SCIENTIFIC COMMITTEE
FOURTEENTH REGULAR SESSION

Busan, Korea
8-16 August 2018

Testing MULTIFAN-CL developments for multispecies/multi-sex assessments, using SW Pacific swordfish

---

WCPFC-SC14-2018/SA-IP-10

Yukio Takeuchi[1], Nick Davies[2], Dave Fournier[3], Graham Pilling[1], and John Hampton[1]

[1] Oceanic Fisheries Programme, The Pacific Community (SPC)
[2] Te Takina Ltd, Whangarei, New Zealand
[3] Otter Research Ltd, North Saanich, British Columbia, Canada

Abstract

This paper summarizes the current developments to the multi-species/multi-sex functionality of MULTIFAN-CL. These developments are used to implement a preliminary sex-disaggregated MULTIFAN-CL model for swordfish in the southwest Pacific Ocean. A specific sub-set of results from that evaluation are presented and compared to the diagnostic case model from the 2017 sex-aggregated assessment for this stock.

Management quantities such as the depletion of female spawning biomass from the sex-disaggregated model are very similar to those developed for the sex-aggregated 2017 diagnostic case. Despite that overall similarity, there are model-specific differences. For example, the pattern of recruitment by model region is notably different in the two-sex model estimates, with the majority of recruits occurring in Region 2 (eastern region). Estimated selectivity of key fleets are also different in this region. Several potential future improvements for the model are suggested, and should be considered prior to the application of two-sex population dynamics within WCPO assessments.

Introduction

One of the recent major developments of MULTIFAN-CL was the extension of model dynamics to the multi species/sex model from the original single species/sex model (Davies et al., 2017, 2018). Since key tuna and billfish species have sex differentiated growth dynamics (e.g. Farley 2016), it is desirable to extend MULTIFAN-CL functionality to explicitly model a sex-structured population and dynamics.

During development of the 2017 south Pacific swordfish assessment (Takeuchi et al., 2017), an explicitly modelled sex-structured population model was developed, where sex-specific biological information was incorporated but the majority of fishery data were sex aggregated. However, this attempt was unsuccessful as several additional important features were needed to stabilize the model estimation given that the limited sex specific data could not be incorporated into the model fit within the time available.

Since SC13, additional developments to MULTIFAN-CL have been undertaken, in particular effort deviations can now be shared across sexes. This feature can substantially reduce the number of independent parameters to be estimated, and is expected to stabilize the two-sex MULTIFAN-CL model estimation, particularly where only sex aggregated fishery data are available.

This new MULTIFAN-CL sex-structured functionality is tested by conducting a preliminary two-sex evaluation, using the diagnostic case model of the 2017 sex-aggregated South Pacific swordfish assessment as a basis. Results from two test models incorporating sex structure are prepared. The first applied the fixed biological parameters used in the 2017 assessment equally to both sexes. The second applied fixed sex-specific growth estimates to each sex.

Changes of MULTIFAN-CL for two-sex model after SC13

The key development to MULTIFAN-CL's functionality for two-sex model development following SC13 has been the implementation of shared effort deviations among one or more of fisheries. This section introduces the feature.

The feature is primarily intended to allow sharing of effort deviation parameters across sex for the same fishery, but this feature can potentially be used as a general setting. The only limitation to the shared effort deviation currently implemented is that it requires fisheries that share effort deviations to occur concurrently. This limitation is clearly not a concern in the case of a two-sex model. If effort deviations are shared across sexes, the effort deviation penalties are calculated once for the fishery and applied to both sexes. This avoids applying the effort deviation penalty twice.

Outline of two-sex model structure

The two-sex version of MULTIFAN-CL allows sex-specific population dynamics to be modelled. The sex ratio at recruitment is assumed to be 1:1 for each region and season. Natural mortality and maturity at age parameters are sex-specific. Although MULTIFAN -CL accepts maturity at age for each sex as input parameters, only maturity at age for the female component is used to calculate spawning potential. Growth curve parameters include two parameters to define the standard deviation of mean length at age for each sex. Growth curve parameters can be estimated within the model or assumed at fixed values. Age specific natural mortality is usually not internally estimable (unless well-informed by data), and therefore must be supplied by the user.

Fishery selectivity parameterizations

For the two sex model, two forms of selectivity functions were implemented in 2017 that can share selectivity parameters across sex based on "scaled length at age" (Davies et al., 2017). One is a cubic spline, which is an extension of cubic spline age-based selectivity within the single sex model. In the case of the single sex model, it is parametrized on the scaled length, which maps the L_1 and L_{max} parameters of the growth curve from 0 to 1. For a two-sex model, the scaled length was re-defined to map the smallest L_1 and largest L_{max} among male and female from 0 to 1. Similarly, a logistic selectivity function for the two-sex formulation was implemented on the scaled length at age among the sexes. For the single-sex version, the logistic selectivity function is parametrized only on the age. Therefore, the shape of the equivalent estimated two-sex version may not match that for the single sex case.

The current implementation of selectivity functions shared across sexes has the following limitation. The single sex MULTIFAN-CL allows analysts to control the behaviour of the selectivity function (e.g non-decreasing from certain age class or zero selectivity from first age class to a certain age class). These finer controls of selectivity function behaviour often improve the stability of the model estimate. In the case of the shared selectivity function for the two-sex model, analysts can still use those controls by age class as in the single sex model. However, since mean length at age between sexes can be different, the user must *a priori* know which gender has the lower length at age for an age class as part of this process. This may be challenging when the growth curve is estimated internally.

Calculation of predicted size composition

The fit to sex-aggregated size composition data is calculated reflecting the sex ratio of the predicted catch-at-size.

Disaggregated fisheries data

The two-sex feature in MULTIFAN-CL was extended to allow the aggregated or dis-aggregated options for each of the three types of fisheries data individually, i.e. for catches, length frequencies, and weight frequencies. For an individual fishing incident, each data type can be input either aggregated or disaggregated among the sexes. While this flexibility is possible, the models presented here use sex aggregated fisheries data only.

Two-sex MULTIFAN-CL test runs - southwest Pacific swordfish as an example

The two-sex model developments of MULTIFAN-CL were tested using southwest Pacific swordfish as an example. As a two-sex assessment model was initially attempted in 2017, the file structure and available sex-disaggregated information were available for this purpose.

Model settings

Three models were developed for evaluation and comparison:

Model 0

Model 0 is a single-sex model, identical to the 2017 diagnostic case model. Model 0 is used as a baseline against which to compare the results from following two two-sex models.

Model 1

Model 1 is identical to Model 0, except it introduces sex structured population dynamics. The same biological parameters used in the 2017 diagnostic case model are applied to both sexes. As a result, this model is expected to produce results directly comparable to the 2017 diagnostic case model. Any potential differences can be expected from the use of different parametrizations for the selectivity functions, in particular the logistic selectivity function (in Model 0 it is parametrized on age, in Models 1 and 2 it is parametrized on scaled length).

Model 2

Model 2 is also sex structured, but a sex specific growth curve obtained from otolith ageing data (Farley et al., 2016) is used. Sex-specific and age-specific natural mortality are calculated using the same algorithm applied in the 2017 single sex assessment model. In the case of the two-sex model, sex specific growth curve parameters are used to empirically derive average natural mortality.

Models 1 and 2 have fixed growth curve parameters, but the CV of growth curve is estimated by sex. These models therefore have one more estimated parameter compared with the 2017 diagnostic case model which estimate one CV parameter for the growth curve.

