(dat.ID$GausSel==F,"B/B0 F=M Lc=Lc_opt =", "Y/R' F=M Lmean=Lopt="),BFM1B0,"\n")
cat("B/B0     =",BB0.med,paste("(",format(BB0.lcl,digits=3),"-",format(BB0.ucl,digits=3),
  ")"),sep=""),"\n")
cat(ifelse(dat.ID$GausSel==F,"Y/R' F=M Lc=Lc_opt =", "Y/R' F=M Lmean=Lopt="),YRFM1,"\n")
cat("Y/R'     =",YR.med,paste("(",format(YR.lcl,digits=3),"-",format(YR.ucl,digits=3),
  ")"),sep=""),"(linearly reduced if B/B0 < 0.25)\n\n")
cat("Estimates for last year",EndYear,":\n")
last <- which(Ldat$Year==EndYear)
if(dat.ID$GausSel==F){
  cat("Lc      =",Ldat$Lc[last],paste("(",format(Ldat$Lc.lcl[last],digits=3),
  "-.",format(Ldat$Lc.ucl[last],digits=3),ifelse(dat.ID$mm.user==F,"") cm, Lc/Linf = ",") mm, Lc/Linf = ",)
  format(Ldat$Lc[last]/Ldat$Linf[last],digits=2), ("(",format(Ldat$Lc.lcl[last]/Ldat$Linf[last],digits=3),"-",
  format(Ldat$Lc.ucl[last]/Ldat$Linf[last],digits=3),")"),sep=""),"\n")
  cat("alpha    =",Ldat$alpha[last],"(",Ldat$alpha.lcl[last],"-",Ldat$alpha.ucl[last],") \n")
  cat("Lmean/Lopt =",format(Ldat$Lmean[last]/(Ldat$Lr.Lopt[last]*Ldat$Linf[last]),digits=2),
  ", Lc/Lc_opt =",format(Ldat$Lc[last]/Lc_opt.med,digits=2),
  ", L95th =", Ldat$L95[last],ifelse(dat.ID$mm.user==F,"cm","mm"),
  ", L95th/Linf =",format(Ldat$L95[last]/Ldat$Linf[last],digits=2),
  ", Lm50 =", dat.ID$Lm50,ifelse(dat.ID$mm.user==F,"cm","mm"),
  ", Mature =",format(Ldat$perc.mat[last]*100,digits=2),"%\n")
} else if(dat.ID$GausSel==T){
  cat("GLmean/Linf=",format(Ldat$GLmean[last]/Ldat$Linf[last],digits=2)," ,SD/Linf =",Ldat$SD[last]/Ldat$Linf[last],"\n")
  cat("GLmean  =",Ldat$GLmean[last]," ,SD =",Ldat$SD[last],"\n")
}
}
cat("F/K      =",format(Ldat$FK[last],digits=2),"(",Ldat$FK.lcl[last],"-",Ldat$FK.ucl[last],")\n")
cat("F/M      =",format(Ldat$FK[last]/Ldat$MK[last],digits=2),"(",Ldat$FM.lcl[last],"-",Ldat$FM.ucl[last],")\n")
cat("Z/K      =",Ldat$ZK[last],"(",Ldat$ZK.lcl[last],"-",Ldat$ZK.ucl[last],")\n")
cat("Y/R'     =",format(Ldat$YR[last],digits=2),"(",Ldat$YR.lcl[last],"-",Ldat$YR.ucl[last],") (linearly reduced if B/B0 < 0.25)\n")
cat("B/B0     =",format(Ldat$BB0[last],digits=2),"(",Ldat$BB0.lcl[last],"-",Ldat$BB0.ucl[last],")\n")
cat("B/Bmsy   =",format(Ldat$BB0[last]/BFM1B0,digits=2),"(",Ldat$BB0.lcl[last]/BFM1B0,"-",Ldat$BB0.ucl[last]/BFM1B0,"")\n")
if(dat.ID$Comment != "") cat("Comment:",dat.ID$Comment,"\n")

# point out questionable or impossible results
# negative rates
if(Ldat$MK[last] < 0 | Ldat$FK[i] < 0) cat("Data unsuitable for LF analysis, negative mortality rates are impossible\n")
# Biomass larger than unexploited
if(Ldat$BB0[last] > 1.1) cat("Data unsuitable for LF analysis, biomass exceeds carrying capacity\n")

