

# Update on the MARAM hake predation model, focusing on the natural mortality-at-age vectors to be used for the Reference Set of Operating Models for the 2018 Hake OMP review

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## Summary

The Panel at the 2017 International Stock Assessment Workshop recommended single selections for natural mortality-at-age vectors for the two hake species for the Operating Models for OMP testing, and that these be based on the hake predation model. Here this model is used to provide near finalised proposals for the two vectors to be used. Certain recent updates to the predation model are also summarised.

## Introduction

An update is provided to the results presented previously for the MARAM hake cannibalism and inter-species predation model (Ross-Gillespie 2016). The natural mortality-at-age vectors presented here are to be used as input to the standard stock assessment models for the 2018 hake OMP review, as recommended by the Panel for the 2017 International Stock Assessment Workshop (IWS 2017) (Cox *et al.* 2017).

Following comments from IWS 2016 (Dunn *et al.* 2016) and further model exploration, some modifications were made to the Ross-Gillespie (2016) model, a list of which is given below.

1. The input data have been updated (the Ross-Gillespie 2016 model extended only to 2013, and the new model now extends to 2017).
2. The hake-on-hake preference-by-length counts are converted to preference-by-age counts externally to the model using the standard hake assessment model growth curve parameters. These preference data have been updated using more recent growth curve parameter estimates.
3. Some updates have been made to match the latest standard stock assessment model specifications (Rademeyer and Butterworth 2017), in particular updates have been made to the selectivity functions.
4. The Ross-Gillespie (2016) model does not use a selectivity-weighted weight-at-length function. This has now been implemented.
5. The catch-at-length data are incorporated into the negative log-likelihood using a power of 0.35 (see Ross-Gillespie and Butterworth 2018 for more information).

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6. The  $P_{lim}$  constraint placing an upper bound on the predation rate has been removed (see the Appendix for more information).
7. The basal natural mortality vector has been modified to allow for larger values at low ages (see the Appendix for more information).
8. A penalty has been added to prevent the survey  $q$  values from becoming too small for the summer and autumn surveys (see the Appendix for more information).

## Results and discussion

Results are shown here for the new Base Case (BC), from which the natural mortality-age-age vectors are to be used for the Reference Set of Operating Models (OMs) for the 2018 hake OMP revision. The fits are shown alongside the original Ross-Gillespie (2016) fits and the standard stock assessment model (henceforth referred to as the Rademeyer model) results<sup>2</sup>, as well as a version of the updated predation model with the predation component switched off<sup>3</sup>.

While the hake predation model is not yet finalized in every respect, the Panel for IWS 2017 nonetheless recommended that early estimation of the predation natural mortality-age-age vectors for each of the two hake species by the predation model be used for the Reference Set OMs for the OMP review, since these vectors have a better underlying basis than the somewhat arbitrary natural mortality-age-age vectors assumed earlier for the standard stock assessment model. Note should be taken of the fact that the fits of the predation model to the historical ICSEAF data are now much better than was the case for the PhD model. Furthermore, the estimated depletion level for *M. paradoxus* is more optimistic than estimated by the PhD model and is also therefore now more consistent with results obtained by a hake predation model developed independently (OLRAC 2016).

The natural mortality-age-age vectors that are being proposed for input to the Reference Set OMs for the 2018 hake OMP review are thus the "Updated predation BC" 1984-2017 averages in Panel (B) (dark blue lines) of Figure 2, although smoothing will first be applied to the vectors at younger ages for *M. paradoxus*. Alternatives to these vectors could be used for sensitivity tests pursued subsequent to the Reference Set finalization.