Figure 1 presents the growth curve for Model 0 (2017 diagnostic case run) and the sex-specific growth curve estimated using otolith aging data (Farley et al., 2016) used in Model 2. Figure 2 compares natural mortality vectors used for test runs. Sex specific natural mortality vectors are recalculated using the algorithm described in Davies et al. (2013) to each gender separately.

Regional structure and diffusion coefficients are fixed at the values used within the 2017 diagnostic case (Model 0) and are shared across sexes in Models 1 and 2.

In the case of the two-sex models, spawning potential is calculated based on the female spawning biomass only. Depletion estimates from two-sex models presented in this report are also based on the ratio of female spawning potential to unfished female spawning potential.

Results

Table 1 compares total negative likelihood and likelihood components of each model. Total likelihoods of model 1 and 2 are marginally poorer. This may be because particular flag settings, particularly those for the selectivity functions of the two-sex models, had not yet been optimised within this trial.

Figure 3 compares the temporal trends of estimated depletion for Models 0 to 2. Depletion estimates from Models 0 and 1 are comparable throughout the assessment period, and converged to be almost identical in the most recent decade. Temporal trends of estimated depletion from Model 2 suggest slightly lower depletion compared to those of the other Models, with the exception of peak around 1980s, and again estimates converge in the most recent decade. Figure 4 compares the predicted yield as a function of fishing mortality multiplier for Models 0 and 2. Maximum sex-aggregated yield is estimated to be slightly lower in the two-sex model, achieved at slightly higher fishing mortality levels.

Figure 5 and Figure 6 compare estimated spawning potential and recruitment by model region respectively, from Models 0 to 2. Spawning potential and recruitment from Model 0 are divided by 2 implicitly assuming 1:1 sex ratio for adult biomass and recruitment, i.e. they correspond to half the quantities reported in 2017 assessment. Those presented for Models 1 and 2 are female-specific. Notable differences from the single sex model (Model 0) to the two-sex model (Model 2) are seen in the proportion of recruitment by region, with recruitment primarily resulting in the eastern region (region 2). The average proportion of recruitment from the western region (Region 1) of the two-sex model (Model 2) is only about 0.5%, while that estimated within the 2017 diagnostic case model run (Model 0) is about 35%. Another notable difference is the higher spawning potential and recruitment in Model 2 with sex-specific dynamics compared to Model 0 and Model 1. This is likely the result of the different natural mortality at age in Model 2 compared to the other models. In particular, Model 2 has substantially higher natural mortality for juvenile males which may indirectly impact the scaling of female abundance through the assumption of 50:50 sex ratio at recruitment.

Figure 7 compares selectivity at mean length at age from Models 0 to 2. Although the expectation was that the selectivity estimated within the single sex model (model 0) and two-sex model with same biological parameters applied across sexes (Model 1) were likely to be similar, the estimated selectivities for distant longline fisheries (Fisheries 7, 8 and 9) in eastern region (Region 2) differ. One potential cause of this difference may be the parametrization of the logistic selectivity function for the two-sex model.

Figure 8 and Figure 9 presents observed and predicted length composition data aggregated over all time periods by fishery from the three Models, while Figure 10 compares the fit to CPUE for the Models. Figure 11 compares estimated effort deviations for those fisheries having standardized CPUEs among the models, while Figure 12 compares estimated effort deviations for fisheries without standardized CPUE among the models.

Discussion

A test application of the two-sex MULTIFAN-CL functionality to south-western Pacific swordfish appears to have been successful.

- Model 1, which modelled the sex structured population but applied the same biological parameters from 2017 diagnostic case run (Model 0) to each sex, produced very similar results compared to Model 0. Nevertheless, there are a few minor differences between the model fits. More testing is needed to check if there are any unrecognized problems which might cause the differences in the current two-sex version of MFCL.
- Comparisons of selectivity at mean length at age of 2017 diagnostic case model (Model 0) and the two-sex model with identical biological parameters applied to both sexes (Model 1) in Figure 7, highlighted the potential differences in model fit due to different parametrizations of the implemented selectivity functions for the two-sex model when compared to age based selectivity functions used for single sex model. Further investigation of the cause of these different estimated selectivities is warranted.
- Both the 2017 south-western Pacific swordfish assessment and the two two-sex analyses presented in this report assumed two regions (Eastern and Western regions) for the population. However, there is some evidence to suggest a larger proportion of females can be found at the higher latitudes, and further developments of the swordfish model spatial structure could be considered to reflect this.
- There is a limited amount of sex-separated size composition data from some fisheries, but such data would provide key information to differentiate population dynamics by sex. It is possible to simultaneously use sex-aggregated and sex-specific size data for the same fishery observations, so the next iteration of this assessment should investigate that possibility, noting that care will be needed to appropriately weight the size data in the likelihood.

Several potential future improvements for the model are suggested, and should be considered for the application of two-sex population dynamics within WCPO assessments:

- Currently available options for fishery selectivity for the two-sex model are limited to cubic spline curve and logistic curve forms. Development of additional selectivity function options for the two-sex model should be explored. One candidate may be parametric selectivity functions to model dome-shaped selectivity e.g. double normal selectivity.
- Usually assessments using MULTIFAN-CL condition selectivity to assign zero selectivity to certain age classes, or flat or decreasing selectivity from a certain age class. Those features are also available for two-sex model. However analysts must be aware of the sex that has lower or larger length at age to properly set up the selectivity. A development to allow analysts to use length (bin) or scaled length instead of the age class for this purpose would be useful.
- Current implementation of the two-sex version of MULTIFAN-CL requires externally estimated sex specific and age dependent natural mortality. Additional model development could allow MULTIFAN-CL to internally estimate sex-specific age-dependent natural mortality.
- A sex-specific growth curve can be internally estimated if conditional age-at-length data by sex are available. Shared growth curve parameters may be effective in stabilizing the estimations. In particular, the facility to share the L1 (length at first age class) parameter of the growth curve function may be desirable.
- Test runs presented in this report applied fixed movement parameters. Further tag release-recapture data may allow movement parameters to be estimated internally. However an additional model development to correctly apportion aggregated tag release data by sex within MULTIFAN-CL is therefore necessary that accounts for sex-specific lengths at age and the selectivity of the method used to release tagged fish. However, to date probably no tag release recapture data with sex id is available for tuna and billfish assessed at WCPFC.

In conclusion, recent developments to MULTIFAN-CL for two-sex model functionality appear promising for future assessments of those species known to have very different biological parameters by sex. Nevertheless, further model developments are needed to undertake a full assessment using the two-sex version of MULTIFAN-CL.

References

Davies, N., Pilling, G., Harley, S. and Hampton, J. 2013. Stock assessment of swordfish (*Xiphias gladius*) in the southwest Pacific Ocean. WCPFC-SC9-2013/SA-WP-05.

Davies, N., Fournier, D., Takeuchi, Y., Bouyé, F., and Hampton, J. 2017. Developments in the MULTIFAN-CL software 2016-17. WCPFC-SC13-2017/SA-IP-05

Davies, N., Fournier, D., Takeuchi, Y., Bouyé, F., and Hampton, J. 2018. Developments in the MULTIFAN-CL software 2017-18. WCPFC-SC14-2018/SA-IP-02

Farley, J., Clear, N., Kolody, D., Krusic-Golub, K., Eveson P. and Young, J. (2016). Determination of swordfish growth and maturity relevant to the southwest Pacific stock. WCPFC-SC12-2016/SA-WP-11.

