Report of the OMMP Technical Webinar on incorporation of half-sibling pairs in the CCSBT OMs for the 2017 update of stock status

Introduction

The work plan for the 2017 reconditioning of the CCSBT Operating Models (OM) and assessment of stock status included the incorporation of a new data series: Half-Sibling Pairs (HSP) from close-kin mark recapture. This data series was presented and reviewed at OMMP8, however, there was insufficient time available for its incorporation into the OMs prior to that meeting. In anticipation of this, a web meeting of the OMMP technical group was scheduled for 20/21 July 2017 to review the fits of the HSP data and decide whether the new data series would be included in the 2017 reconditioning of the OMs.

The meeting was chaired by Dr Ana Parma and the webinar presentation facilitated by Dr Jim Ianelli.

Incorporation of Half-sibling pairs into OM

The working paper (Attachment 1) was circulated prior to the web meeting and presented by Dr Hillary. In summary, 140 well-defined HSPs and 4 clear full-sibling pairs (FSPs) have been identified from the juvenile capture years 2006 to 2015. The HSP data are included in the OM likelihood in a way that only information on the adult mortality and trend in adult abundance is used in the fit; a coefficient q_{hsp} is estimated so that the information on absolute adult abundance is not used. Initial runs of the OM with a steepness range of h = 0.6, 0.7 and 0.8 resulted in some combinations of h=0.6 crashing. A slightly modified grid of 0.62, 0.7 and 0.8 over-came this problem. The fits to all data series, including the HSP, were consistently good, with no obvious misfit. The HSP data are strongly consistent with the POPs and the general estimated adult dynamics: low adult ***total*** mortality for the dominant reproducing ages (10-25), slightly decreasing abundance prior to around 2010 with a slight increasing trend from 2010 to the present. The estimates of q_{hsp} are not so different from 1 as to raise any substantive questions. On the basis of these results the meeting decided that proceeding with inclusion of the HSP data in the current likelihood model (using the method outlined in CCSBT-OMMP/1706/04) is most appropriate at this time.
Examination of mitochondrial DNA haplotypes demonstrated that 65 of the 140 HSP shared common haplotypes, which strongly indicates they had the same mother, and this ratio is consistent with a ~ 50:50 female:male sex ratio. This and related analysis strongly suggest that male and female adult abundance, mortality and reproductive dynamics are similar and, therefore, there is no pressing case to account for sex-structured dynamics in the OM based in these results.

The crashed runs using the original steepness setting of 0.6 were associated with some combinations of the low M_{10} elements of the grid and appeared to be caused by catch equation “running out of fish”. It was agreed that this should be investigated in more detail and confirmed at ESC22. In addition, the code changes, to allow for these crashed models to no longer affect the grid sampling, would be finalised and may allow the steepness values of 0.6, 0.7 and 0.8 to be used in the reference set.

The group reviewed the log-likelihood plots for M_{10} (Fig 8, Attachment 1) and estimates of total Z for the adult component of the population covered by the HSP data (Fig 9, Attachment 1).

