

## Prior incoherence within a Bayesian assessment of the Southern Hemisphere humpback whale breeding stock B population.

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The descriptions of the model used as well as the associated population dynamics are given in the Appendix.

### Outline of problem encountered

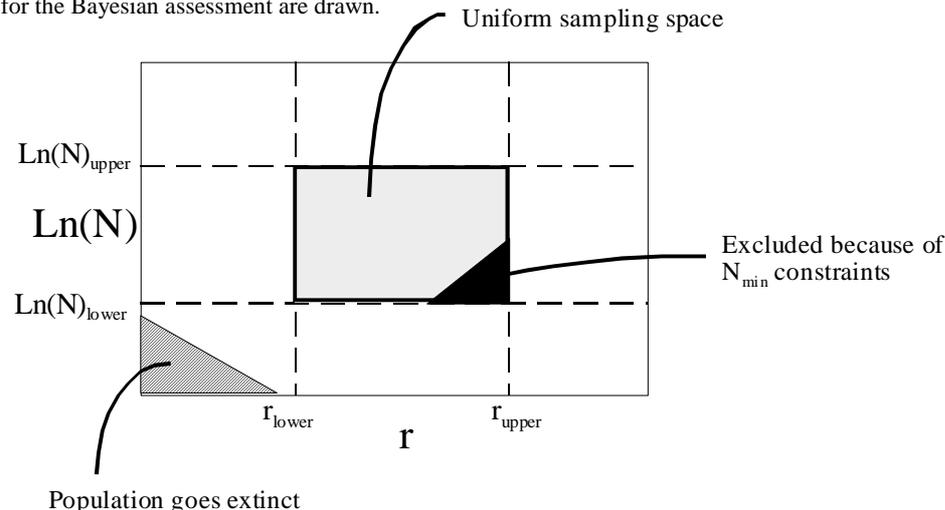
In very simple terms, a Bayesian analysis involves drawing estimatable parameter values from some prior distribution, computing population dynamics and assigning a likelihood value to each combination based on comparisons to data containing information on population size and/or trend. A posterior distribution may then be constructed and conclusions drawn about the parameter estimates. In Model Ia (see Appendix)  $r^{B1}$ ,  $r^{B2}$ ,  $\ln(\tilde{N}_{targ}^{B1})$ ,  $\ln(\tilde{N}_{targ}^{B2})$  are the parameter values drawn from priors for the intrinsic growth rate and the log of the recent abundance for the two populations under consideration.

At the 2010 IWC conference in Morocco, values for the minimum number of haplotypes were put forward to inform  $N_{min}$  (the lowest size the population could have reached, taken to be 4 times the minimum number of haplotypes (Jackson *et al.* 2006)) and were accepted as a reference case (IWC (2010)). In the assessment procedure, any parameter values ( $r$  and  $\ln(\tilde{N}_{targ})$ ) that lead to population estimates going below  $N_{min}$  are penalised by adding 1000 to the negative log likelihood for each year the population is below  $N_{min}$  (i.e. the longer the population remains below  $N_{min}$ , the greater the penalty will be). For the B2 population, the introduction of these new  $N_{min}$  values results in some parameter values being rejected that may otherwise provide good fits to the trend and abundance data (in particular certain combinations of low  $\ln(\tilde{N}_{targ}^{B2})$  and high  $r^{B2}$ ). As such, the final assessment results yield a lower  $r^{B2}$  and, as a direct consequence of the favoured high  $\ln(\tilde{N}_{targ}^{B2})$ , a higher  $K^{B2}$  than expected (see Tables 1 and 2, and Figures 2a-b and 3a-b).

Essentially, there are now two independent pieces of information informing the realised prior distributions of the  $r^{B2}$  and  $\ln(\tilde{N}_{targ}^{B2})$  parameters (namely the  $N_{min}$  constraints in addition to the standard explicit prior distribution). This results in incoherent joint prior distributions and can turn an uninformative prior distribution into one that is in fact informative (Brandon *et al.* 2007).

A coherent joint prior thus needs to be constructed and an approach to do this is outlined in Brandon *et al.* (2007): The essence of the problem is that by introducing a (in this case higher)  $N_{min}$  constraint, a range of  $r^{B2}$  and  $\ln(\tilde{N}_{targ}^{B2})$  values are excluded, as they do not respect this biological realism. Therefore the parameter space that is sampled is effectively no longer uniform, as a section has been excluded. This is illustrated in Figure 1 below.

