BAYESIAN ASSESSMENTS OF SOUTHERN HEMISPHERE HUMPBACK WHALE BREEDING SUB STOCKS C1 AND C3, INCLUDING ALLOWANCE FOR INTERCHANGE ON THE BREEDING GROUNDS

SUSAN J. JOHNSTON AND D. S. BUTTERWORTH[1]

Contact e-mail: Susan.Holloway@uct.ac.za

ABSTRACT

Bayesian stock assessment results for breeding sub-stocks C1 and C3 using models which allow for interchange on the breeding grounds as well as mixing on the feeding grounds are illustrated for two models – the sabbatical model and the resident model (for which interchange is set to zero.

KEYWORDS: HUMPBACK WHALES, BAYESIAN ASSESSMENT, INTERCHANGTE

INTRODUCTION

This document reports Bayesian stock assessment results for breeding stock C, which is considered to consist of two sub-stocks:

C1: east coast of South Africa and Mozambique

C3: where C3 refers to C2+3 (strictly C2 refers to whales wintering around the Comoros Islands, and C3 refers to whales wintering in the coastal waters of Madagascar).

There are several sources of trend data available for sub-stock C1, whereas no direct measurements of trend from the breeding area for sub-stock C3 are available. Although historic catches from the breeding grounds are available for each sub-stock's breeding area, the historic catches from the feeding grounds (south of 40°S) are for both sub-stocks combined. The mixed modelling approach reported here allows for mixing of the C1 and C3 sub-stocks on both the feeding grounds and breeding grounds.

In Butterworth and Johnston (2008), four alternate models were put forward, with three of these allowing for different possible mechanisms of interchange between the C1 and C3 breeding substocks. Here we present results for resident (no interchange) and sabbatical (incorporate interchange) models.

DATA

The data used for these analyses are deliberately identical with those adopted for the assessment reported in IWC (2008).

Historic Catch data

There are two sources of historic catch data that relate to breeding sub-stocks C1 and C3.

i) Catches north of 40°S

C1	those from "SCape", "Natal", and "Mozamb" from Allisons's database (Allison pers. commn) [note the total for each category is SCape =68, Natal=10330 and Mozamb=3995]
C3	those from "W Indian Ocean" from Allisons's database.

ii) Catches south of 40°S
This series refers to catches recorded for 10°E-60°E and thus includes both C1 and C3 whales. Table 1a and Figure 1 show these three historic catch series.

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[1] MARAM (Marine Resource Assessment and Management Group), Department of Mathematics and Applied Mathematics, University of Cape Town, Rondebosch, 7701, South Africa

Absolute abundance data

The absolute abundance data considered in these analyses are presented in Table 1b. For breeding stock C1, an estimate of 5965 (CV = 0.17) for the 2003 season has been provided by Findlay *et al.* (in press). For breeding stock C3, upper and lower abundance estimates are suggested in Cerchio *et al.* (2008); these were obtained using the MARK program applied to capture-recapture data from both photo-ID and genotypic data. These estimates are 6737 (CV=0.31) and 7715 (CV=0.24) for the year 2005. These estimates are for sub-stock C3 – primarily for Antongil Bay in the northeast of Madagascar. The lower of these estimates (6737) is used in the initial step of model fitting procedure (backwards method) where given a random value of r^{C3} a corresponding value of K^{C3} is needed – and this is done by fitting exactly to a recent population abundance estimates (in this case the 6737 in 2005 for C3). This C3 estimate is however not incorporated in the likelihood function because the capture-recapture data that underlie it are used instead.

Trend information

Two sources of direct information on trend for sub-stock C1 are used. These are reported in Table 2, and comprise:

i) Cape Vidal sightings per unit effort data for the 1988-2002 period (Findlay and Best 2006). These are obtained from shore-based surveys of northwards-migrating humpback whales at Cape Vidal, South Africa each year between 1988 and 1991, and in 2002.

ii) Aircraft sightings per unit effort 1954-1975 from the Durban whaling ground (reported in Best 2003).

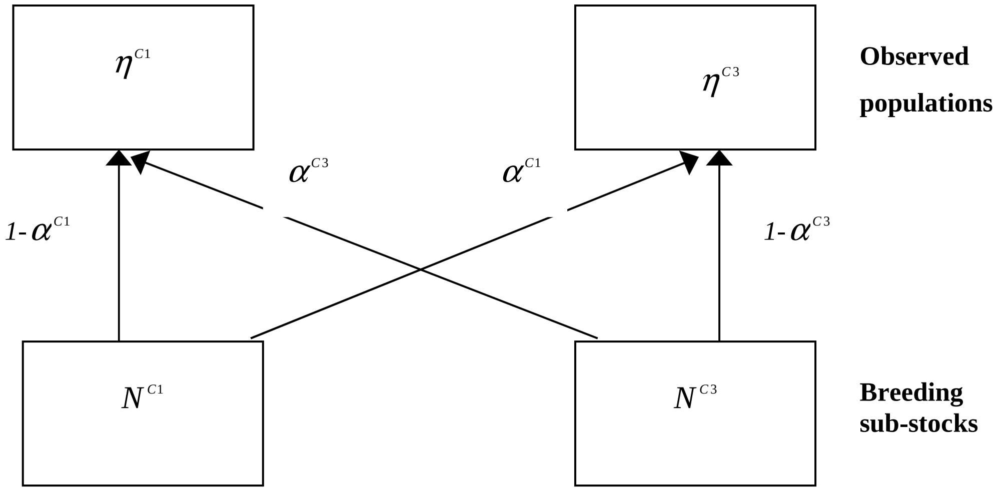
Capture-recapture data

The capture-recapture data used here are reported in Cerchio *et al*. (2008a and b). These consist of photo-ID mark-recapture data from Antongil Bay (C3) (Cerchio *et al.* 2008a), as well as photo-ID mark-recapture data for C1 (Cerchio *et al.* 2008b). The data span the period 2000-2006 and are reproduced in Tables 3a-c. The years 2000 and 2004 for C1 and the year 2002 for C3 are however excluded due to poor temporal coverage of capture effort.

