PROGRESS ON RECOMMENDATIONS FROM 2016 REVIEW PANEL REPORT REGARDING HAKE

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Panel Comments and Prioritised research recommendations

Responses to these comments are shown in *red italics.*

A. Hake

A.1 Assessment

A.1.1 (H). A "historical" analysis should be undertaken in which the results (time trajectories of biomass in absolute terms and relative to MSYL) are plotted for the reference sets of operating models proposed for the next update to the hake OMP as well as those on which OMP-2014 and earlier OMPs were based. Such "historical" analyses provide a way to understand the changes in estimated stock status due to changes to the assumptions on which the operating models are based, rather than changes due, for example, to estimates of incoming recruitment as further resource monitoring data become available.

Time constraints have precluded this methodological retrospective analysis, but a retrospective analysis for the current methodology (i.e. without allowance for changes in methodology over time) is provided in MARAM/IWS/2017/Hake/P3.

A.2 GeoPop

A.2.1 Provide brief comments on the papers presented applying the GeoPop approach to hake

MARAM/IWS/DEC16/HakeGeoPop/P1 and MARAM/IWS/DEC16/HakeGeoPop/P2 summarize the application of the GeoPop model to survey data for Namibia and South Africa. A key conclusion from MARAM/IWS/DEC16/HakeGeoPop/P2 is that there is one main nursery ground for *M. paradoxus* on the West Coast and a minor nursery ground on the South Coast, while MARAM/IWS/DEC16/HakeGeoPop/P1 identified three potential stocks of *M. capensis* off Namibia and South Africa. The results from fine-scale spatial models such as GeoPop can be used to provide parameter values and data for spatial stock assessment models for hake, ideally if they produce estimates of movement rates by age-class. However, the current version of GeoPop can provide only estimates of the relative abundance of age-classes spatially and not the rates of movement between regions that lead to that non-homogeneous spatial abundance. The results from GeoPop could be used and included in spatial modelling for hake in the short-term, as follows.

(a) Compare the spatial distributions by age from GeoPop with the raw survey data at the level of the spatial cells used in the spatial model (Rademeyer, 2013, 2014) to assess the extent to which GeoPop mimics the actual data.
(b) Compare the outputs from the spatial model with those from GeoPop to assess whether the spatial model is able to replicate the patterns in distribution even without formally including the GeoPop results into the likelihood function (or in the form of penalty terms) for the spatial model.
(c) Include the spatial distribution information from GeoPop into the likelihood function of the spatial model; it will then be necessary to downweight the spatial

(but not trend) information from the survey data when formulating the likelihood function.

The Panel endorses the future work outlined in MARAM/IWS/DEC16/HakeGeoPop/P2, particularly (a) modelling growth and fishery removals more realistically, and (b) formulating GeoPop so that it outputs the probability of fish of a given age moving from each of the spatial cells in the spatial model to each of the other spatial cells. The latter may require formulating GeoPop as a dynamic rather than an equilibrium model.

The analyses suggested in (a) to (c) above are reported in MARAM/IWS/2017/Hake/BG9. Regarding the first, it is reported for the comparison that "abundance trends with region are broadly similar (Figure 1), and proportions-at-length match closely except for a few regions at the lowest length for M. capensis". The overall conclusion is that "the addition of the GeoPop data leads to increasing M. capensis but decreasing M. paradoxus estimates of abundance over recent years; there is little impact on nearly all estimates of movement parameters".

A.3 Modelling predation

A.3.1 Review the two hake predation models presented, with a particular view towards identifying why (or suggesting approaches to determine why) they provide appreciably different estimates of current depletion (relative to pristine) for the *M. paradoxus* population.

The differences between the two hake predation models are difficult to evaluate because the models differ in a large number of respects. In particular, the models differ substantially in estimates of absolute biomass, especially for *M. paradoxus*, even when there is no predation. Thus, the comparison of the models should proceed by first selecting as many common assumptions as possible (minimally the no predation models should be based on the same reference case specifications). Only once the differences between the two predation models when there is no predation are understood (or eliminated), should attempts be made to compare "with predation" variants of those models. The comparison of the models "with predation" should start with the same or similar initial conditions (for 1916) because these can influence the subsequent dynamics substantially. Analyses in which the basal natural mortality rate for animals of age 15+ are set to same value for the two predation models may also assist these comparisons.