Figure 1: Illustration of the parameter space available for sampling. The outside box contains a large range of possible ( $r$ ,  $\ln(N)$ ) combinations, while the inner box encloses a reduced range that represents what are considered realistic parameter values, from which the ( $r$ ,  $\ln(N)$ ) values for the Bayesian assessment are drawn.



An approach for dealing with an  $(r^{B2}, \ln(\tilde{N}_{targ}^{B2}))$  parameter combination that does not adhere to the  $N_{min}$  constraint is to re-sample the parameter values until a biologically feasible combination has been found. Various re-sampling schemes are given in Brandon *et al.* (2007). The paper emphasises that no one method has been conclusively deemed better than the others and all schemes produce slightly different results. In the case of a data-poor assessment, these differences can be quite substantial. Thus sensitivity to re-sampling scheme needs to be investigated. It is proposed to explore the following three re-sampling methods for the breeding stock B case:

If a biologically infeasible solution is obtained for a particular parameter combination  $(r^{B1}, r^{B2}, \ln(\tilde{N}_{targ}^{B1}), \ln(\tilde{N}_{targ}^{B2}))$ , then  $r^{B1}$  and  $\ln(\tilde{N}_{targ}^{B1})$  are kept and one of the following procedures is followed:

- (i) Re-sample both  $r^{B2}$  and  $\ln(\tilde{N}_{targ}^{B2})$ .
- (ii) Keep  $r^{B2}$  and re-sample  $\ln(\tilde{N}_{targ}^{B2})$ .
- (iii) Keep  $\ln(\tilde{N}_{targ}^{B2})$  and re-sample  $r^{B2}$ .

The proposed approach, as well as its implementation and related issues around the problem encountered are to be discussed at the International Fisheries Stock Assessment Review Workshop, December 2010.