METHODS

Sabbatical interchange modelling approach

The sabbatical interchange model considered is shown schematically below (see also Butterworth and Johnston (2009). There are two breeding substocks C1 and C3 of sizes N^{C1} and N^{C3} respectively. However each year there is a probability α^{C1} that an animal from sub-stock C1 travels to the C3 region instead of C1, and similarly a probability α^{C3} that one from sub-stock C3 travels to the C1 region instead of C3. Note that the model thus assumes that an animal "visits" only one of these two regions in any one year. The observed numbers in regions C1 and C3 each year are then given by η^{C1} and η^{C3} respectively, and these are the variables to which observations apply (both capture-recapture and survey data).



The following equations then apply:

Breeding sub-stock population dynamics

$$N_{y+1}^{B,C1} = N_y^{B,C1} + r^{C1} N_y^{B,C1} \left(1 - \left(\frac{N_y^{B,C1}}{K^{C1}} \right)^{\mu} \right) - C_y^{C1} \qquad (1)$$

$$N_{y+1}^{B,C3} = N_y^{B,C3} + r^{C3} N_y^{B,C3} \left(1 - \left(\frac{N_y^{B,C3}}{K^{C3}} \right)^{\mu} \right) - C_y^{C3} \qquad (2)$$

where

$N_y^{B,C1}$	is the number of whales in the breeding population C1 at the start of year *y*,
$N_y^{B,C3}$	is the number of whales in the breeding population C3 at the start of year *y*,
r^{C1}	is the intrinsic growth rate (the maximum per capita the population can achieve, when its size is very low) for breeding population C1,
r^{C3}	is the intrinsic growth rate for breeding population C3,
K^{C1}	is the carrying capacity of breeding population C1,
K^{C3}	is the carrying capacity of breeding population C3,
μ	is the “degree of compensation” parameter; this is set at 2.39, which fixes the MSY level to MSYL = 0.6*K*, as conventionally assumed by the IWC Scientific Committee,
C_y^{C1}	is the total catch (in terms of animals) in year *y* from breeding population C1, and
C_y^{C3}	is the total catch (in terms of animals) in year *y* from breeding population C3.

Feeding stocks

Mixing of the breeding populations in the feeding area (defined by 10°E – 60°E) yields:

$$N_y^F = N_y^{B,C1} + N_y^{B,C3} \tag{3}$$

which is assumed to reflect complete mixing of sub-stocks C1 and C3 in the feeding area.

Observed populations

$$\eta_y^i = (1-\alpha^i)N_y^i + \alpha^j N_y^j \qquad \begin{Bmatrix} i \\ j \end{Bmatrix} = \begin{Bmatrix} C1 \\ C3 \end{Bmatrix} or \begin{Bmatrix} C3 \\ C1 \end{Bmatrix} \tag{4}$$

where

η_y^i	is the observed population size in year *y* in breeding region *i*,
α^i	is the probability that animal from breeding population *i* moves (for one year) to observation area for breeding population *j* instead of that for breeding population *i*.

Catches

$$C_y^{C1} = C_y^{C1,B} + C_y^{C1,F} \tag{5}$$

$$C_y^{C3} = C_y^{C3,B} + C_y^{C3,F} \tag{6}$$

where

$C_y^{C1,B}$	are the catches of animals in year *y* from the C1 sub-stock in either breeding area,
$C_y^{C1,F}$	are the catches of animals in year *y* from the C1 sub-stock in the feeding area,
$C_y^{C3,B}$	are the catches of animals in year *y* from the C3 sub-stock in either breeding area, and
$C_y^{C3,F}$	are the catches of animals in year *y* from the C3 sub-stock in the feeding area.

Table 1a provides the reported breeding area catches ($C_y^{C1,B,reported}$ and $C_y^{C3,B,reported}$), but only the combined catch ($C_y^F = C_y^{C1,F} + C_y^{C3,F}$) for the feeding area. To split this feeding ground catch, it is assumed that the catches each year are proportional to their relative abundances in the feeding area (given that complete mixing is assumed). Thus the breakdown of feeding ground catches is calculated as follows:

$$C_y^{C1,F} = C_y^F \frac{N_y^{C1,B}}{\left(N_y^{C1,B} + N_y^{C3,B}\right)} \qquad \text{and} \tag{7}$$

$$C_y^{C3,F} = C_y^F \frac{N_y^{C3,B}}{\left(N_y^{C1,B} + N_y^{C3,B}\right)} \tag{8}$$

The reported breeding ground catches are also split proportional to the relative abundance of each breeding sub-stock in each area as follows:

$$C_y^{C1,B} = C_y^{C1,B,reported}\frac{(1-\alpha^1)N_y^{C1,B}}{\left((1-\alpha^1)N_y^{C1,B}+\alpha^3 N_y^{C3,B}\right)} + C_y^{C3,reported}\frac{\alpha^1 N_y^{C1,B}}{\left(\alpha^1 N_y^{C1,B}+(1-\alpha^3)N_y^{C3,B}\right)} \quad (9)$$

$$C_y^{C3,B} = C_y^{C1,B,reported}\frac{\alpha^3 N_y^{C3,B}}{\left((1-\alpha^1)N_y^{C1,B}+\alpha^3 N_y^{C3,B}\right)} + C_y^{C2+3,reported}\frac{(1-\alpha^3)N_y^{C3,B}}{\left(\alpha^1 N_y^{C1,B}+(1-\alpha^3)N_y^{C3,B}\right)} \quad (10)$$