Takeuchi, Y. Pilling, G. and Hampton, J. (2017). Stock Assessment of Swordfish (*Xiphias gladius*) in the Southwest Pacific Ocean. WCPFC-SC13-2017/SA-WP-13

WCPFC (2017). Scientific Committee 10th Regular Session summary report. Rarotonga, Cook Islands
9 - 17 August 2017. 228p.

Figures and tables

Table 1. Negative of likelihoods components and numbers of parameters of Models 0 to 2.

	SRR	Effort	catchability	Length	Weight	catch	Total	Number of params
Model 0	11.7603	1105.082	97.28123	-16943.32	-10359.64	3.478441	-26085.36	2266
Model 1	10.1667	1141.101	101.3977	-16960.83	-10360.71	3.602105	-26065.27	2268
Model 2	10.6248	1191.588	102.2867	-16969.11	-10357.57	3.794685	-26018.39	2268

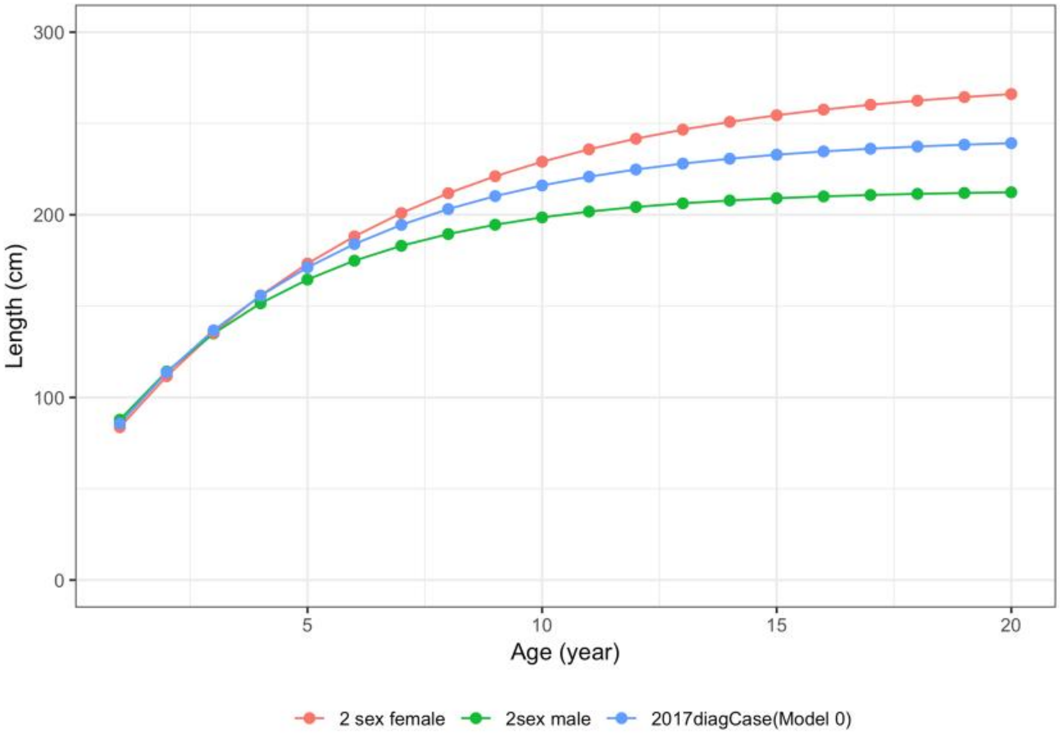

Figure 1. Comparison of growth curves used for 2017 diagnostic case (Model 0) and Model 2 with sex specific growth curves from otolith ageing.

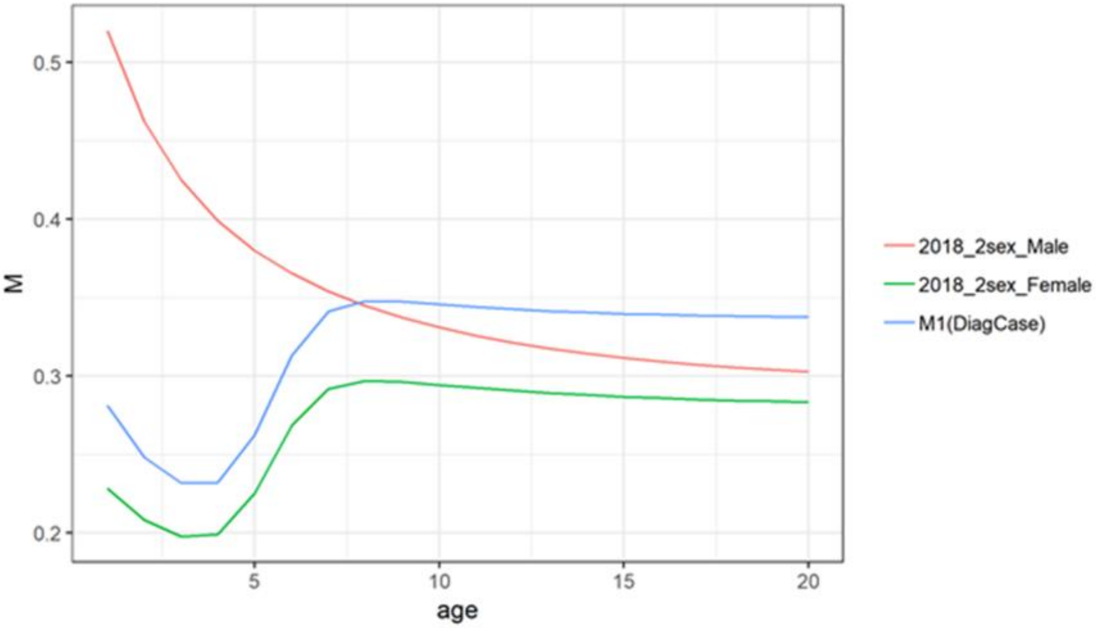

Figure 2. Comparison of annual natural mortality vectors used for 2017 diagnostic case (Model 0) and two-sex model with sex specific growth curve (Model 2).

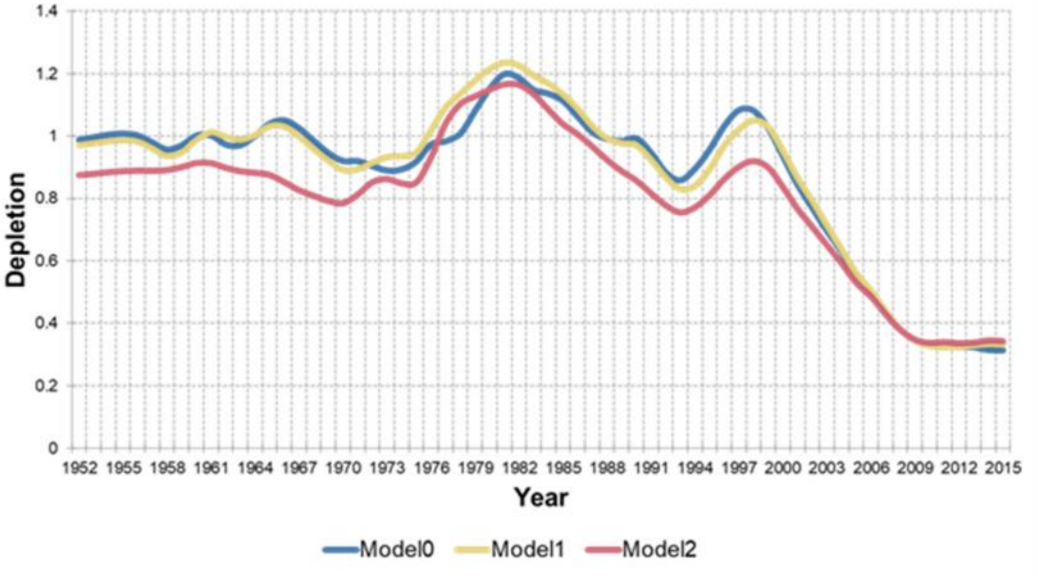

Figure 3. Comparison of time series of depletion ($SB/SB_{F=0}$) of Models 0 to 2. $SB_{F=0}$ was calculated from the average of unfished spawning biomass from 2005 to 2014.