The apparently "uninformative" log-likelihood profile for the HSP as a function if M_{10} was discussed, given that the HSP data series should, in principle, be informative on total mortality of adults. It was noted that the estimation of the q_{hsp} parameter in the OMs is one factor that would contribute to this apparent lack of information in the HSP data series. Adult natural mortality is a scaling factor when it comes to adult abundance, so it is not just through its contribution to the signal in total mortality that M_{10} will play a role in the HSP data. Once the absolute abundance information is removed, via the q_{hsp}, parameter, that information is lost from the HSP data series. Second, the strong negative correlation between *M* and *F* (i.e. a relatively wider combination of these values can result in the very precise *Z* estimates, which is where the HSP signals are contained) is also likely to contribute to this result. It is evident form Figure 9 (Attachment 1) that following the quota reductions in the mid and late 2000s there is a general decline in Z over this period, followed by a stable trend in the most recent decade. In addition, the estimates are quite precise and indicate a relatively high adult survival (*ca*. 90% and higher for the main reproducing adult population). This shows that even without the HSP data the estimates of adult *Z* are precise and relatively low. These low values appear to be consistent with the HSP data (the fits are good). Dr Hillary noted that this was examined further by exploring cases where the adult *Z* was increased (or decreased) outside of the range, but held adult relative abundance the same. In these cases, it was clear that the HSP data quickly become informative. In particular, for increasing *Z*, the rate of decay in the predicted number of HSPs between ever more distant comparison cohorts begins to rapidly increase (as one would expect). The only way to reproduce the observed HSP data in this case would be to have a decreasing adult abundance from 2003 to 2012 (thus keeping the HSP probability from decreasing too quickly and not fitting the data well). The POPs clearly do not agree with this trend, so it is, apparently, not a viable alternative prediction of the HSP data. The general explanation for the flat log-likelihood for HSP in Figure 8 seems to be: (a) the HSP data are very consistent with existing estimates of total mortality and adult abundance trends and, therefore (b) that **within the current range of M_{10} values** there is little additional information on this parameter in these data (though not total mortality).

Given these results and the review of the HSP fits and diagnostics, the OMMP agreed that the HSP data series should be incorporated in the reference set for the 2017 reconditioning. It was also agreed that an additional sensitivity tests should be included:

i) Setting q_{hsp} =1.

The Chair thanked Dr Hillary and colleagues for their inter-sessional work and the clear, concise working paper.

Meeting closed at 8:48am on 21 July 2017 (Canberra time).

Summary of initial incorporation of the Half-Sibling Pair (HSP) data in the CCSBT Operating Model

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This document briefly summarises the fits to the various data sets with the HSP data included in the CCSBT Operating Model, the estimates of total reproductive output, and what the mitochondrial DNA analyses of the HSPs revealed in terms of sex ratio of parents of HSP and sex-specific population demographics.

Final HSP data set

The final HSP data set is comprised of 140 well-defined HSPs and 4 clear full-sibling pairs (FSPs), covering the juvenile capture years 2006 to 2015 (assumed to be the cohorts 2003-2012 i.e. all juveniles are 3 years old for the purposes of the results presented here). Table 1 summarises the number of comparisons by juvenile capture year, and Table 2 the number of detected HSPs. The false-negative discard rate resulting from the critical value of the PLOD value (above which there will be no false-positive pairs) was 0.106, so the probability of a true HSP appearing above the critical PLOD value is 1-0.106 = 0.894 (see the π_η parameter in CCSBT-OMMP/1706/4).

The number of HSPs per comparison is highest when comparing fish from the same cohorts, as one would expect, given no adult mortality has occurred between cohorts and if there are batch-spawned egg survival effects ("lucky litters"). As the number of years between samples increases, we see that the number of HSPs decrease (and faster than the decrease in number of comparison would predict) as we see the effect of adult mortality begin to dominate other factors (like changing spawning abundance and adults increasing their relative reproductive output as they age). Empirically, the HSP data seem consistent with low adult mortality rates, a relatively stable adult population from 2003 to 2012, and paced increases in relative reproductive output as adult's age from being first spawners to fully-fledged adults.

Table 1: Number of comparisons between juveniles in the 10 capture years.

	2006	**2007**	**2008**	**2009**	**2010**	**2011**	**2012**	**2013**	**2014**	**2015**
2006	800745	1633140	1623012	1653396	1614150	1169784	1041918	1096356	1087494	1158390
2007	-	831405	1653780	1684740	1644750	1191960	1061670	1117140	1108110	1180350
2008	-	-	821121	1674292	1634550	1184568	1055086	1110212	1101238	1173030
2009	-	-	-	852165	1665150	1206744	1074838	1130996	1121854	1194990
2010	-	-	-	-	812175	1178100	1049325	1104150	1095225	1166625
2011	-	-	-	-	-	426426	760452	800184	793716	845460
2012	-	-	-	-	-	-	338253	712718	706957	753045
2013	-	-	-	-	-	-	-	374545	743894	792390
2014	-	-	-	-	-	-	-	-	368511	785985
2015	-	-	-	-	-	-	-	-	-	418155

Table 2: Number of HSPs above the false-positive threshold PLOD value between juveniles captured in the years in bold.