<u>Bayesian estimation framework</u>

Priors

Prior distributions are defined for the following parameters:

i) r^{C1} ~ U[0, 0.106] (as there are appreciable trend data to inform on *r* for C1)

ii) r^{C3} ~ Post BS A (as there are no trend data to inform on *r* for C3)

iii) $\ln\tilde{\eta}_{target}^{C1,obs} \sim U[\ln\eta_{target}^{C1,obs} - 4CV,\ \ln\eta_{target}^{C1,obs} + 4CV]$

iv) $\ln\tilde{\eta}_{target}^{C3,obs} \sim U[\ln\eta_{target}^{C3,obs} - 4CV,\ \ln\eta_{target}^{C3,obs} + 4CV]$

v) $\alpha^{C1} \sim U[0,0.6]$

vi) $\alpha^{C3} \sim U[0,0.6]$

The uninformative r^{C1} and informative r^{C3} priors are bounded by zero (negative rates of growth are biologically implausible) and 0.106 (this corresponds to the maximum growth rate for the species agreed by the IWC Scientific Committee (IWC, 2007)). The prior distributions from which target abundance estimates ($\tilde{\eta}_{target}^{C1,obs}, \tilde{\eta}_{target}^{C3,obs}$) are drawn at random are uniform on a natural logarithmic scale. The lower and upper bounds are set by four times the CV. For these *N* targets, the Findlay *et al.* (in press) estimate is used for C1, and the lower Cerchio *et al.* (2008a) estimate is used for C3. The upper bound on the α priors is to exclude results corresponding to interchange symmetry $N^{C1} \leftrightarrow N^{C3}$ $\alpha^{C1/C3} \to 1-\alpha^{C3/C1}$.

Using the randomly drawn vector of values of $\tilde{\eta}_{target}^{C1,obs}$, $\tilde{\eta}_{target}^{C3,obs}$, r^{C1}, r^{C3}, α^{C1} and α^{C3}, a downhill simplex method of minimization is used to calculate K^{C1} and K^{C3} such that the model estimates of η_{target}^{C1} and η_{target}^{C3} are identical to the randomly drawn values $\tilde{\eta}_{target}^{C1,obs}$ and $\tilde{\eta}_{target}^{C3,obs}$.

For each simulation, using the r^{C1}, r^{C3}, α^{C1}, α^{C3} and calculated K^{C1} and K^{C3} values, a negative log likelihood is then computed by comparing the model estimates of the (potentially) observed populations (the η_y^{C1} and η_y^{C3}) to observed data – the recent absolute abundance estimate for C1, aircraft SPUE data for C1, relative abundance trend data from the breeding grounds for C1 (Cape Vidal data), and the capture-recapture photo-ID data for C1 and C3. The components of the negative log likelihood are calculated as follows.

The model treats the SPUE estimates from Cape Vidal (C1) as relative indices of abundance. It is assumed that the observed relative abundance index is log-normally distributed about its expected value:

$$I_{SPUE,Vidal,y}^{C1} = q_{SPUE,Vidal}^{C1}\eta_y^{C1}e^{\varepsilon_y} \quad (11)$$

where

$I^{C1}_{SPUE,Vidal,y}$	is the Cape Vidal survey-based relative abundance (SPUE index) for year y for breeding sub-stock C1,
$q^{C1}_{SPUE,Vidal}$	is the catchability coefficient for the Cape Vidal index for breeding sub-stock C1,
η^{C1}_{y}	is the model estimate of observed population size at the start of year y for breeding sub-stock C1, and
ε_y	is from $N\left(0,\left(\sigma^{C1}_{SPUE,Vidal}\right)^2\right)$ (see equation 18 below)

The model treats the aircraft SPUE abundance estimates slightly differently as follows, in particular to take proper account of zero sightings in some years. A Poisson distribution is assumed. The expected number of sightings in year y is:

$$\hat{n}^{S}_{y} = q_{SPUE,aircraft}\,\eta^{C1}_{y} E_y \qquad (12)$$

where

E_y	is the aircraft searching effort in year y.

The associated “catchability” coefficient is calculated as follows:

$$q_{SPUE,aircraft} = \frac{\sum\limits_{y} \overline{n}^{S}_{y}}{\sum\limits_{y} \eta^{C1}_{y}.E_y} \qquad (13)$$

where

$\overline{n}^{S}_{y}$	is the observed number of whale sightings in year y.

Capture-recapture

Captures: $n^i_y = p^i_y \eta^i_y \qquad i = C1, C3 \qquad (14)$

Recaptures: $m^{i,j}_{y,y'}$ refers to humpbacks captured in region *i* in year *y* and recaptured in region *j* in year *y*’, where the expected numbers in terms of the interchange model are:

$$\hat{m}^{i,j}_{y,y'} = p^i_y[(1-\alpha^i)N^i_y e^{-M(y'-y)}\alpha^i + \alpha^j N^j_y e^{-M(y'-y)}(1-\alpha^j)]p^j_{y'} \qquad (15)$$

$$\hat{m}^{i,i}_{y,y'} = p^i_y[(1-\alpha^i)N^i_y e^{-M(y'-y)}(1-\alpha^i) + \alpha^j N^j_y e^{-M(y'-y)}\alpha^j]p^i_{y'} \qquad (16)$$

where:

$$\begin{Bmatrix} i \\ j \end{Bmatrix} = \begin{Bmatrix} C1 \\ C3 \end{Bmatrix} or \begin{Bmatrix} C3 \\ C1 \end{Bmatrix} ; \begin{Bmatrix} i \\ i \end{Bmatrix} = \begin{Bmatrix} C1 \\ C1 \end{Bmatrix} or \begin{Bmatrix} C3 \\ C3 \end{Bmatrix}$$

where:

n^i_y	= number of animals captured in breeding region *i* in year *y*
$m^{i,j}_{y,y'}$	= number of animals captured in *i* in year *y* that were recaptured in *j* in year y'

$\hat{m}^{i,j}_{y,y'}$ = model predicted number of animals in *i* captured in year *y* that were recaptured in *j* in year y'

M = natural mortality rate (set here to equal 0.03)

p^{i}_{y} = probability animal is seen in *i* year *y*.