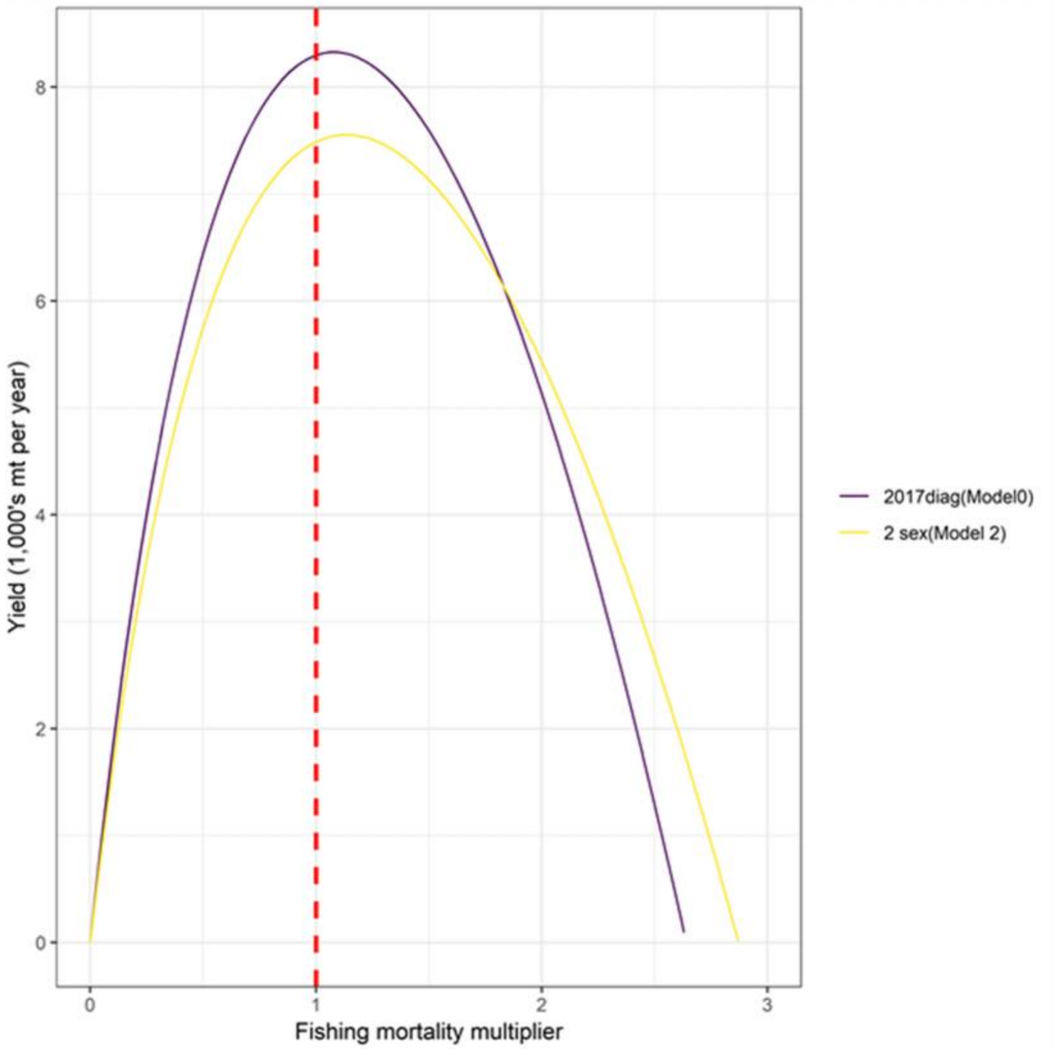

Figure 4. Estimated yield as a function of fishing mortality multiplier for 2017 diagnostic case model (Model 0) and two-sex model (yellow curve, Model 2). Predicted yield from the two-sex model represents sex aggregated yield.