## Acknowledgements

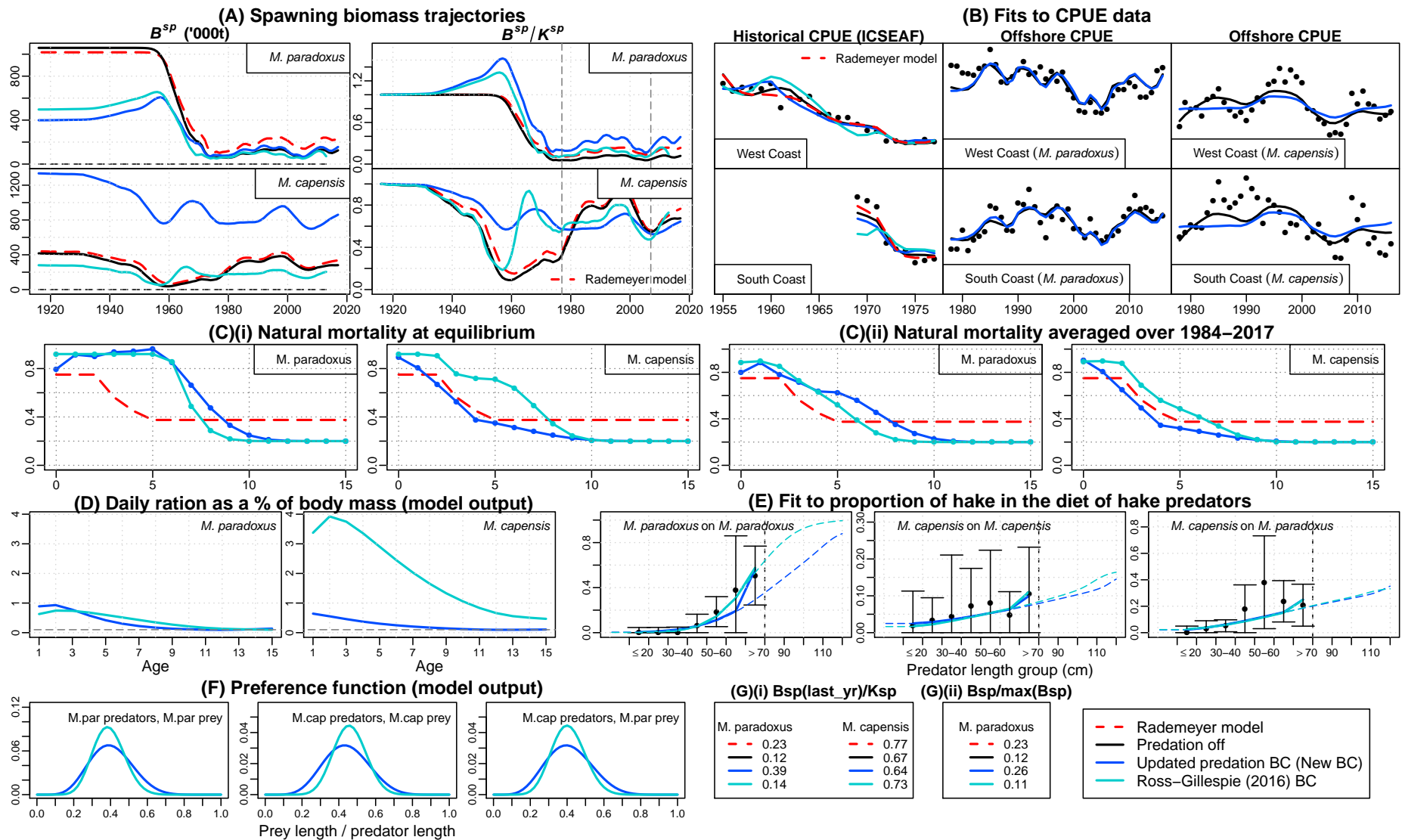
Computations were performed using facilities provided by the University of Cape Town's ICTS High Performance Computing team: <http://hpc.uct.ac.za>.

<sup>2</sup>The results reported for the Rademeyer model use a power of 0.35 for incorporating the catch-at-length data into the negative log-likelihood (see Ross-Gillespie and Butterworth 2018 for more details).