The contributions of the various data to the negative of the log-likelihood function are then given by equation (17) below, where the absolute abundance estimate for C1 ($N^{C1,obs}_{target}$) refers to that of Findlay *et al.* (in press):

$$
\begin{aligned}
-\ln L = {} & [\bar{n}^{C1}_{SPUE,Vidal}\ln\sigma^{C1}_{SPUE,Vidal} + \frac{1}{2\sigma^{C1\ 2}_{CPUE}}\sum_y\left(\ln I^{C1}_{SPUE,Vidal,y} - \ln q^{C1}_{SPUE,Vidal} - \ln\eta^{B,C1}_{y}\right)^2] + \\
& \left[\sum_y\{q_{SPUE,aircraft}\eta^{C1}_y E_y - n_y\ln(q_{SPUE,aircraft}\eta^{C1}_y E_y)\}\right] + \\
& [\frac{1}{2CV^2}\left(\ln N^{C1,obs}_{target} - \ln\eta^{B,C1}_{target}\right)^2] + \\
& \sum_i\sum_j\sum_{y=y_o}^{y_f-1}\sum_{y'=y+1}^{y_f}[-m^{i,j}_{y,y'}\ln\hat{m}^{i,j}_{y,y'} + \hat{m}^{i,j}_{y,y'}]
\end{aligned}
\qquad (17)
$$

The $\sigma^{C1}_{SPUE,Vidal}$ parameter is the residual standard deviation which is estimated in the fitting procedure by its maximum likelihood value:

$$\hat{\sigma}^{C1}_{SPUE,Vidal} = \sqrt{1/\bar{n}^{C1}_{SPUE,Vidal}\sum_y\left(\ln I^{C1}_{SPUE,Vidal,y} - \ln q^{C1}_{SPUE,Vidal} - \ln\eta^{C1}_y\right)^2} \quad \text{for Vidal SPUE data} \qquad (18)$$

where

$\bar{n}^{C1}_{SPUE,Vidal}$ is the number of data points in the Cape Vidal SPUE series, and

$q^{C1}_{SPUE,Vidal}$ is the multiplicative bias, estimated by its maximum likelihood value:

$$\ln\hat{q}^{C1}_{SPUE,Vidal} = 1/\bar{n}^{C1}_{SPUE,Vidal}\sum_y\left(\ln I^{C1}_{SPUE,Vidal,y} - \ln\eta^{C1}_y\right) \qquad (19)$$

This is a short cut to avoid integrating over priors for the *q*'s and σ^2 's, and in fact corresponds to the assumption that these priors are uniform in log-space and proportional to σ^{-3} respectively (Walters and Ludwig 1994).

The negative log likelihood is then converted into a likelihood value (*L*). The integration of the prior distributions of the parameters and the likelihood function then essentially follows the Sampling-Importance-Resampling (SIR) algorithm presented by Rubin (1988) as described in Zerbini (2004). For a vector of parameter values θ_i, the likelihood of the data associated with this vector of parameters (L) as described above is calculated then modified by an importance function and stored as $\tilde{L}$. This process is repeated until an initial sample of n_1 θ_i s is generated.

To improve calculation efficiency, given that high α values correspond to very low likelihoods, an importance function was introduced for each α value. In effect this means replacing the existing uniform priors on the α values by:

$$\alpha^{C1} \sim \sigma^{C1} N(0,1)$$
$$\alpha^{C3} \sim \sigma^{C3} N(0,1)$$

where α^{C1} and α^{C3} are bound by [0,0.6], and σ^{C1} and σ^{C3} are set at 0.1, and then modifying the likelihood *L* to:

$$\tilde{L}_i = L_i / \left\{ e^{-(\alpha_i^{C1})^2/2(\sigma^{C1})^2} e^{-(\alpha_i^{C3})^2/2(\sigma^{C3})^2} \right\}$$

This sample is then resampled with replacement n_2 times with probability equal to weight w_j, where:

$$w_j = \frac{\tilde{L}\,(\theta_j / data)}{\sum_{j=1}^{n1} \tilde{L}\,(\theta_j / data)} \qquad (20)$$

The resample is thus a random sample of size n_2 from the joint posterior distribution of the parameters (Rubin 1988).

Values of n_1 (original number of simulations) are 500 000 and the value of n_2 (number of resamples) is 1000. Tests showed that no sample contributed more than 0.5% of the total weight, and that at least 80% of the resamples were unique values.

Nmin constraints

$N_{\min}$ constraints of 248 and 496 whales are imposed for sub-stocks C1 and C3 respectively. These values are 4 times the number of haplotypes estimated by Rosenbaum *et al.* (2006) for these sub-stocks.

The Resident model

The resident model is identical to the sabbatical model, except that no interchange between breeding regions C1 and C3 is allowed. This results in both α^{C1} and α^{C3} being set equal to zero. Equation (15) is thus not required, and the single recapture that indicates interchange is excluded from the likelihood.

RESULTS

The Bayesian sabbatical and resident model results are reported in Tables 4a and b respectively. Figures 1 and 2 illustrate the resident model C1 and C3 population trajectories, and Figures 3 and 4 illustrate those for the sabbatical model. Figures 5a and b compare the median C1 and C3 population trends estimated between the sabbatical and resident models. Table 5 compares the estimates of population numbers in the breeding areas given in Table 1b with those predicted by the two models.

DISCUSSION

The interchange probability estimates are small: parameter medians of 0.051 and 0.016 for C1 and C3 respectively (Table 4b), though the 95%ile for the former is somewhat larger at 0.156.

The effect of making allowance for interchange is to reduce the abundance of the C3 population somewhat, but the results for C1 hardly differ in median terms (Figure 5). The $N_{\min}$ constraint did not come into play for either model.