The first two steps in this process were identified to be (1) to set up a common data base with the most up-to-date data to ensure that the two models use the same data, and (2) to set up the full specifications for the Rademeyer model to ensure that the methodologies for the two predation models and the single-species model are as comparable as possible. The first step has been completed and the second is in its final stages (it involved quite a lengthy process of cross-checking code with the documented specifications). The next step (comparing the "predation-off" models) is yet to commence.

A.3.2.1 (H). The hake predation model in MARAM/IWS/DEC16/Hake_Pred/P2 includes an upper bound on predation mortality. The predicted diets should be constrained if predation mortality is constrained, but this is not the case at present. The "switch" behaviour evident for this model may be due to the complexity of the likelihood surface, and the Panel recommends that this be explored further using 'jittering'. Care should be taken that predation mortality does not hit its upper bound in the first year of the model (1916).

The predation model presented at the 2016 International Stock Assessment Workshop was based on the 2014 single-stock specifications and included data up to 2014 only. Following the workshop, the model was updated to incorporate the latest data up to 2016 and to match the latest single-stock specifications. These changes have resulted in a new base case needing to be developed, a process which is still underway. The 2016 panel recommendations are being considered in this process.

A.3.2.2 (H). The hake predation model in MARAM/IWS/DEC16/Hake_Pred/P1 should be extended to: (a) allow for time-varying amounts of hake in the diets of hake predators, (b) consider a constraint that the basal natural mortality rate decreases with age, and (c) consider iterating the calculation of natural mortality to avoid assuming that the total mortality rate for year *y* is the same as that for year *y*-1 when computing predation mortality (or consider shorter time-steps).

Not yet addressed – the work currently in progress needs to be completed first.

A.3.2.3 (H). The proportion of the consumption of hake by prey age-class for age 15+ hake in MARAM/IWS/DEC16/Hake_Pred/P2 is very high compared to that of age 14 hake. One reason for this is that there are more 15+ than 14 hake, but the full set of reasons needs to be explored.

This has been investigated, but will need to be re-evaluated once the new base case model has been developed to see whether this issue persists.

A.3.2.4 (H). Plot the time-trajectories of the proportions of hake in the diets of predators by hake species and age-class. This information may assist in understanding the reasons for the differences between the two models.

This has been investigated, but the plots will need to be redone for the new base case once it has been finalised.

A.3.2.5 (H). The preference function should be a function of length. However, this would complicate fitting the model to the diet data (currently predators and prey categorized by length) because it would be necessary to convert predator and prey numbers from age to length using age-length keys and this would lead to high variability in model predictions. MARAM/IWS/DEC16/Hake_Pred/P2 overcomes this problem by explicitly modelling populations by length as well as age. This problem could also be overcome by basing the diet data on predator ages rather than predator lengths so it only necessary to convert prey ages to prey lengths when constructing the likelihood function.

No progress on this as of yet.

A.3.2.6 (M). Consider a sensitivity test in which the basal natural mortality rates are higher at low and old ages than at intermediate ages. The support for such a sensitivity test could be explored by examining age-composition information for longline-caught fish, ideally those caught during the early years of the longline fishery when untrawlable grounds were first intensively fished.

Sensitivity to the basal mortality rate is being considered in the development of the new base case. The longline data have not been explored yet.

A.3.2.7 (M). The diet data for the west and south coast should be combined. This can be achieved by weighting the diet data by coast by a measure of the numerical abundance by age-class on the west and south coasts, e.g. from the results of the surveys. Alternatively, a spatial predation model could be developed.

This has not yet been attempted.

A.3.2.8 (M). The Panel reiterates the recommendations from the 2013 and 2014 Panels, which are important to implement.

(a) Scale hake prey-by-species information upwards to account for unidentified hake prey. This applies primarily to *M. capensis* predators because they consume both hake species. However, ignoring unidentified hake will underestimate the proportion of hake in the diet of *M. paradoxus.*

(b) Plan, and then implement, a review of the sampling strategy for diet data given the results of the current model as well as other needs for diet data. This recommendation pertains to DAFF.

These have yet to be undertaken.