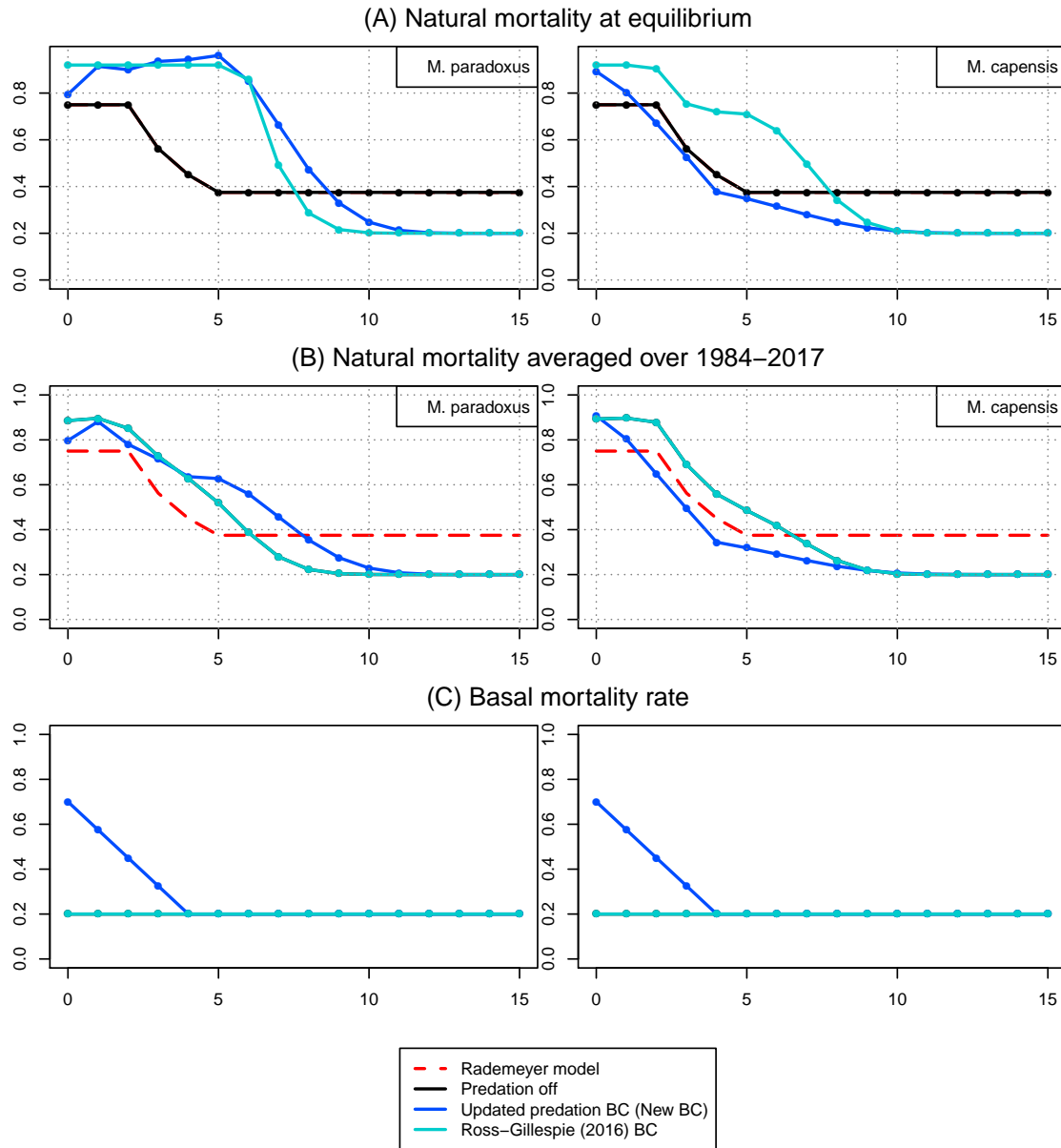
<sup>3</sup>Note that there are some differences between the "predation off" model and the standard Rademeyer model: the predation model is sex-aggregated, uses the Baranov approximation for the catch equation, uses a Beverton-Holt stock recruitment relationship and does not fit to age-length keys but instead fixes the growth curve parameters at the values estimated by the standard stock assessment model.

## References

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- Rademeyer, R.A. and Butterworth D.S. 2017. Specifications of the Sout African Hake 2017 Reference Case Assessment. International Stock Assessment Workshop Document MARAM/IWS/2017/Hake/P2rev. 1-40.
- Ross-Gillespie, A. 2016. Modelling cannibalism and inter-species predation for Cape hake species *Merluccius capensis* and *M. paradoxus*. PhD thesis. University of Cape Town. 1-195.
- Ross-Gillespie, A. and Butterworth, D.S. 2018. Investigating the suitability of the negative log-likelihood term for the catch-at-length data in the hake assessment model. DAFF document FISHERIES/2018/FEB/SWG-DEM/05. 1-11.



**Figure 1:** A selection of model outputs are shown for the Rademeyer model, a version of the hake predation model with predation "turned off", the new proposed Base Case for the updated predation model, and the original Ross-Gillespie (2016) model. The plots in section (A) show the spawning biomass trajectories in absolute and relative terms. Those in section (B) show the fits to the commercial CPUE data. The ones in sections (C) display the natural mortality-age-age vectors. Daily ration as a percentage of body mass (which is a model output) is shown in section (D), while the fits to the proportion of hake in the diet of hake predators are shown in section (E). The model-estimated preference functions are shown in section (F), while the depletion levels are listed in section (D) for (i)  $B_{last\_yr}^{SP}/K^{SP}$  and (ii)  $B_{last\_yr}^{SP}/\max(B^{SP})$ , where *last\_yr* is the last year considered in the model, namely 2017 for the Rademeyer and updated predation model, and 2013 for the Ross-Gillespie (2016) model.



**Figure 2:** The natural mortality-age-age vectors (which comprise a predation component and a basal natural mortality rate that is due to natural sources other than hake) are shown (A) for pristine pre-exploitation equilibrium and (B) averaged over 1984-2017. Panel (C) shows the basal natural mortality vector, which is time-invariant and fixed on input. The natural mortality-age-age vectors that are being proposed for input to the hake OMP models are the "Updated predation BC" 1984-2017 averages in Panel (B) (dark blue lines), although smoothing will first be applied to the vectors at younger ages for *M. paradoxus*.

## Appendix A

### Details of and results for the pre-BC runs and the sensitivity runs conducted

Further details of the changes made to the Ross-Gillespie (2016) model are provided Results for the “pre-BC” runs (i.e. the runs in the developmental phase leading up to the BC) and for the sensitivity runs investigating the effects of these changes are also provided here.