Clearly other variants of these models could be investigated. For example, one might set $r^{C1} = r^{C3}$. However, at this stage the intent of this paper is to illustrate the methodology for the two models rather than to provide immediately definitive results.

REFERENCES

Best, P. 2003. How low did they go? An historical comparison of indices of abundance for some baleen whales on the Durban whaling ground. Paper SC/55/SH18 submitted to the IWC Scientific Committee, 11pp.

Butterworth, D.S. and Johnston, S.J. 2009. Report on discussions on modelling studies of possible interchange between the C1 and C3 breeding substocks of Southern Hemisphere humpback whales, Cape Town, December 2008. IWC document, SC/F09/SH1.

Cerchio, S, Ersts, P., Pomilla, C., Loo, J., Razafindrakoto, Y., Leslie, M., Andrianrivelo, N., Minton, G., Dushane, J., Murray, A., Collins, T. and Rosenbaum, H. (2008a) Revised estimation of abundance for breeding stock C3 of humpback whales, assessed through photographic and genotypic mark-recapture data from Antongil Bay, Madagascar, 2000-2006. IWC document SC/60/SH32.

Cerchio, S., Findlay, K., Ersts, P., Minton, G., Bennet, D., Meyer, M.A., Razafindrakoto, Y., Kotze, P.G.H., Oosthuizen, H., Leslie, M., Andrianarivelo, N. and Rosenbaum, H. 2008b. Initial assessment of exchange between breeding stocks C1 and C3 of humpback whales in the western Indian Ocean using photographic mark-recapture data, 2000-2006. IWC document SC/60/SH33.

Findlay, K., Meyer, M, Elwen, S., Kotze, D., Johnson, R., Truter, P., Uamusse, C., Sitoe, S., Wilke, C., Kerwath, S., Swanson, S., Stavarees, L. and J. van der Westhuizen. (in press). Distribution and abundance of humpback whales, *Megaptera novaeangliae*, off the coast of Mozambique, 2004. J. Cetacean Res. Manage. (Special Issue).

Findlay, K. and P. Best. 2006. The migration of humpback whales past Cape Vidal, South Africa, and a preliminary estimate of the population increase rate. Paper SC/A06/HW16 submitted to the IWC southern hemisphere humpback workshop, Hobart, April 2006.

IWC. 2007. Report of the international Whaling Commission, Annex H, Report of the Sub-Committee on Southern Hemisphere whale stocks. Annex H. *J.Cetacean Res.Manage. Suppl.*

IWC. 2008. Report of the international Whaling Commission, Annex H, Report of the Sub-Committee on Southern Hemisphere whale stocks. Annex H. *J.Cetacean Res.Manage. Suppl.*

Rosenbaum, H.C., Pomilla, C, Olavarria, C., Baker, C.S., Leslie, M.C., Mendez, M.C., Caballero, S., Brassuer, M., Bannister, J., Best, P.B., Bonatto, S., Collins, T., Engel, M.H., Ersts, P.J., Findlay, K.P., Florez-Gonzalez, L., Garrigue, C., Hauser, C., Jenner, N., Meyer, M., Minton, G., Poole, M. and Y. Razafindrakoto. 2006. Paper SC/A06/HW59 submitted to the IWC southern hemisphere humpback workshop, Hobart, April 2006.

Rubin, D.B. 1988. Using the SIR algorithm to simulate posterior distributions. Pp. 395-402. In. J.M. Bernado, M.H. DeGroot, D.V. Lindlley and A.F.M Smith (eds). *Bayesian Statistics 3: Proceedings of the Third Valencia International Meeting.* June 1-5, 1987. Clarendon Press, Oxford. 805pp.

Walters, C. and Ludwig, D. 1994. Calculation of Bayes posterior probability distributions for key population parameters. *Can. J. Fish. Aquat. Sci.* 51: 713-722.

Zerbini, A.N. 2004. Status of the Southern Hemisphere humpback whale breeding stock A: preliminary results from a Bayesian assessment. Paper SC/56/SH17 presented to the IWC Scientific Committee, 18pp.

Table 1a: Historic catch series for sub-stocks C1 and C2+3 (Allison, pers. commn).

Season	C1 Breeding grounds	C3 Breeding grounds	C1+C3 Feeding grounds	Season	C1 Breeding grounds	C3 Breeding grounds	C1+C3 Feeding grounds	Season	C1 Breeding grounds	C3 Breeding grounds	C1+C3 Feeding grounds
1900	0	0	0	1926	124	0	0	1952	111	0	208
1901	0	0	0	1927	86	0	0	1953	89	0	66
1902	0	0	0	1928	62	0	0	1954	28	0	50
1903	0	0	0	1929	99	0	4	1955	49	0	28
1904	0	0	0	1930	134	0	150	1956	36	0	4
1905	0	0	0	1931	72	0	2	1957	34	0	66
1906	0	0	0	1932	307	0	38	1958	39	0	120
1907	0	0	0	1933	162	0	54	1959	38	0	152
1908	104	0	0	1934	514	0	554	1960	36	0	72
1909	149	0	0	1935	418	0	1870	1961	40	4	28
1910	632	0	0	1936	300	0	2684	1962	38	1	74
1911	1580	0	0	1937	242	1223	780	1963	38	0	40
1912	2313	25	0	1938	177	1752	0	1964	3	3	48
1913	1805	0	0	1939	200	1240	4	1965	2	1	76
1914	830	0	0	1940	176	0	0	1966	0	0	196
1915	334	0	0	1941	79	0	0	1967	8	8	66
1916	94	0	0	1942	156	0	0	1968	0	0	0
1917	7	0	0	1943	80	0	0	1969	0	0	0
1918	9	0	0	1944	115	0	0	1970	0	0	0
1919	91	0	0	1945	116	0	0	1971	0	0	0
1920	148	0	0	1946	93	0	0	1972	0	0	0
1921	251	0	0	1947	89	0	0	1973	1	0	0
1922	285	0	0	1948	182	0	34	1974	0	0	0
1923	183	0	0	1949	190	1333	396	1975	0	0	0
1924	187	0	0	1950	151	714	74				
1925	372	0	0	1951	103	0	212				

Table 1b

Absolute abundance estimates considered in analyses for sub-stocks C1 and C3

Breeding sub-stock	**Abundance estimate**	**Year applicable**	**Source**
C1	5965 (CV = 0.17)	2003	Findlay *et al.* (in press)
C3 lower	6737 (CV = 0.31)	2005	Cerchio *et al.* (2008a)
C3 upper	7715 (CV = 0.24)	2005	Cerchio *et al.* (2008a)

Table 2: Relative abundance trend data for sub-stock C1. For SPUE, effort is in hours and n^s is the number of whales sighted.