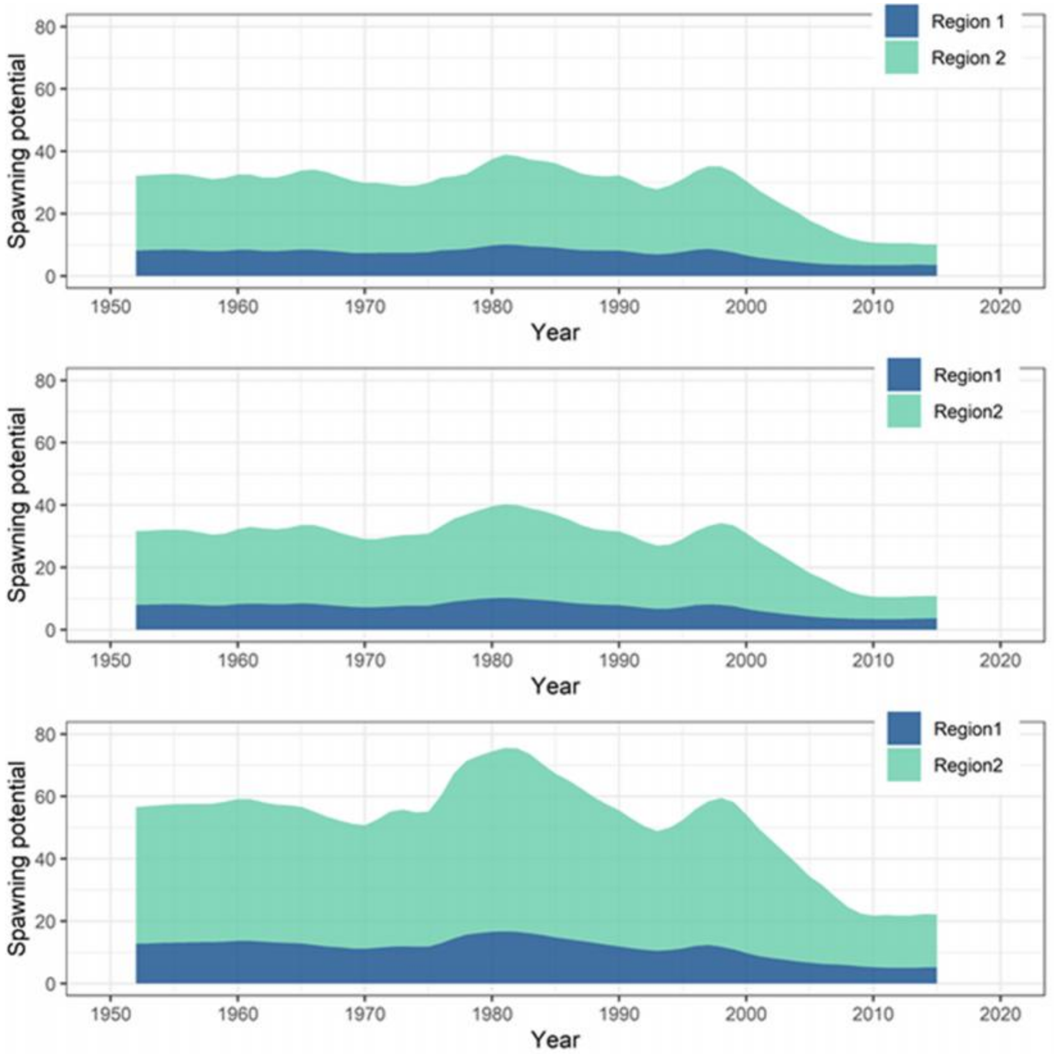

Figure 5. Comparisons of trends of spawning potential from Model 0 (Top), Model 1 (centre) and Model 2 (bottom). Spawning potential of Model 0 was divided by 2, implicitly assuming 1:1 sex ratio for the single sex model. Spawning potential of Models 1 and 2 are female spawning biomass only.

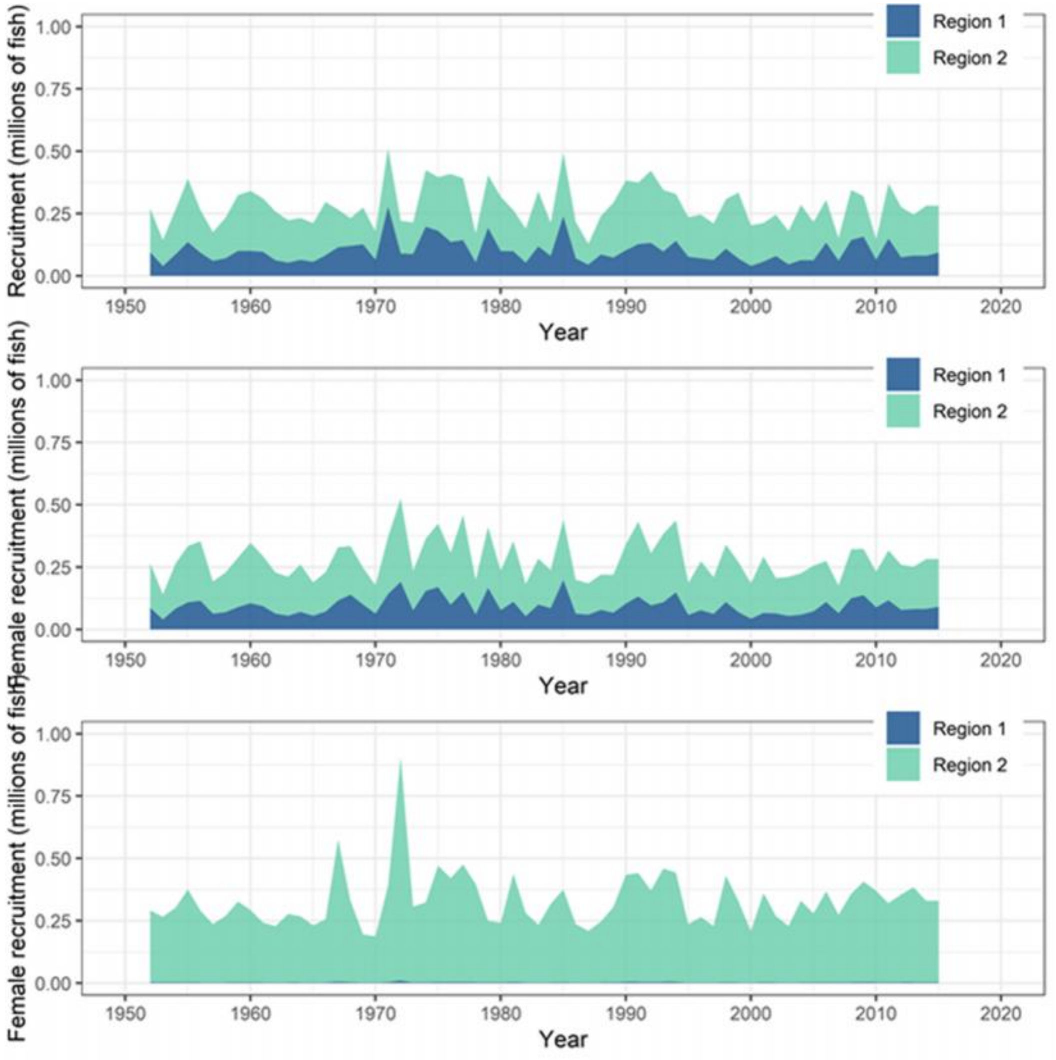

Figure 6. Comparisons of trends of recruitment from Model 0 (Top), Model 1 (centre) and Model 2 (bottom). Recruitment of Model 0 was divided by 2 to make direct comparison to those from two-sex models easier. Recruitment estimates of Models 1 and 2 are female recruitments only.