#### The $P_{lim}$ constraint

The Ross-Gillespie (2016) base case (BC) hake predation model was developed through an iterative process in which various alterations (such as introducing a parameter to allow *M. capensis* preference to shift from predominantly *M. capensis* prey to *M. paradoxus* prey as the *M. capensis* predators grow older) were made and sensitivities were tested. Following the above-mentioned updates, the predation model BC had to be re-developed. For the PhD work, the final step in this process involved the introduction of a  $P_{lim}$  parameter, which served to limit the predation natural mortality rate. The basis for including such a parameter was the concept of competition, since very large predator cohorts would be competing for available prey and consequently the predation natural mortality on that prey would have some natural upper boundary. The PhD approach was relatively simple, but prevented the natural mortality from reaching what was considered excessive levels (e.g. values well above  $1 \text{ yr}^{-1}$ ). After the above-mentioned updates were implemented, however, it was found that the natural mortality no longer reached such high levels and the  $P_{lim}$  parameter was thus discarded from the BC, although sensitivity tests were still run to test the impact of  $P_{lim}$  (see Sensitivity 2).

#### Basal natural mortality rate

However, a new feature in the natural mortality-at-age vectors became evident, namely that under equilibrium conditions that for *M. paradoxus* exhibited a dome-shape (see Figure A.1) suggesting that natural mortality was lower at the smallest ages. Bearing in mind that the hake predation model assumes that hake are the primary predators of smaller hake, this lower natural mortality at the smallest ages is consistent with the hake preference data, which indicate that the smallest *M. paradoxus* fish are desirable to at most age 1 and 2 hake predators, while the intermediate ages are preferred by a much larger range of hake predators. Given that a monotonic natural mortality vector seems more biologically realistic, it is most likely that the smallest hake are consumed predominantly by non-hake predators. To account for this, the basal natural mortality vector (which is a natural mortality rate accounting for all natural sources of natural mortality not caused by hake) was adjusted so that it was highest for age 0 hake and decreased linearly to age 4 hake (the Ross-Gillespie (2016) model assumed an age-independent natural mortality vector of  $0.2 \text{ yr}^{-1}$ ). Several variations of this basal natural mortality vector were tested, and it was found that a basal natural mortality rate of 0.7 at age 0 decreasing linearly to 0.2 at age 4 gave the nearest to a monotonic natural

mortality-at-age vector for *M. paradoxus* (see the Pre-BC runs).

## Constraining the estimates of the survey $q$ s

One of the recommendations of the panel for the 2016 International Stock Assessment Workshop was to undertake a "jittering" exercise, whereby the "converged" vector of estimable parameters is perturbed by a small percentage, and the minimisation is reinitiated in order to see whether minimisation ends with the same values as before. The aim of this exercise is to ensure as far as possible that the maximum likelihood estimate is a global rather than a local minimum. This exercise was undertaken for the predation model, and the results of the different jittered runs indicated that the pristine spawning biomass for *M. capensis* is not well determined, and furthermore is often unrealistically high. In order to address this in an objective manner, a constraint was added to the lower bound of the survey catchability constant,  $q$ , for the summer and autumn surveys so that these  $q$  values lie above 0.67 (bearing in mind that a high overall biomass estimated in the model would require a small  $q$  value to match the survey biomass estimates). The constraint was applied to the summer and autumn surveys and to the surveys conducted with the old gear only, as these surveys provide the longest time series. While the value of 0.67 is somewhat arbitrary, it seems nonetheless reasonable to assume that the swept-area estimates from the summer and autumn surveys must be reflecting at least 67% of the actual biomass. Sensitivity to the value of 0.67 was tested (see Sensitivity 1).

## Results

Pre-BC: Basal natural mortality-at-age vector

Figure A.1 shows a summary of the fits for four different basal natural mortality-age-age vectors. The run Pre-BC(a) (which assumes an age-independent basal natural mortality rate of  $0.2 \text{ yr}^{-1}$ ) uses the basal natural mortality vector that was assumed for the PhD model and yields a dome-shaped natural mortality vector for *M. paradoxus* at equilibrium. By increasing the basal natural mortality rate for younger ages, this dome-shape can be flattened. Note that the same basal natural mortality rate was assumed for both species. A basal natural mortality vector with a value of  $0.7 \text{ yr}^{-1}$  at age zero decreasing linearly to  $0.2 \text{ yr}^{-1}$  at age four yielded the nearest to a monotonic natural mortality vector for *M. paradoxus* (Pre-BC(d)).

Sensitivity 1: Alternative bounds on the survey  $q$ 's

The BC is a version of run Pre-BC(d) which enforces a lower bound of 0.67 on the summer and autumn survey  $q$  values. Two other lower boundaries were tested (0.50 and 0.80) and the results are shown in Figure A.2. The boundaries were implemented as hard boundaries (i.e. values below the threshold were not accepted). As the different thresholds did not yield noticeably different results (in particular with reference to the estimated natural mortality-age-age vectors), the choice of 0.67 was retained for the BC.

Sensitivity 2: Reintroducing  $P_{lim}$

Figure A.3 shows the results for three different values for  $P_{lim}$ . These plots show that as the limit is lowered, the behaviour of the predation model becomes more similar to that of the standard stock assessment model in that the predation release effect evident in the *M. paradoxus* population decreases and eventually disappears.