Year	Cape Vidal (Findlay and Best 2006)	Year	Aircraft SPUE and effort from Durban 1954-75		
			SPUE	n^s	Effort
1988	358	**1954**	2.868	5	174.35
1989	249	**1957**	0	0	325.49
1990	359	**1958**	0	0	423.40
1991	587	**1959**	0.223	1	448.58
2002	1673	**1960**	0	0	585.00
		1961	1.289	9	698.22
		1962	0.257	2	779.71
		1963	0.180	2	1119.99
		1964	0.197	2	1016.33
		1965	0	0	1102.26
		1966	1.336	13	972.86
		1967	0.710	6	844.95
		1968	0.294	2	681.36
		1969	1.254	9	717.87
		1970	0.536	4	745.83
		1971	0.426	3	704.31
		1972	0.966	7	724.51
		1973	1.720	11	639.23
		1974	1.514	8	528.32
		1975	1.871	10	534.35

Table 3a: Photographic capture-recapture data from BS C1 – from SC/60/SH33 (Cerchio *et al.* 2008b)

[*n* = number of different individuals sighted each year, *m* = total recaptures between pairs of years]

n							
	2000	2001	2002	2003	2004	2005	2006
	3	24	49	115	21	134	112

m							
	2000	2001	2002	2003	2004	2005	2006
2000	X	0	0	0	0	0	0
2001		X	1	0	0	0	0
2002			X	1	1	0	1
2003				X	0	0	0
2004					X	1	0
2005						X	2
2006							X

Table 3b Photographic capture-recapture data from C3 – from SC/60/SH33 (Cerchio *et al.* 2008a)

[*n* = number of different individuals sighted each year, *m* = total recaptures between pairs of years]

N							
	2000	2001	2002	2003	2004	2005	2006
	89	159	16	126	151	144	158

m							
	2000	2001	2002	2003	2004	2005	2006
2000	X	2	1	3	1	0	1
2001		X	1	3	3	3	2
2002			X	3	0	0	0
2003				X	2	1	3
2004					X	4	3
2005						X	4
2006							X

Table 3c: Photographic capture-recapture data between C1 and C3 – from SC/60/SH33 (Cerchio *et al.* 2008a)

[*n* = number of different individuals sighted each year, *m* = total recaptures between pairs of years; the entries above the diagonal in the matrix reflect animals first seen in C3 and later re-sighted in C1, whereas entries below the diagonal reflect the reverse, animals first seen in C1 and later re-sighted in C3.

n							
	2000	2001	2002	2003	2004	2005	2006
C1	89	159	16	126	151	144	158
C3	3	24	49	115	21	134	112
Total							

m		**C1**						
		2000	2001	2002	2003	2004	2005	2006
C3	2000	X	0	0	0	0	0	0
	2001	0	X	0	0	0	0	0
	2002	0	0	X	0	0	0	0
	2003	0	0	0	X	0	0	0
	2004	0	0	0	0	X	0	0
	2005	0	0	0	0	0	X	0
	2006	0	0	0	1	0	0	X

Table 4a: **Resident** model assessment results (posterior medians with 5th and 95th percentiles in parenthesis).

	BS C1		**BS C2+3**
***r* prior**	**U[0, 0.106]**		**Post BS(A)**
Historic catch	**Feeding grounds split proportional to abundance**		**Feeding grounds split proportional to abundance**
Recent abundance	**5965 (2003)**		**None**
Trend information	**Cape Vidal and aircraft SPUE trend data only**	**None**	**None**
Capture-recapture Data	**“All” photo-ID data***		**“All”photo-ID data***
r	0.092 [0.069; 0.104]		0.065 [0.022; 0.090]
K	8414 [8060; 9369]		11279 [9473; 15387]
α	-		-
N_{min}	333 [256; 688]		2969 [1124; 6494]
N_{2006}	7406 [6415; 8056]		10449 [8005; 13477]
η_{2006}	7406 [6415; 8056]		10449 [8005; 13477]
N_{min}/K	0.040 [0.031; 0.073]		0.263 [0.116; 0.426]
N_{2006}/K	0.880 [0.709; 0.967]		0.993 [0.620; 1.000]
N_{2020}/K	0.995 [0.966; 0.999]		0.999 [0.747; 1.000]
N_{2040}/K	1.000 [0.999; 1.000]		1.000 [0.894; 1.000]

* As per the decision of IWC (2008), these exclude data from the years 2000 and 2004 for C1, and 2002 for C3, because of poor temporal coverage of capture effort. Further, for the resident model, the one recapture that reflects movement between C1 and C3 is excluded.

Table 4b **Sabbatical** model assessment results (posterior medians with 5th and 95th percentiles in parenthesis).