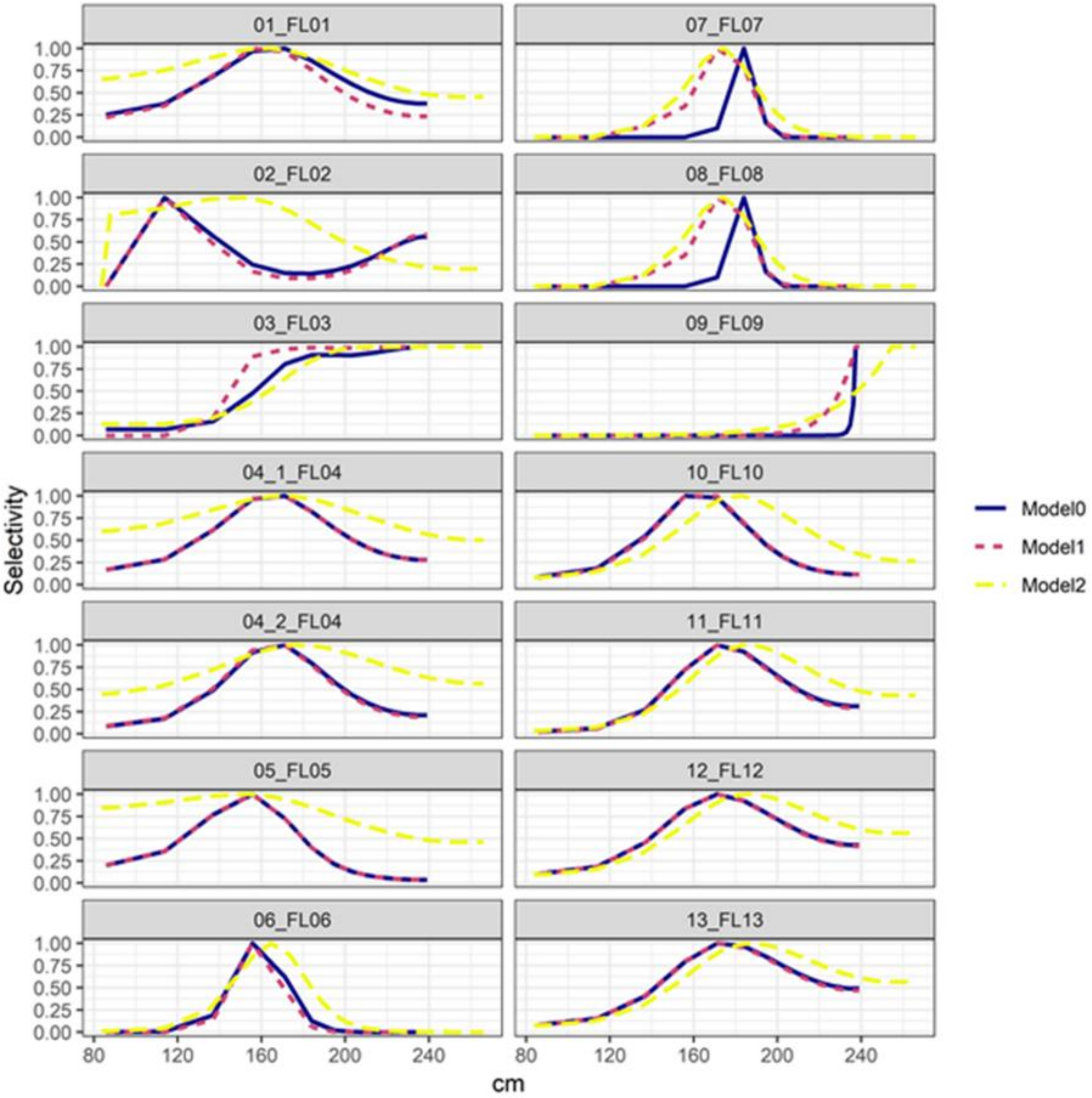

Figure 7. Comparison of estimated selectivity at mean length at age of Models 0 to 2

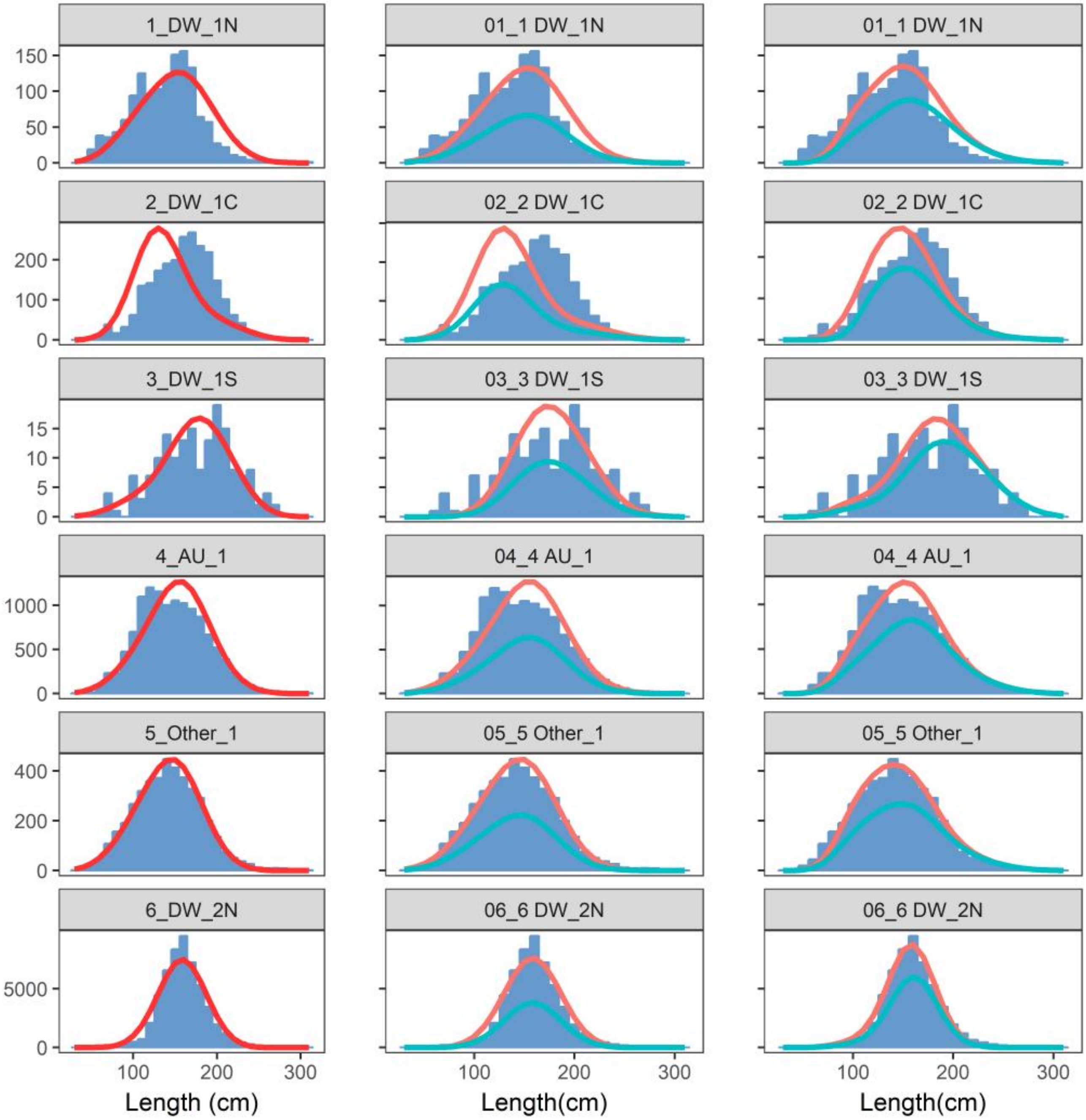

Figure 8. Aggregated observed and predicted length composition by fishery (1-6,down) and Models 0, 1 and 2 (left, centre and right, respectively). For Models 1 and 2, predictions by sex are stacked in the plot. The area between the red and green lines represents the predicted male length composition. The area below the green line represents the predicted female length composition.