Since the natural mortality rates for the predation model are no longer excessively high as they were for the PhD model, there is no need for this constraint.

Table [A.1](#) summarises the estimates of depletion which are reported in the Figures. Depletion levels are shown for (i) current spawning biomass relative to pristine spawning biomass and (ii) current spawning biomass relative to the maximum spawning biomass. The latter has been shown for *M. paradoxus* only, as it is for this species only that the model-predicted biomass trajectory exceeds the pristine level owing to a predation release experienced by *M. paradoxus* when the *M. capensis* predator population was reduced by heavy fishing in the middle of the previous century (*M. capensis* values would be the same for column (i) and (ii)). Since there are no data available prior to 1950, it could be argued that the predation model *M. paradoxus* biomass trajectory from 1950 onwards can be compared directly to the standard stock assessment model trajectory from the same period (treating the maximum biomass estimate from the predation model as equivalent to the pristine biomass level in the standard model as there are no data to inform the biomass trend before this time), and that the depletion values reported in column (ii) are comparable to the standard stock assessment depletion values from column (i).

**Table A.1:** The depletion levels reported section (G) of Figure 1 of the main text and in Figures A.1 -A.3 of this Appendix are repeated here. Note that the depletion levels correspond to the last year in the model, which is 2013 for the PhD model and 2017 for all the others.

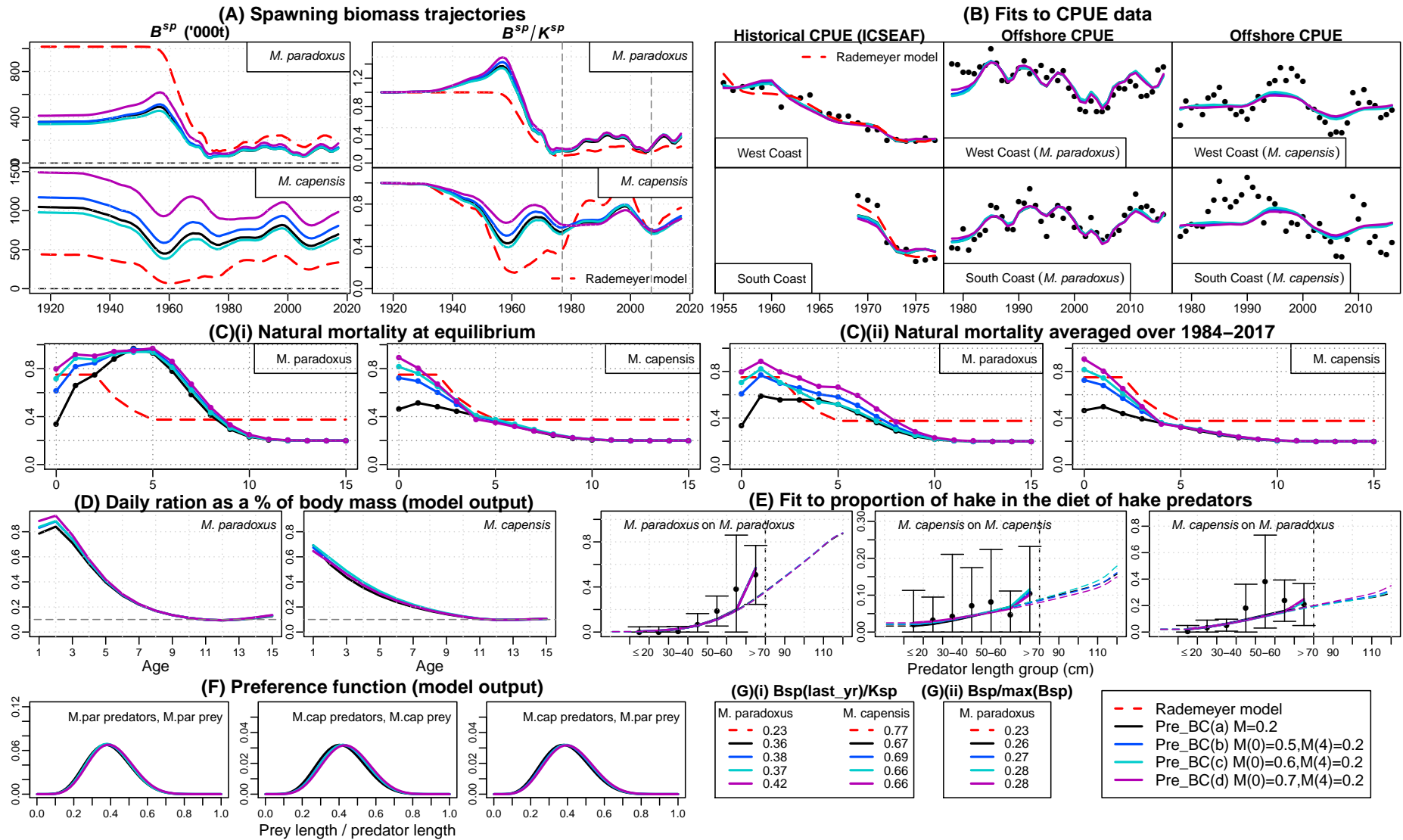
Run	(i) $B_{sp}/K_{sp}$		(ii) $B_{sp}/\max(B_{sp})$
	<i>M. Paradoxus</i>	<i>M. Capensis</i>	<i>M. Paradoxus</i>
Rademeyer model	0.23	0.77	0.23
Predation off	0.12	0.67	0.12
PhD model	0.14	0.73	0.11
New BC	0.39	0.64	0.26
Pre-BC (no $q$ boundary)			
(a) $M(0)=M(4)=0.2$	0.36	0.67	0.26
(b) $M(0)=0.5, M(4)=0.2$	0.38	0.69	0.27
(c) $M(0)=0.6, M(4)=0.2$	0.37	0.66	0.28
(d) $M(0)=0.7, M(4)=0.2$	0.42	0.66	0.28
Sensitivity 1: Alternative bounds on $q$			
(a) $q \geq 0.50$	0.40	0.65	0.27
New BC ( $q \geq 0.67$ )	0.39	0.64	0.26
(b) $q \geq 0.80$	0.37	0.64	0.24
Sensitivity 2: Reintroducing $P_{im}$			
New BC (No $P_{im}$ )	0.39	0.64	0.26
(a) $P_{im}=0.06$	0.38	0.65	0.26
(b) $P_{im}=0.05$	0.34	0.63	0.30
(c) $P_{im}=0.04$	0.22	0.61	0.22