	BS C1		**BS C2+3**
***r* prior**	**U[0, 0.106]**		**Post BS(A)**
Historic catch	**Feeding grounds split proportional to abundance**		**Feeding grounds split proportional to abundance**
Recent abundance	**5965 (2003)**		**None**
Trend information	**Cape Vidal and aircraft SPUE trend data only**	**None**	**None**
Capture-recapture data	**“All” photo-ID data**		**“All” photo-ID data**
r	0.091 [0.068; 0.104]		0.064 [0.024; 0.089]
K	8092 [6920; 9180]		10766 [9179; 14904]
α	0.051 [0.006; 0.165]		0.016 [0.001; 0.078]
N_{min}	361 [259; 831]		2076 [836; 4953]
N_{2006}	7190 [5976; 8013]		9831 [7353; 12320]
η_{2006}	6916 [5956; 7775]		9963 [7563; 12562]
N_{min}/K	0.045 [0.033; 0.095]		0.191 [0.089; 0.351]
N_{2006}/K	0.902 [0.733; 0.982]		0.967 [0.561; 1.000]
N_{2020}/K	0.996 [0.968; 1.000]		0.997 [0.727; 1.000]
N_{2040}/K	1.000 [0.999; 1.000]		1.000 [0.887; 1.000]

Table 5: Comparison between population estimates reported in Table 2b with the model estimates showing 1.65s.e as 90% confidence intervals the Table 1b estimates on the left, and 90% probability intervals for the model estimates on the right.

C1 (2003)	
Findlay *et al.* (in press): 5965 [4292; 7638]	Resident Model η_{2003}^{C1} : 6735 [5545; 7756]
	Sabbatical Model η_{2003}^{C1} : 6395 [5252; 7474]
C3 (2005)	
Cerchio (2008a) lower estimate: 6737 [3291; 10183]	Resident Model η_{2005}^{C3} : 10404 [7869; 13466]
Cerchio (2008a) upper estimate: 7115 [4660; 10770]	Sabbatical Model η_{2005}^{C3} : 9909 [7395; 12544]

Figure 1a: Resident model fit to C1 trend data (Cape Vidal and aircraft SPUE), as well as the recent abundance estimate (2003). The model trajectory is the Bayesian posterior median values of η_y^{C1}, the whales in the C1 breeding grounds. The vertical line shows 2006.

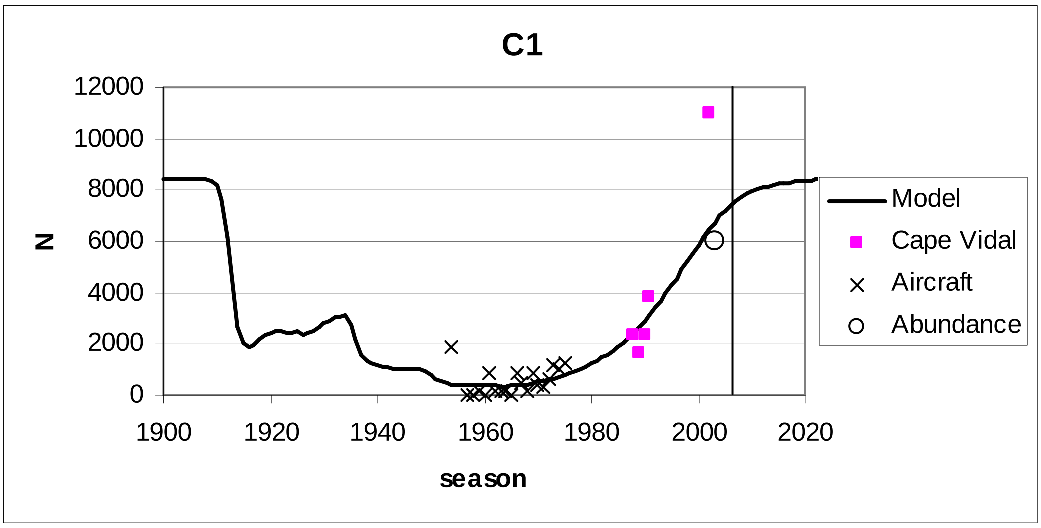


Figure 1b: Resident model C1 population (N_y^{C1}) trajectories, showing the median and 95% probability envelopes. The vertical line shows 2006.

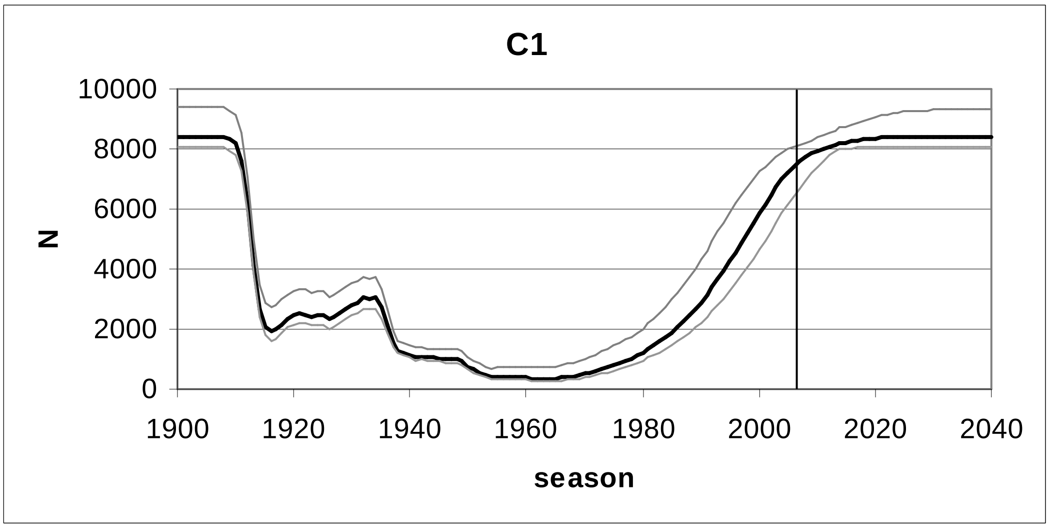


Figure 2a: Resident model trajectories of is the Bayesian posterior median values of η_y^{C3}, the whales in C3 breeding grounds. The vertical line shows 2006. The squares show the upper and lower abundance estimates from Cerchio (2008a) for comparative purposes – these estimates are not used in fitting the model because the capture-recapture data underlying them are used instead.