	2006	**2007**	**2008**	**2009**	**2010**	**2011**	**2012**	**2013**	**2014**	**2015**
2006	3	4	4	4	0	2	1	0	1	2
2007	-	6	3	6	2	2	2	0	0	2
2008	-	-	5	3	3	3	0	5	1	1
2009	-	-	-	8	6	1	3	7	4	0
2010	-	-	-	-	3	5	3	3	1	3
2011	-	-	-	-	-	6	1	1	2	3
2012	-	-	-	-	-	-	2	2	0	0
2013	-	-	-	-	-	-	-	2	1	2
2014	-	-	-	-	-	-	-	-	4	3
2015	-	-	-	-	-	-	-	-	-	3

Fits to the various data sets upon including the HSP data

The likelihood function for the HSP data is defined in CCSBT-OMMP/1709/4. A scaling factor (q_{hsp}) is estimated within the OM so that *only* the adult total mortality and general turn-over rate information within the HSPs, *not* their absolute abundance information, is used (see paper in CCSBT-OMMP/1709/4 for the reasons behind this decision). The POPs are used primarily for their information on absolute abundance and the age structure of the reproducing adult population; the HSPs for total mortality and abundance trend. Additionally, we do not include intra-cohort comparisons in the OM runs (to avoid the potential biasing of the information in the data due to 'lucky litter' effects).

Difficulties arose when running the grid with the default set of three steepness values: h = 0.6, 0.7 and 0.8 (some resulted in crashes). So, to obtain a workable grid sample for the web meeting: h = 0.62, 0.7 and 0.8 were used and no runs crashed.

Figures 1, 2 and 3 shows the OM fits to the three main non-CKMR data sets: longline CPUE, the aerial survey, and the tagging data, respectively. All three are fine, and are basically identical to those obtained in the initial reconditioning presented in paper CCSBT-OMMP/1706/4 at the OMMP meeting in Seattle.

Figure 1: Longline CPUE fits (magenta dots are observed data, median and 95%iles are blue lines)

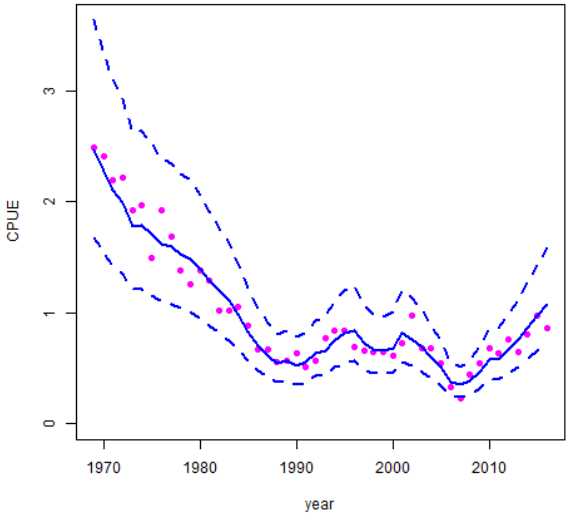


Figure 2: Aerial survey fits (magenta dots are observed data, median and 95%iles are blue lines)