Table A.2: Negative log-likelihood components for various runs.

Run	GLM CPUE	ICSEAF	Surv. abund	Comm. CAI	Survey CAI	NG penalty	Rec. resid.	DR	Preference	Prop hake	DR slope	Total
Predation off	-198.75	-39.70	-34.56	-1172.19	-946.05	0.35	9.57	0.00	0.00	0.00	0.00	-2380.81
Pre_BC(a) M=0.2	-184.92	-38.52	-30.72	-1166.60	-949.01	0.41	7.07	0.31	35.37	70.77	7.60	-2248.18
Pre_BC(b) M(0)=0.5,M(4)=0.2	-184.38	-38.20	-30.11	-1166.75	-950.93	0.42	7.17	0.26	35.30	73.07	8.34	-2245.78
Pre_BC(c) M(0)=0.6,M(4)=0.2	-184.63	-38.68	-30.44	-1166.92	-951.44	0.43	7.68	0.30	35.09	76.11	8.58	-2243.85
Pre_BC(d) M(0)=0.7,M(4)=0.2	-184.00	-37.66	-30.00	-1167.05	-952.53	0.41	6.42	0.23	35.35	74.93	8.84	-2245.05
New BC (q>0.67)	-183.50	-38.11	-29.86	-1167.23	-952.21	0.40	6.67	0.21	35.28	74.81	8.82	-2244.70
Sen1a. q>0.50	-184.16	-37.89	-29.99	-1166.44	-952.46	0.41	6.71	0.19	35.31	75.06	8.97	-2244.27
Sen1b. q>0.80	-183.22	-38.51	-29.71	-1167.24	-951.77	0.39	7.05	0.23	35.25	74.80	8.83	-2243.89
Sen 2a. Plim=0.06	-183.72	-38.02	-29.80	-1167.26	-952.22	0.40	6.78	0.25	35.44	74.80	8.82	-2244.50
Sen 2b. Plim=0.05	-185.03	-37.27	-29.53	-1166.60	-952.26	0.39	6.33	0.11	35.54	74.45	9.07	-2244.76
Sen 2c. Plim=0.04	-187.47	-37.23	-29.02	-1166.07	-952.81	0.42	6.98	0.03	35.62	74.86	8.76	-2245.93

Table A.3: Negative log-likelihood components relative to first line (grey highlight indicates a worse -lnL).