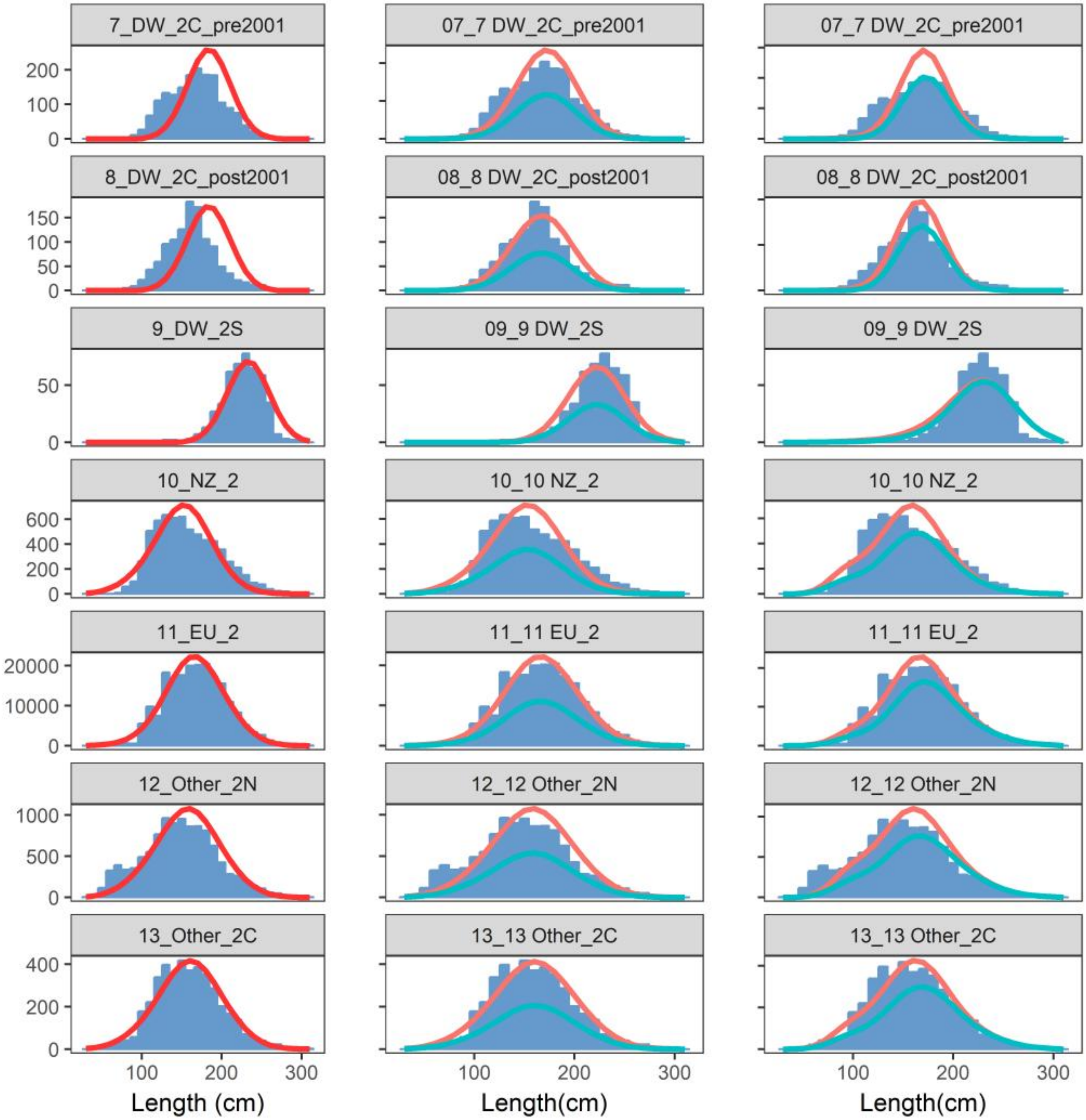

Figure 9 Aggregated observed and predicted length composition by fishery (7-13, down) and Models 0, 1 and 2 (left, centre and right, respectively). For Models 1 and 2, predictions by sex are stacked in the plot. The area between the red and green lines represents the predicted male length composition. The area below the green line represents the predicted female length composition.

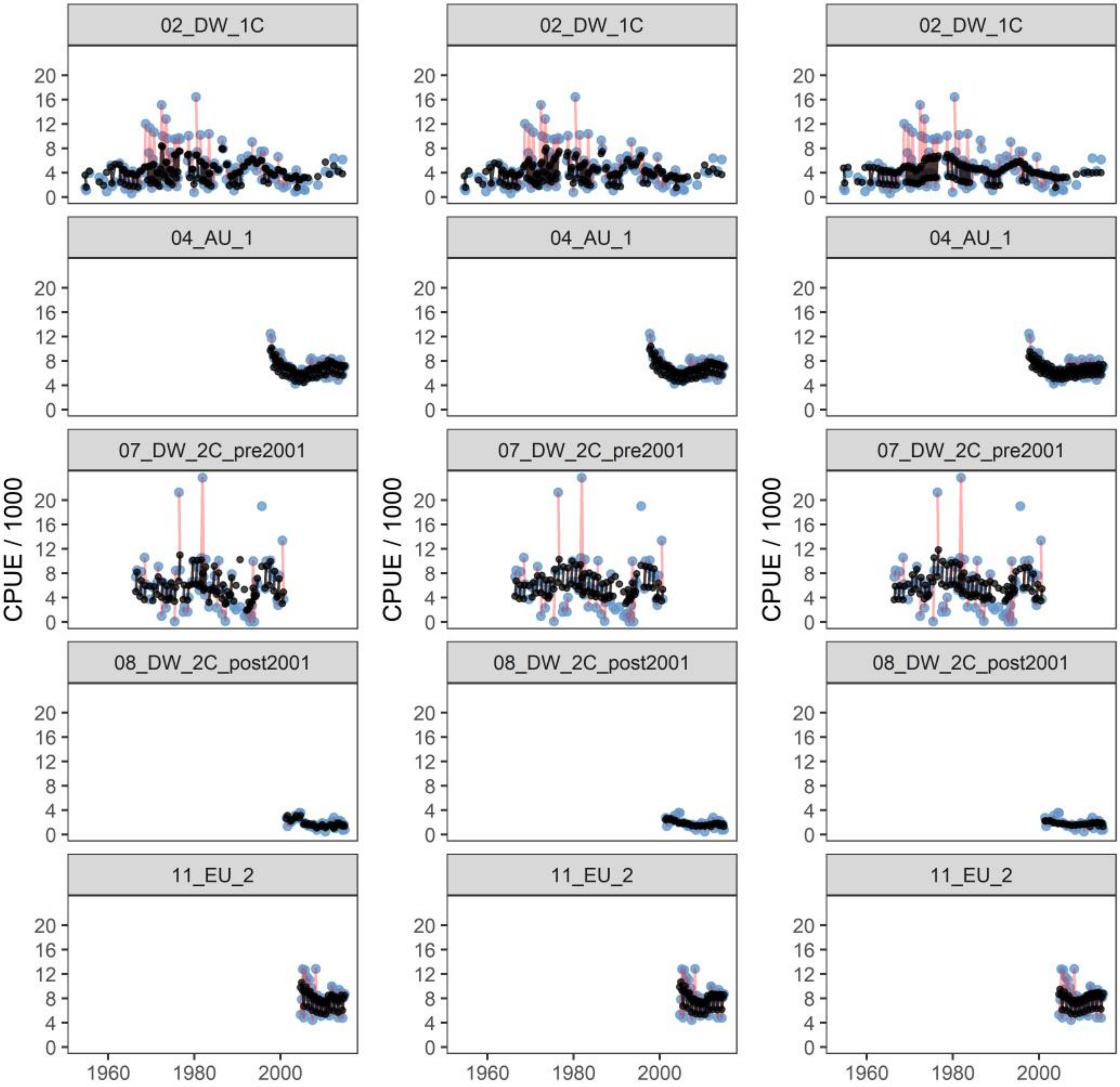

Figure 10. CPUE fits from Model 0 (left) , Model 1 (centre)and Model 2 (right).