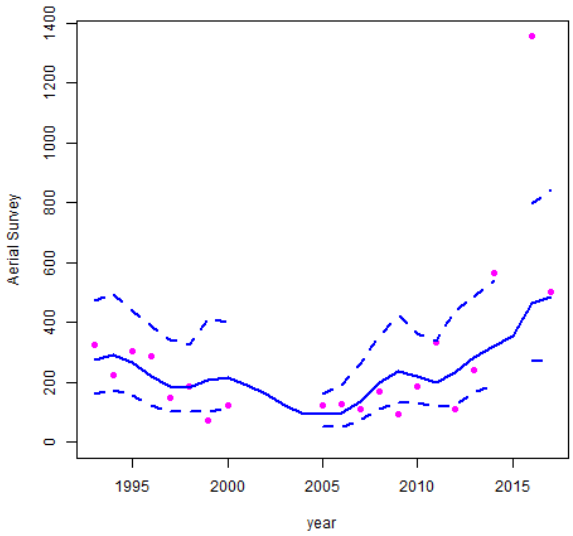
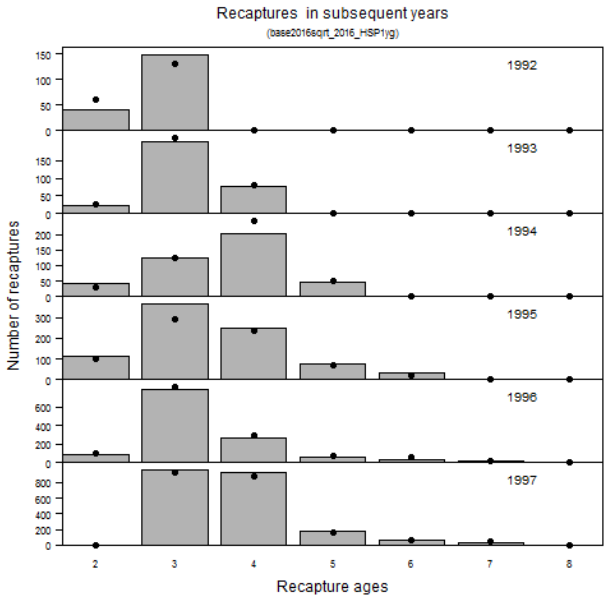


Figure 3: Pooled tagging data fits (grouped by release cohort and recapture age)



Figures 4 and 5 show the POP fitting summary, with the POPs grouped at the juvenile cohort, and adult capture age level, respectively. Both aggregated data sets are fitted well, with the observed data always sitting within the 95% predictive limits, and with no obvious trends in the fits.

Figure 4: CKMR POP fits at the juvenile cohort aggregation level

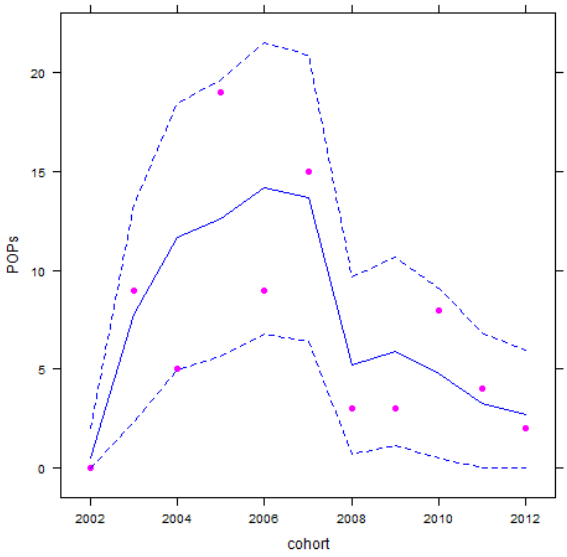
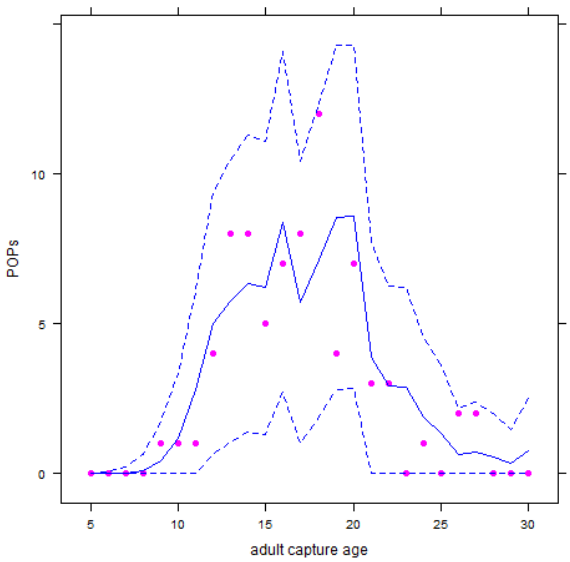