Run	GLM CPUE	ICSEAF	Surv. abund	Comm. CAI	Survey CAI	NG penalty	Rec. resid.	DR	Preference	Prop hake	DR slope	Total
Predation off	-198.75	-39.70	-34.56	-1172.19	-946.05	0.35	9.57	0.00	0.00	0.00	0.00	-2380.81
Pre_BC(a) M=0.2	13.83	1.17	3.84	5.59	-2.96	0.06	-2.50	0.31	35.37	70.77	7.60	132.63
Pre_BC(b) M(0)=0.5,M(4)=0.2	14.37	1.50	4.45	5.44	-4.88	0.07	-2.40	0.26	35.30	73.07	8.34	135.03
Pre_BC(c) M(0)=0.6,M(4)=0.2	14.12	1.02	4.12	5.27	-5.39	0.07	-1.89	0.30	35.09	76.11	8.58	136.96
Pre_BC(d) M(0)=0.7,M(4)=0.2	14.74	2.04	4.56	5.14	-6.48	0.05	-3.15	0.23	35.35	74.93	8.84	135.76
New BC (q>0.67)	15.25	1.58	4.70	4.95	-6.15	0.04	-2.90	0.21	35.28	74.81	8.82	136.11
Sen1a. q>0.50	14.58	1.81	4.57	5.75	-6.40	0.06	-2.86	0.19	35.31	75.06	8.97	136.54
Sen1b. q>0.80	15.52	1.19	4.85	4.95	-5.72	0.04	-2.53	0.23	35.25	74.80	8.83	136.92
Sen 2a. Plim=0.06	15.03	1.68	4.76	4.93	-6.17	0.04	-2.79	0.25	35.44	74.80	8.82	136.31
Sen 2b. Plim=0.05	13.71	2.43	5.03	5.59	-6.21	0.04	-3.24	0.11	35.54	74.45	9.07	136.05
Sen 2c. Plim=0.04	11.28	2.47	5.54	6.12	-6.76	0.07	-2.60	0.03	35.62	74.86	8.76	134.88



**Figure A.1:** The set of summary plots are shown for the **pre-BC** runs, where the basal natural mortality rate is varied. Fits are shown for (a) an age-independent natural mortality rate of  $0.2 \text{ yr}^{-1}$  (the BC assumption for the PhD model) and age-dependent natural mortality vectors that start at (b) 0.5, (c) 0.6 and (d) 0.7 at age 0 and decrease linearly to  $0.2 \text{ yr}^{-1}$  at age 4.