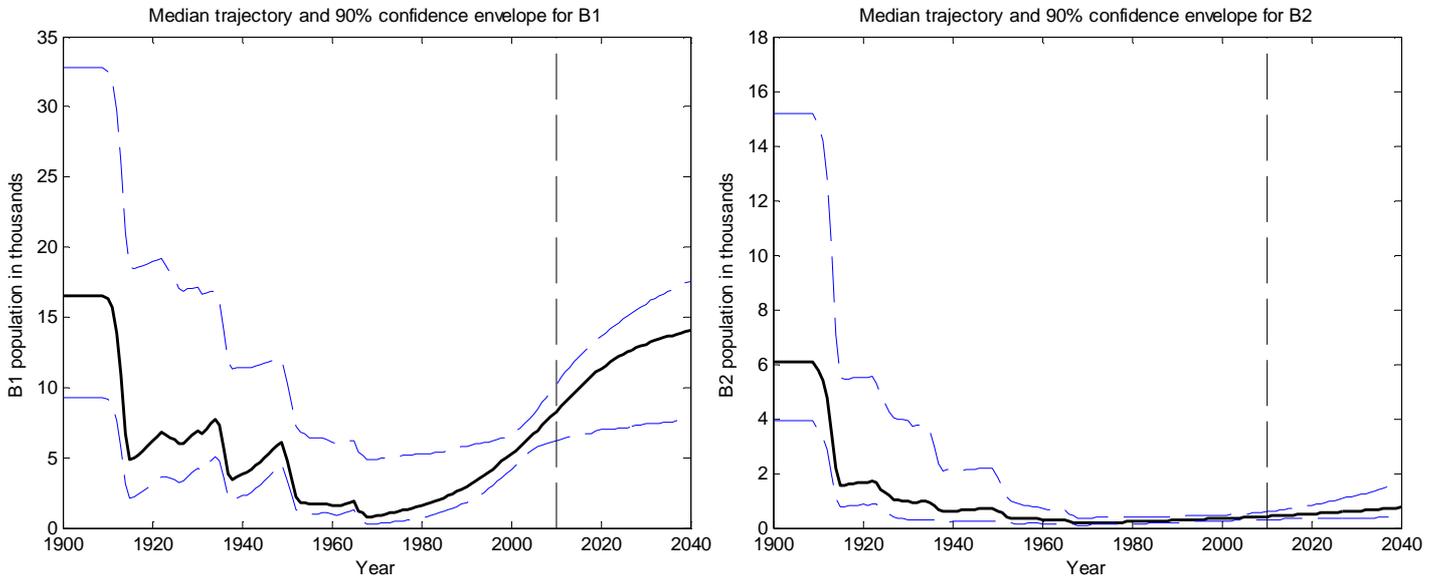
## References

- Brandon, J.R., Breiwick, J.M., Punt, A.E and Wade, P. 2007. Constructing a coherent joint prior while respecting biological realism: application to marine mammal stock assessments. *ICES J. Mar. Sci.* (2007) 64(6): 1085-1100.
- IWC. 2010. Report of the Scientific Committee of the International Whaling Commission, Annex H.
- Jackson, J., Zerbini, A., Clapham, P.J., Garrigue, C., Hauser, N., Poole, M., and Baker, C.S. 2006. A Bayesian assessment of humpback whales on breeding stocks of Eastern Australia and Oceania (IWC Stocks E, E1, E2 and F). Paper SC/A06/HW52 presented to the IWC Workshop on the Comprehensive Assessment of Southern Hemisphere humpback whales, Hobart, Australia, April 2006. 9pp. [Available from the office of this Journal]

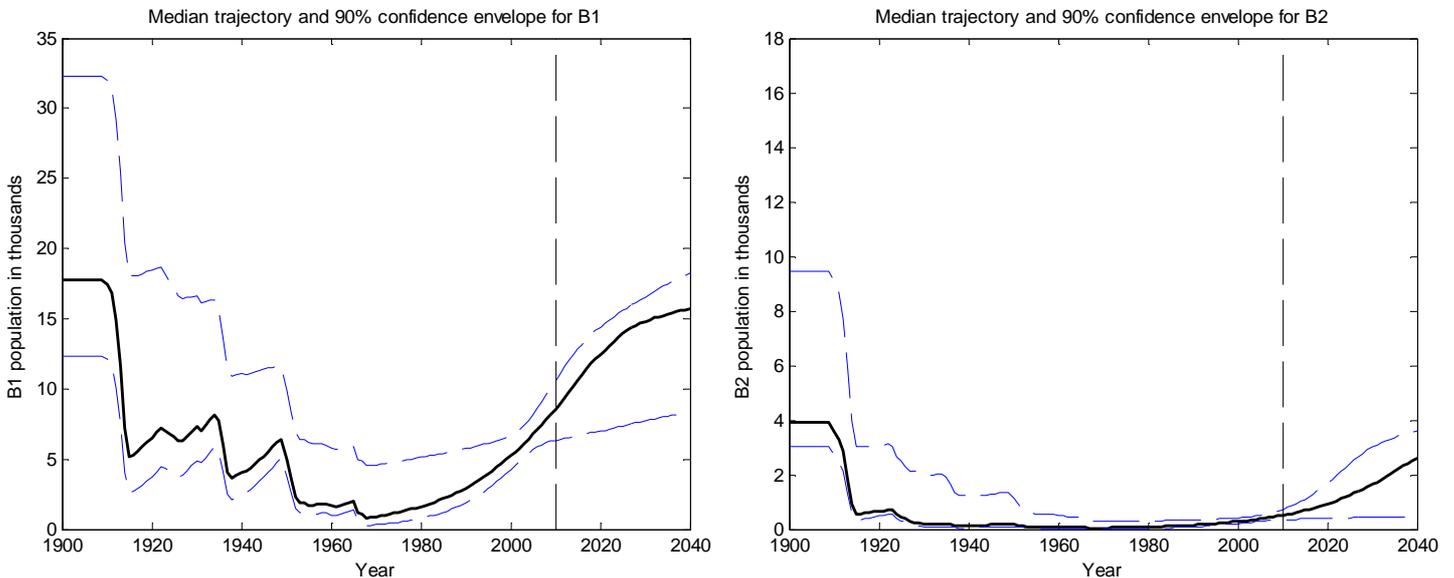
Table 1: Model parameter estimates for case A, where both the  $N_{min}$  constraints are in place ( $N_{min}^{B1} = 272$  and  $N_{min}^{B2} = 96$ ), as well as for case B where an arbitrary  $N_{min}$  constraint of 10 is placed on B2. The posterior medians are given with the 5<sup>th</sup> and 95<sup>th</sup> percentiles in parentheses.