Figure 5: CKMR POP fits at the adult capture age aggregation level



The HSP data are structured at the level of juvenile cohort (with the first cohort being the eldest fish in the pair if they are not from the same cohort). At the full level of disaggregation, they are similar to the POPs, relatively sparse. Figure 6 shows the fits to the data at the full disaggregation level. The data are fitted fairly well at this full disaggregation level, with only two of the points appearing slightly outside the 95% predictive interval (for the best fitting grid run). Figure 7 summarises the fits with the data aggregated to the initial reference cohort level. The fits here are good, with no points appearing outside the predictive interval and no obvious trend in the fits either. The decrease in HSPs

is (like Figure 4) because the later reference cohorts are not compared to as many others as for the earlier ones – it does *not* suggest that the data believe the adult population to be decreasing.

Figure 6: CKMR HSP fits at the full disaggregation level (the panel denotes the reference (oldest) cohort and the x-axis the following (younger) cohorts it is compared against).

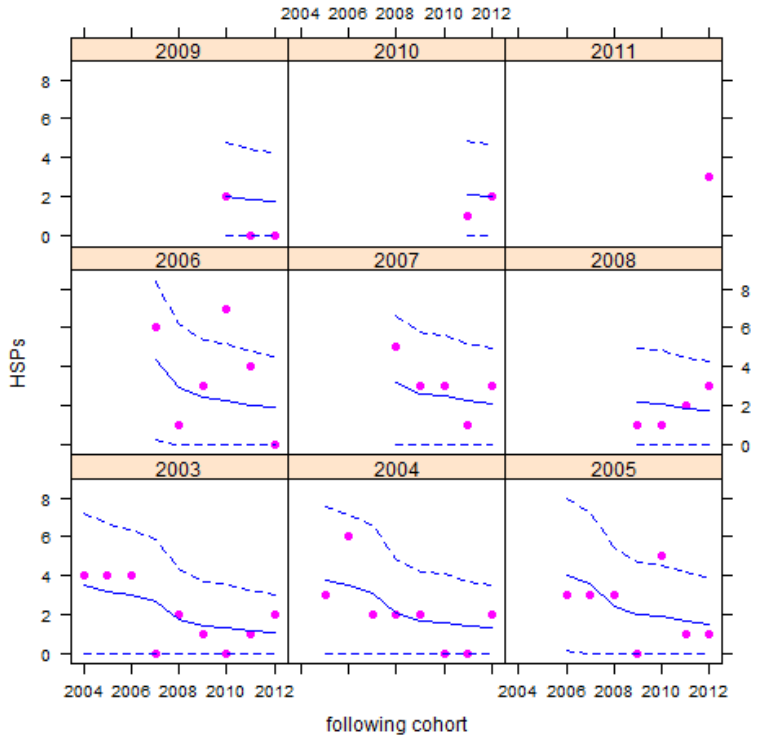
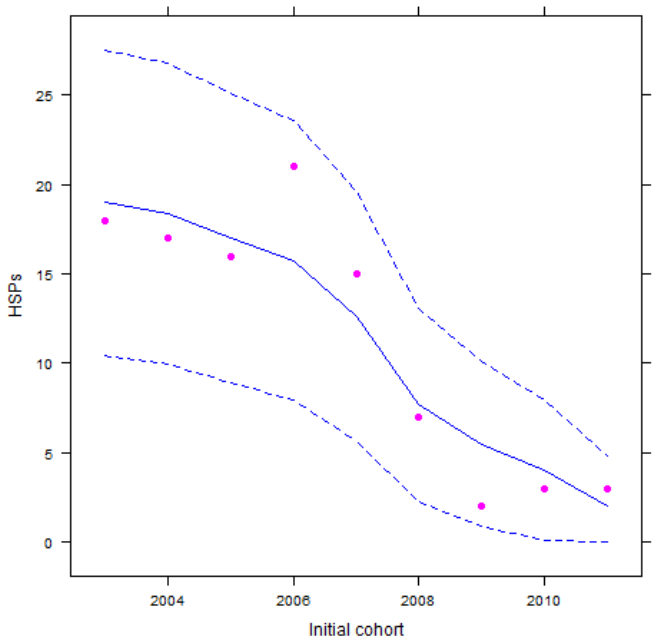