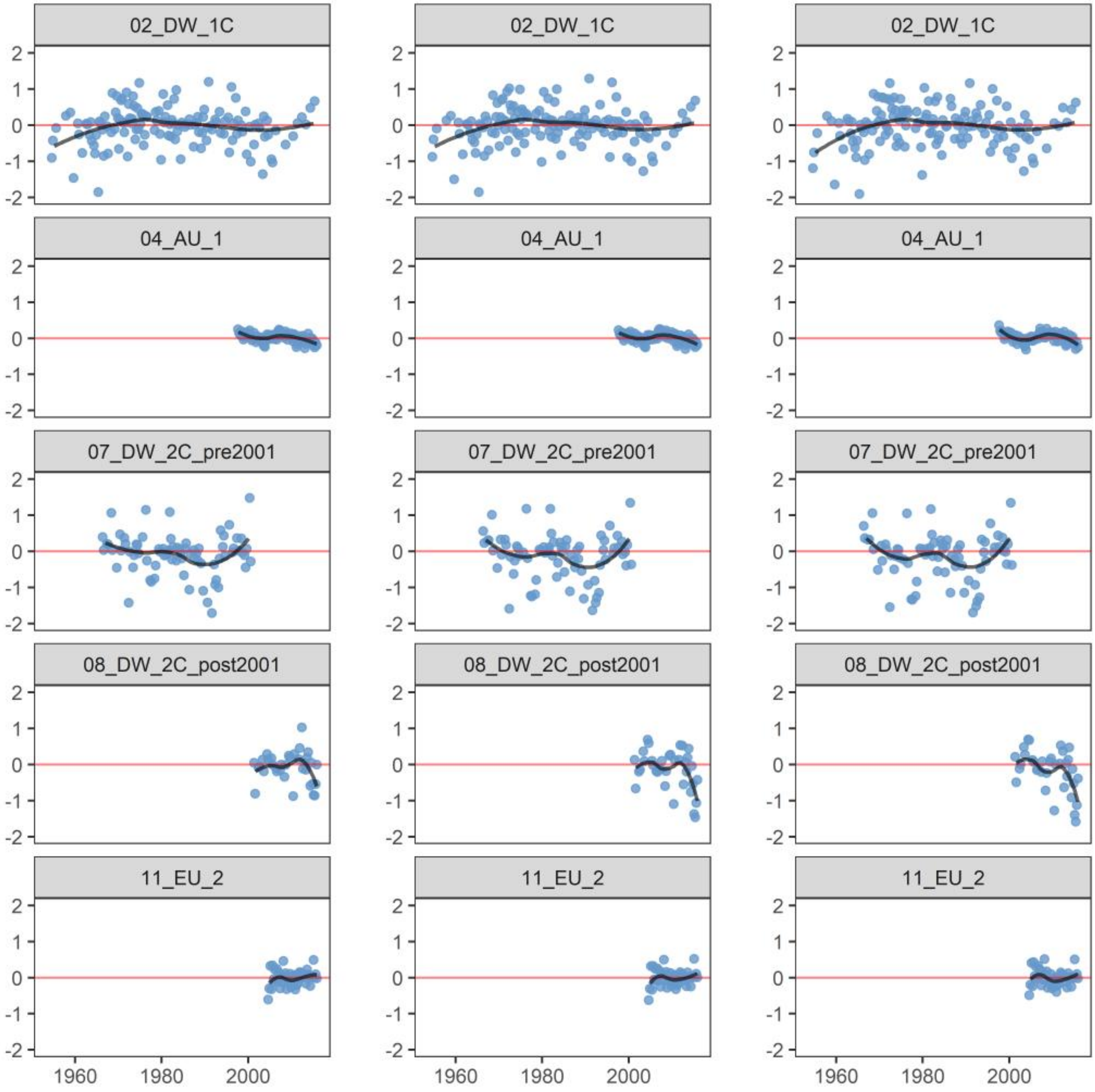

Figure 11. Effort deviations for fisheries having standardised CPUE from Model 0 (left) , Model 1 (centre) and Model 2 (right).

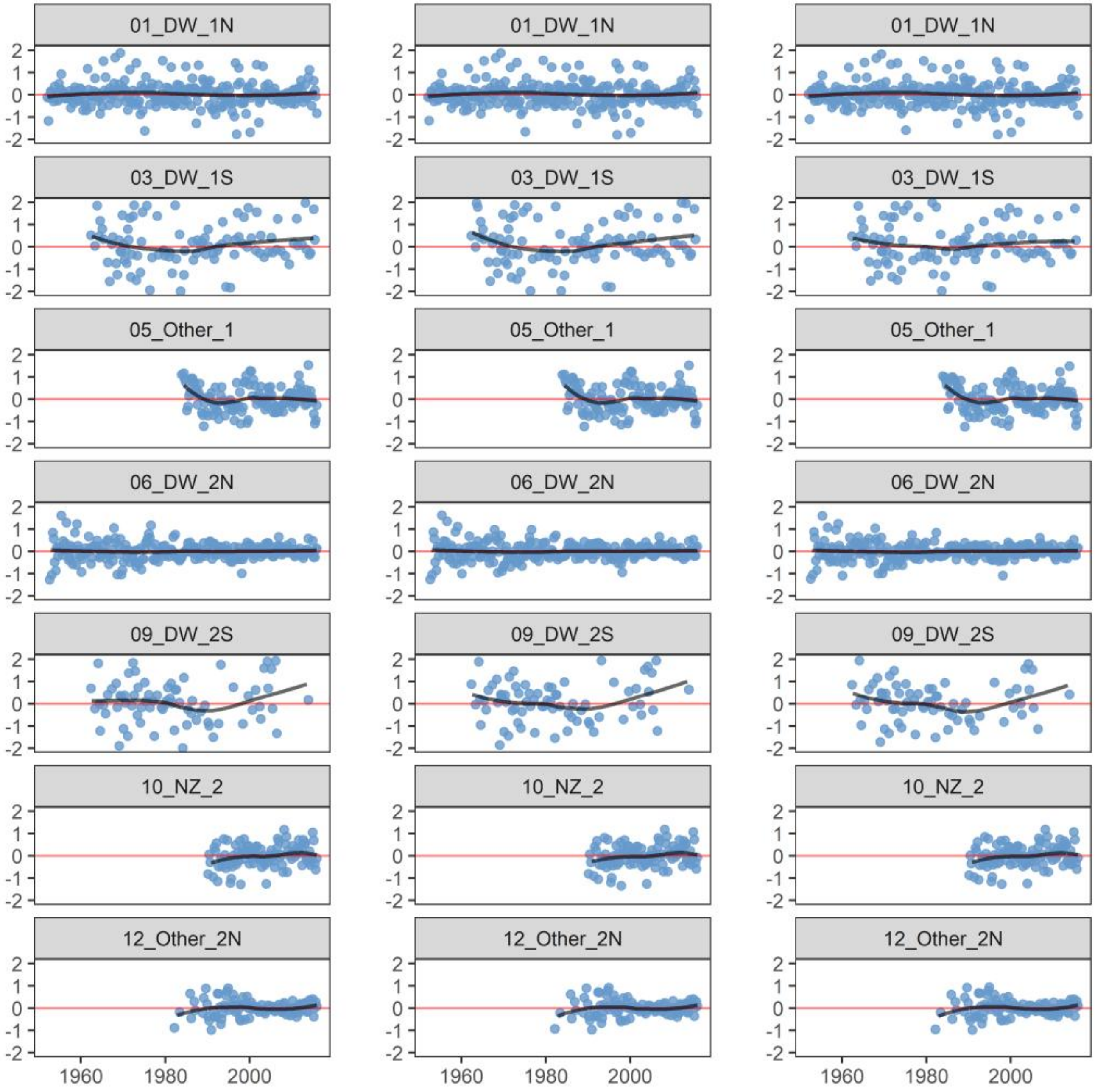

Figure 12. Effort deviations for fisheries without CPUEs from Model 0 (left) , Model 1 (centre) and Model 2 (right).