	A: $N_{min}^{B2} = 96$		B: $N_{min}^{B2} = 10$	
	B1	B2	B1	B2
$r$	0.0619 [0.0081,0.0994]	0.0214 [0.0029,0.0387]	0.0607 [0.0091,0.0967]	0.0628 [0.0094,0.1041]
$K$	16531 [9299,32760]	6100 [3901,15185]	17714 [12367,32280]	3907 [3012,9454]
$N_{min}$	766 [241,4830]	171 [96,365]	791 [267,4508]	42 [10,273]
$N_{min}/K$	0.051 [0.021,0.144]	0.025 [0.016,0.054]	0.046 [0.019,0.143]	0.011 [0.003,0.037]
$N_{2010}$	8287 [6226,10223]	414 [303,592]	8565 [6341,10600]	508 [345,732]
$N_{2010}/K$	0.53 [0.20,0.89]	0.067 [0.026,0.127]	0.49 [0.20,0.78]	0.13 [0.04,0.22]
$N_{2040}/K$	0.99 [0.25,1.00]	0.12 [0.031,0.349]	0.98 [0.26,1.00]	0.69 [0.06,0.99]

Figures 2a-b: Median population trajectories for case A, where the  $N_{min}$  constraint on B2 is 96. The trajectories and their 90% probability envelopes are given. Values to the right of the dashed line are projections into the future under zero catch.

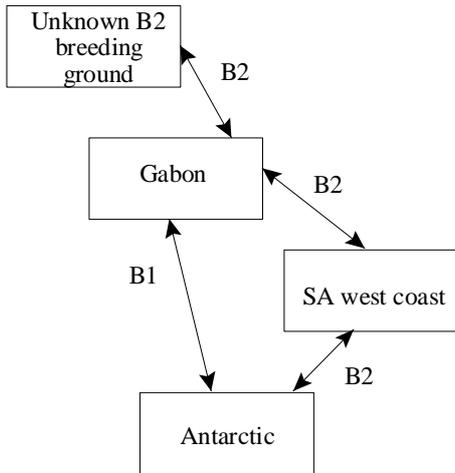


Figures 3a-b: Median population trajectories for case B, where the  $N_{min}$  constraint on B2 is 10. The trajectories and their 90% probability envelopes are given. Values to the right of the dashed line are projections into the future under zero catch.



## Appendix

### Model Ia (As recommended in IWC (2010))



*Model description:* model assumes two independent breeding sub-stocks which can mix on Antarctic feeding grounds. Whales from breeding sub-stock B1 feed in the Antarctic and migrate to Gabon for breeding. Whales from breeding sub-stock B2 feed off WSA and migrate along the West African coast through Gabon to a separate unidentified breeding ground. Additionally, some portion of B2 animals migrate to the Antarctic feeding grounds.

*Model dynamics:*

$$N_{y+1}^{B1} = N_y^{B1} + r^{B1} N_y^{B1} \left[ 1 - \left[ \frac{N_y^{B1}}{K^{B1}} \right]^\mu \right] - C_y^{B1} \quad (1)$$

$$N_{y+1}^{B2} = N_y^{B2} + r^{B2} N_y^{B2} \left[ 1 - \left[ \frac{N_y^{B2}}{K^{B2}} \right]^\mu \right] - C_y^{B2} \quad (2)$$

The catches are given by:

$$C_y^{B1} = p_y^{A,B1} C_y^A + p_y^{G,B1} C_y^G \quad (3)$$

$$C_y^{B2} = p_y^{A,B2} C_y^A + C_y^{WSA} + p_y^{G,B2} C_y^G \quad (4)$$

where

$C_y^A$  is the Antarctic catch in year  $y$ ,

$C_y^G$  is the Gabon catch in year  $y$ ,

$C_y^{WSA}$  is the West Africa catch in year  $y$ ,

$p_y^{A,Bi}$  is the proportion of animals caught in the Antarctic allocated to sub-stock  $i$ , and

$p_y^{G,Bi}$  is the proportion of animals caught in the Gabon breeding area allocated to sub-stock  $i$ .

These proportions are given by:

$$p_y^{A,B1} = \frac{N_y^{B1}}{N_y^{B1} + p_1 N_y^{B2}} \quad \text{and} \quad p_y^{A,B2} = \frac{p_1 N_y^{B2}}{N_y^{B1} + p_1 N_y^{B2}} \quad (5)\&(6)$$

$$p_y^{G,B1} = \frac{N_y^{B1}}{N_y^{B1} + p_2 N_y^{B2}} \quad \text{and} \quad p_y^{G,B2} = \frac{p_2 N_y^{B2}}{N_y^{B1} + p_2 N_y^{B2}} \quad (7)\&(8)$$

where  $p_1$  is the proportion of B2 animals that migrate down to the Antarctic and  $p_2$  is the probability of sighting a B2 animal as it transits through the Gabon breeding area.

Abundance and trend data: Gabon data is fit to  $N_y^{B1} + p_2 N_y^{B2}$ , and the WSA data is fit to  $N_y^{B2}$ . These data comprise either genetic or photo-ID “tag-recapture” results.