Figure 7: CKMR HSP fits aggregated at the reference (oldest) cohort level, with the y-axis the number if HSPs found across all the following (younger) cohorts.



To summarise the fits to the data, relative to the initial conditioning without the HSP data, they look very much the same (including the age and length composition plots omitted for brevity) with the HSP data included. These data are strongly consistent with the POPs and the general estimated adult dynamics: low adult **total** mortality for the dominant reproducing ages (10-25), slightly decreasing abundance prior to around 2010 with a slight increasing trend from 2010 to the present. The estimates of q_{hsp} were almost all less than 1 (between 0.8 and 0.9 i.e. there were slightly *less* HSPs than we might have expected if we make the strong assumption about how absolute HSPs relate to adult abundance). We outlined this can have many interpretations (CCSBT-OMMP/1706/4) and not all relate to actual adult dynamics. At this stage, the estimates of q_{hsp} are really not so different to 1 as to raise any serious questions, so we feel happy enough in proceeding with the current likelihood model (that doesn't use their absolute abundance information).

Figure 8 shows a likelihood profile plot for the M_{10} parameter, across the various data sets. Given the HSP data contain information adult abundance (absolute and trend), RRO-at-age and adult total mortality, it is surprising to see the profile so flat across the grid range of M_{10} values. There is a weak preference for the higher of the two M_{10} values, relative to the lowest value of 0.05. One factor that will almost certainly contribute to this apparent lack of information across the current grid range for M_{10} is the active estimation of the $\underline{q_{hsp}}$ parameter in the OMs. Adult natural mortality is a clear scaling factor when it comes to adult abundance so it is not just through its contribution to the signal in total mortality that M_{10} will play a role in the HSP data. Once you take the absolute abundance information out of the problem, via the q_{hsp}, parameter, that information is lost.

The second factor playing a role is strong negative correlation between M and F at these ages (i.e. a relatively wider combination of these values can result in the very precise Z estimates, which is where the HSP signals are contained). Figure 9 shows the weighted (via adult abundance-at-age) mean Z over the years covered by the HSP data. Following the quota reductions in the mid and late 2000s we see a general decline in Z over this period, followed by a stable trend in the most recent decade. In addition, the estimates are quite precise and indicate a relatively high adult survival (*ca*. 90% and higher for the main reproducing adult population). The main point is this: even without the HSP data the estimates of adult Z are precise and relatively low. They also appear to be very consistent with the actual HSP data (the fits are good). To explore this further we examined a cases where the adult Z was increased (or decreased) outside of the range, but held adult relative abundance the same. In these cases, it was clear that the HSP data quickly become informative. Specifically, for increasing Z, the rate of decay in the predicted number of HSPs between ever more distant comparison cohorts beings to rapidly increase (as one would expect). The only way to reproduce the observed HSP data in this case would be to have a decreasing adult abundance from 2003 to 2012 (thus keeping the HSP probability from decreasing too quickly and not predicting the data well). The POPs clearly do not agree with this trend, so it is not an apparently viable alternative prediction of the HSP data. The general explanation seems to be: (a) the HSP data are very consistent with existing estimates of total mortality and adult abundance trends and, therefore (b) that **within the current range of M_{10} values** there is little additional information on this parameter in these data (though not total mortality).