#-----
# Plot time series of Lc and Lmean
#-----
if(nYears > 1) {

if(dat.ID$GausSel==F){
plot(x=Ldat$Year,y=Ldat$Lmean, bty="l",type="l",
  xlim=c(Ldat$Year[1],Ldat$Year[nYears]),

```

```

    xaxt="n",
    ylim=c(0,max(c(1.1*Lopt.med,max(Ldat$Lmean,na.rm=T),max(Ldat$Lc.ucl,na.rm=T))),lwd=2,
    xlab="Year",ylab = paste("Length",ifelse(dat.ID$mm.user==F,"(cm)","(mm)")),main="Lmean vs Lopt & Lc vs Lc_opt")
axis(1,at=Ldat$Year)
lines(x=Ldat$Year,y=Ldat$Lc,lwd=1,lty="dashed")
#lines(x=Ldat$Year,y=Ldat$Lc.lcl,lty="dotted")
#lines(x=Ldat$Year,y=Ldat$Lc.ucl,lty="dotted")
lines(x=Ldat$Year,y=rep(Lc_opt.med,nYears),col="darkgreen", lty="dashed") # line for Lc_opt
text(x=Ldat$Year[nYears],y=Lc_opt.med,"Lc_opt", adj=c(1,-0.5), col="darkgreen")
lines(x=Ldat$Year,y=rep(Lopt.med,nYears),col="darkgreen") # line for Lopt
text(x=Ldat$Year[nYears],y=Lopt.med,"Lopt", adj=c(1,-0.5), col="darkgreen")
}

#-----
# Plot time series of GLmean relative to Lopt
#-----
if(dat.ID$GausSel==T){
  plot(x=Ldat$Year,y=Ldat$GLmean, bty="l",type="l",
    xlim=c(Ldat$Year[1],Ldat$Year[nYears]),
    xaxt="n",
    ylim=c(0,max(1.1*median(Ldat$r.Lopt)*Linf.med,max(Ldat$GLmean),na.rm=T)),lwd=2,
    xlab="Year",ylab = "Lenght (cm)",main="Lmean vs Lopt")
  axis(1,at=Ldat$Year)
  lines(x=Ldat$Year,y=(Ldat$GLmean.lcl),lty="dotted")
  lines(x=Ldat$Year,y=(Ldat$GLmean.ucl),lty="dotted")
  lines(x=Ldat$Year,y=rep(Lopt.med,nYears),col="darkgreen") # line for Lopt
  text(x=Ldat$Year[nYears],y=Lopt.med,"Lopt", adj=c(1,-0.5), col="darkgreen")
}

#-----
# Plot time series of F/M
#-----
plot(x=Ldat$Year,y=Ldat$FM,
  ylim=c(0,max(max(Ldat$FM.ucl),1.05)),
  bty="l",type = "l", lwd=1.5, xaxt="n",
  main="previous F/M",xlab="Year",ylab="F/M")
axis(1,at=Ldat$Year)
lines(x=Ldat$Year,y=Ldat$FM.lcl,lty="dotted")
lines(x=Ldat$Year,y=Ldat$FM.ucl,lty="dotted")
abline(h=1.0,col="darkgreen")
text(x=Ldat$Year[nYears],y=1,"F=M", adj=c(0.8,-0.5), col="darkgreen")

#-----
# Plot time series of B/B0
#-----
plot(x=Ldat$Year,y=Ldat$BB0,ylim=c(0,min(c(1.1,max(c(0.6,Ldat$BB0.ucl,1.1*BFM1B0))))),
  bty="l",type = "l", lwd=1.5, xaxt="n",
  main="exploited B / B0",xlab="Year",ylab="B / B0")
axis(1,at=Ldat$Year)
lines(x=Ldat$Year,y=Ldat$BB0.lcl,lty="dotted")
lines(x=Ldat$Year,y=Ldat$BB0.ucl,lty="dotted")
abline(h=1.0,col="darkgreen") # B0
text(x=Ldat$Year[nYears],y=1,"B0", adj=c(0.8,-0.5), col="darkgreen")
lines(x=Ldat$Year,y=rep(BFM1B0,nYears),lty="dashed", col="darkgreen")
text(x=Ldat$Year[nYears-1],y=BFM1B0,"B F=M, Lc=opt", adj=c(0.8,-0.5),col="darkgreen")
lines(x=Ldat$Year,y=rep(BFM1B0/2,nYears),lty="dotted", col="red")
text(x=Ldat$Year[nYears-1],y=BFM1B0/2,"proxy 0.5 Bmsy", adj=c(0.8,-0.5),col="red")
} # end of loop for plotting time series

```