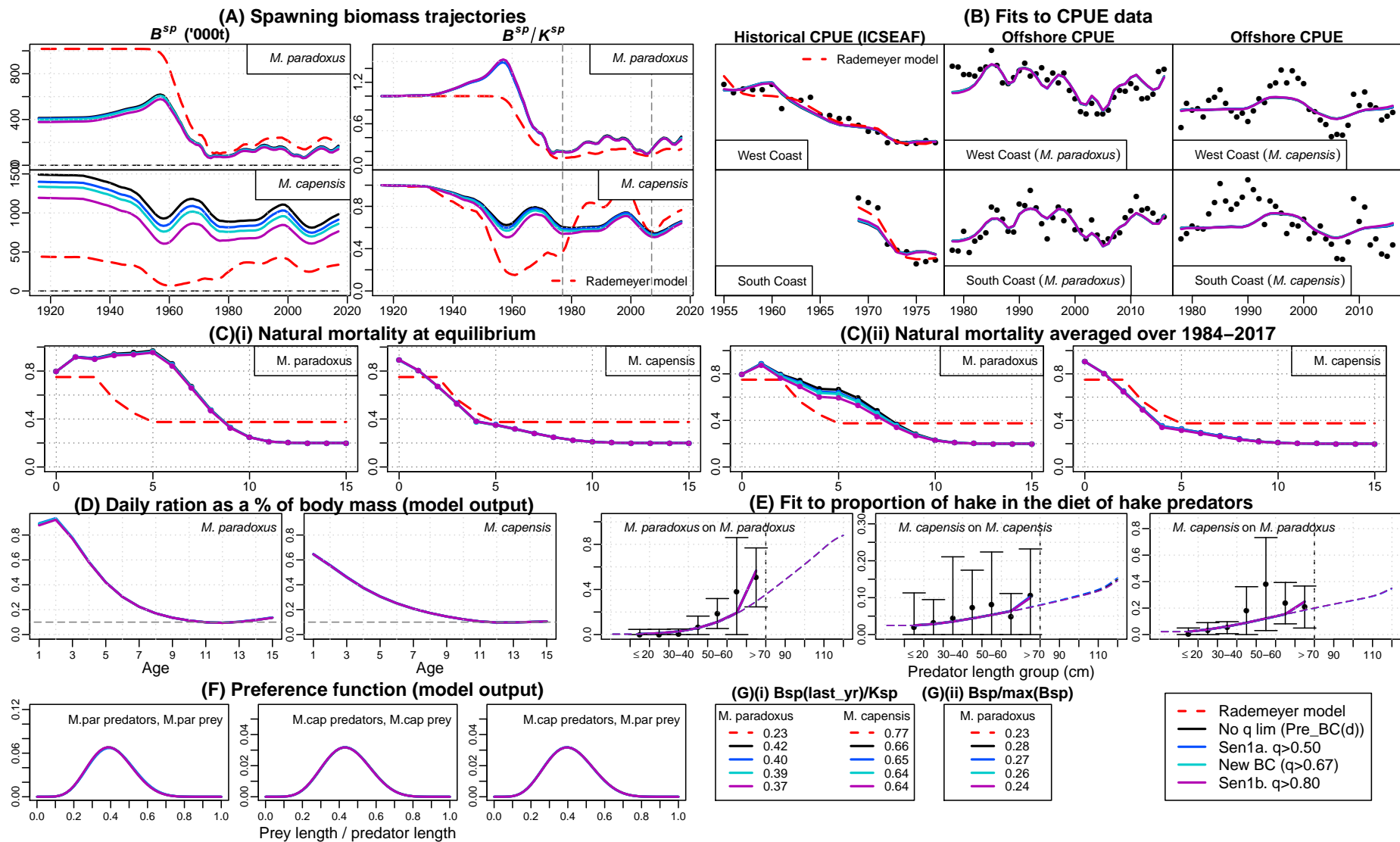
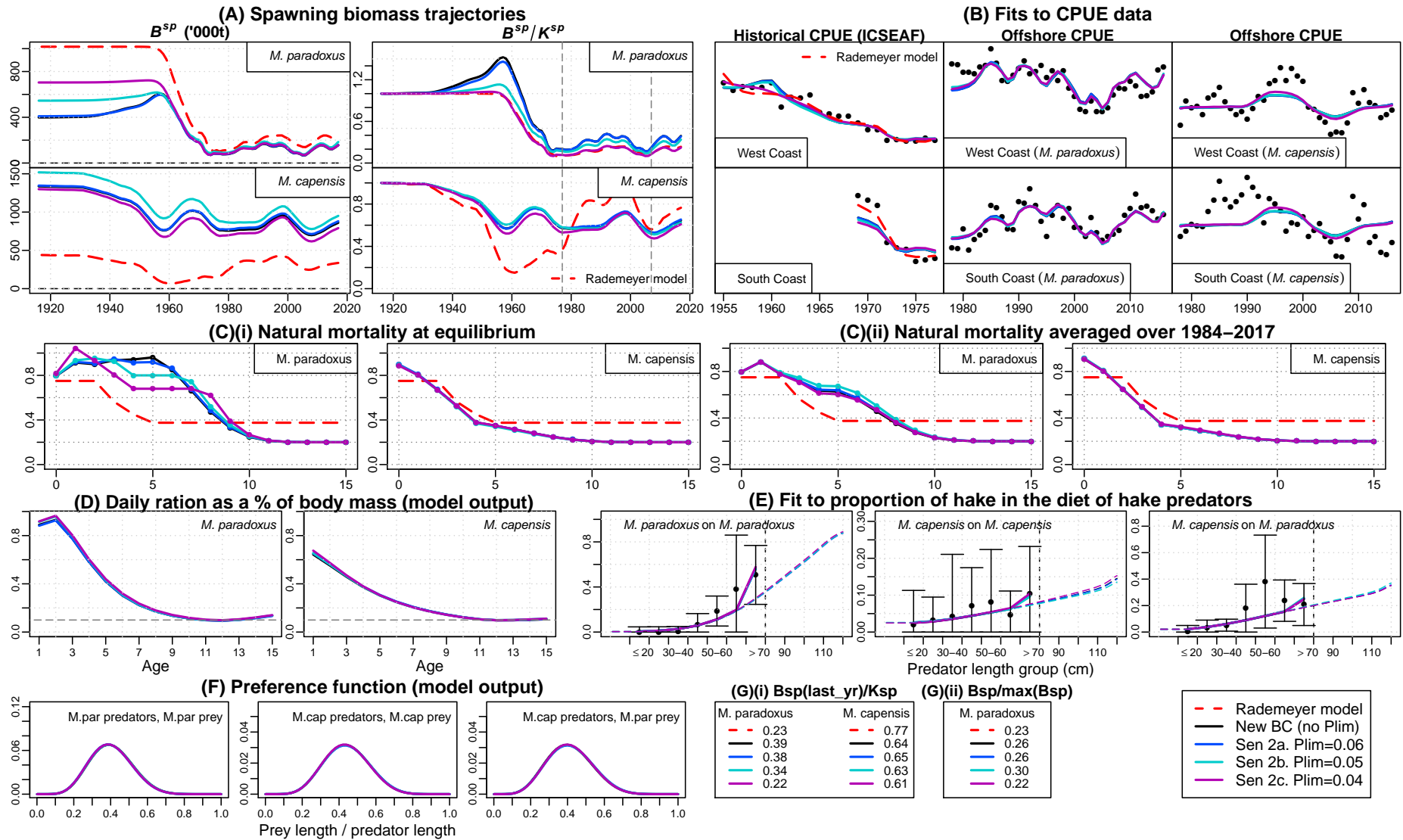


Figure A.2: The summary plots are shown for Sensitivity 1, where the lower boundary for summer and autumn survey  $q$  values is varied.



**Figure A.3:** The summary plots are shown for **Sensitivity 2**, where different values of the  $P_{lim}$  constraint are implemented to test the impact of this constraint. The predation model implements a monthly time-step, so a monthly  $P_{lim}$  constraint of 0.06 equates to an upper limit of  $0.06 \cdot 12 = 0.72$  on the annual predation natural mortality rate.