Figure 8: Log-likelihood profile plots for the various OM data sets for the M_{10} grid parameter.

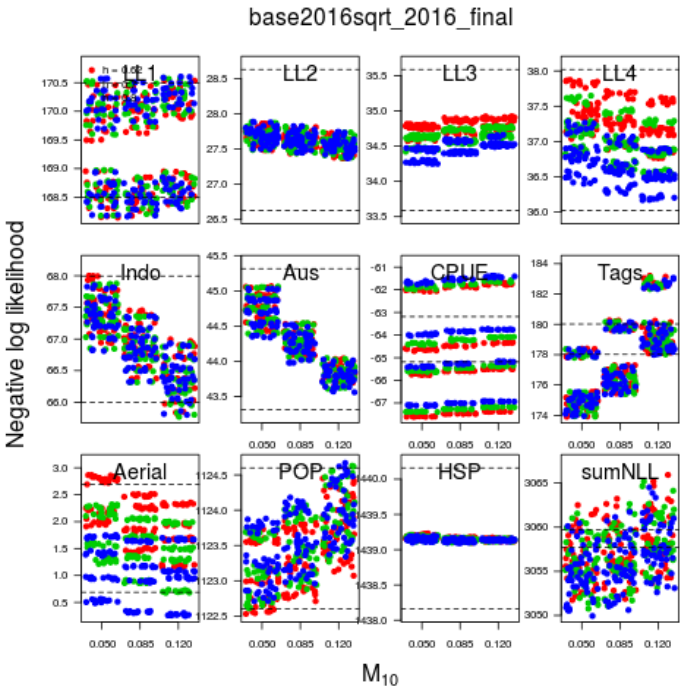
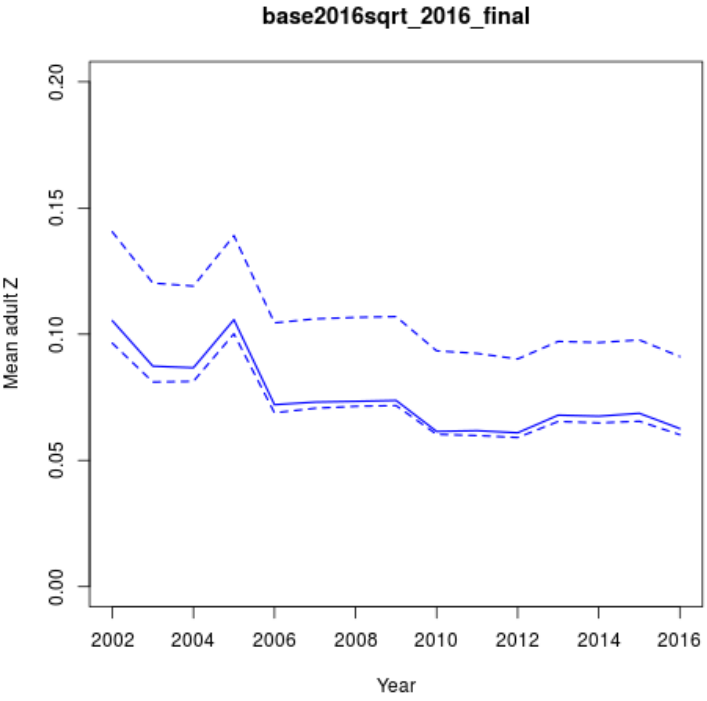


Figure 9: Mean adult total mortality (*Z*), weighted by adult abundance-at-age, across the full grid for the years covered in the HSP data.



What do the mitochondrial DNA (mtDNA) say?

In the OM we do not treat males and females separately. To be clear, we don't assume anything other than a fixed sex ratio either (not an implicit 50/50 ratio) and, if relative reproductive output-at-age/length varies by sex, we are detecting (via the CKMR data) a sexually "averaged" effect. The male and female mix of POPs (accounting for sampling differences in numbers of males and females) strongly suggests that a 50/50 sex ratio is about right. With the HSP data we can also explore if this is true and a little more. For an HSP, and with high diversity among the haplotypes (i.e. there are a lot of them so the chances of sharing one by chance are small), generally speaking if an HSP shares a haplotype it will be a maternal HSP, and a paternal HSP if it does not. In a general overview sense, with 140 actual HSPs and with an informative and diverse array of haplotypes (which we have for SBT), if the male-female abundance ratio is about 50/50 we'd expect to see around 65-75 HSPs share a haplotype. As it turned out 65 of the HSPs had a common haplotype (and are, almost certainly, maternal HSPs) which strongly supports the 50/50 adult abundance sex ratio hypothesis.

Furthermore, by looking at the mean number of years between HSPs that do and do not share a haplotype (i.e. comparing maternal and paternal HSPs), we can look for indications of differential turn-over rates between the sexes. The HSP data (treated as we are in a relative sense) combine information on adult population trend, total mortality, and some information on the rate at which relative reproductive output increases as fish get larger/older. All together this is indicative of the average turn-over rate (renewal of the adult population by maturing animals, total mortality, RRO-at-age). With the mtDNA, we can do a simple empirical analysis to see if these are clearly different just by looking at the mean "distance" in terms of time between birth years among HSPs. Among inter-cohort HSPs, for likely maternal HSPs this number is 3.1 years and for likely paternal HSPs it is 3.05 – given the number of samples (around 50 each) this strongly suggests that *either* the three major population processes this give rise to these data are very similar over the time frame covered, *or* they are different but in just such a way as to result in the same mean time between birth years. Purely from an Occam's razor perspective, this seems to strongly indicate that male and female adult abundance, mortality and reproductive dynamics are very similar. This is clearly very encouraging for the OM given we lack the data to fully sexually disaggregate the whole life-history of each of the sexes.

Summary

In summary, 140 well-defined HSPs and 4 clear full-sibling pairs (FSPs) have been identified from the juvenile capture years 2006 to 2015. The HSP data is included in the OM likelihood in a way that only the adult mortality and trend in adult abundance information is used in the fit; the information on absolute adult abundance is not used. Initial runs of the OM with a steepness range of h = 0.6, 0.7 and 0.8 resulted in some combinations of h=0.6 crashing. A slightly modified grid of 0.62, 0.7 and 0.8 over-came this problem. The fits to all data series, including the HSP, were consistently good, with no obvious mis-fit or trends in fit. The HSP data are strongly consistent with the POPs and the general estimated adult dynamics: low adult **total** mortality for the dominant reproducing ages (10-25), slightly decreasing abundance prior to around 2010 with a slight increasing trend from 2010 to the present. The estimates of q_{hsp} are not so different from one to raise any substantive questions. We consider proceeding with inclusion of the HSP data in the current likelihood model (using the method described above that uses HSP data for information on total adult mortality and abundance trend (not absolute abundance)) is most appropriate at this time. Examination of mitochondrial DNA haplotypes demonstrated that 65 of the 140 HSP shared common haplotypes, which strongly indicates they had the same mother, and this ratio is consistent with a ~ 50:50 female:male sext ratio. This and related analysis strongly suggest that male and female adult abundance, mortality and reproductive dynamics are similar and, therefore, there is no pressing case to account for sex-structured dynamics in the OM based in these results.