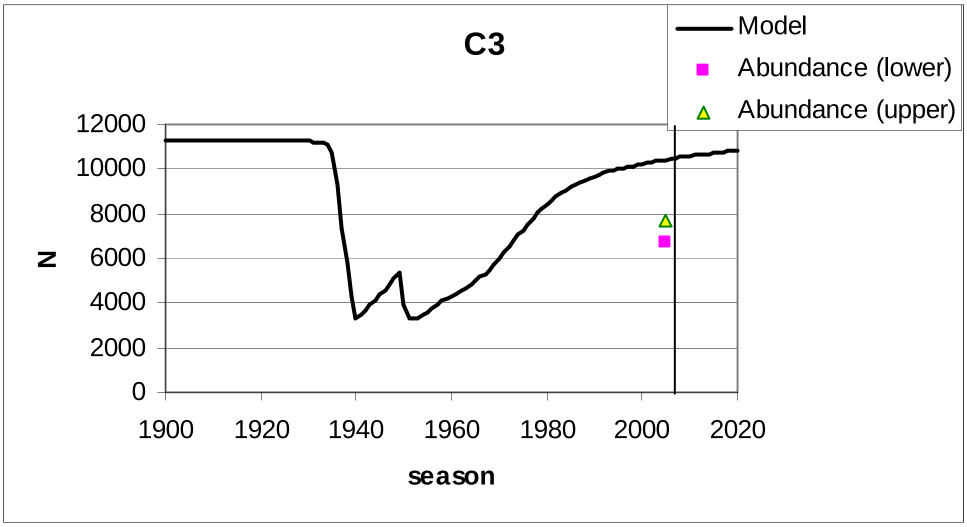


Figure 2b: Resident model C3 population (N_y^{C3}) trajectories, showing the median and 95% probability envelopes. The vertical line shows 2006.

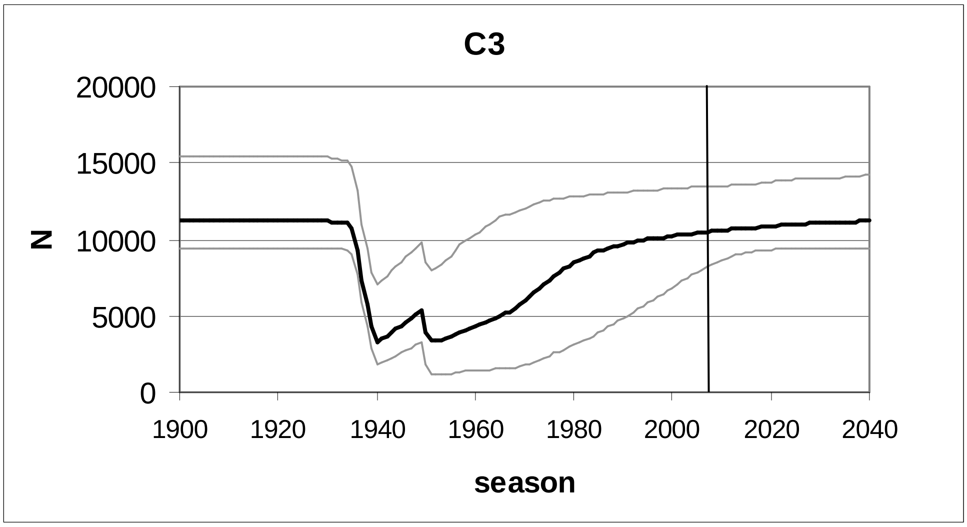


Figure 3a: Sabbatical model fit to C1 trend data (Cape Vidal and aircraft SPUE), as well as the recent abundance estimate (2003). The model trajectory is the Bayesian posterior median values of η_y^{C1}, the whales in C1 breeding grounds. The vertical line shows 2006.

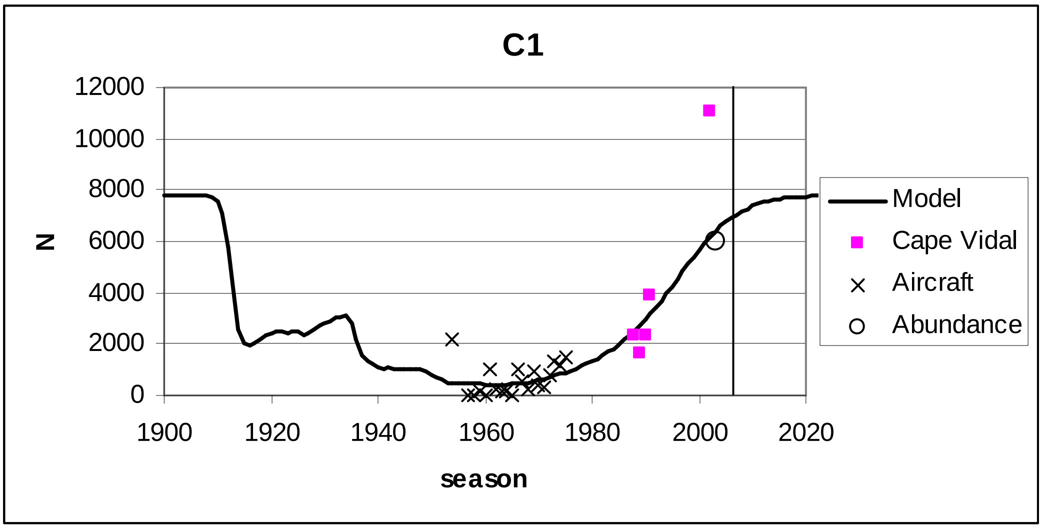


Figure 3b: Sabbatical model C1 population (N_y^{C1}) trajectories, showing the median and 95% probability envelopes. The vertical line shows 2006.

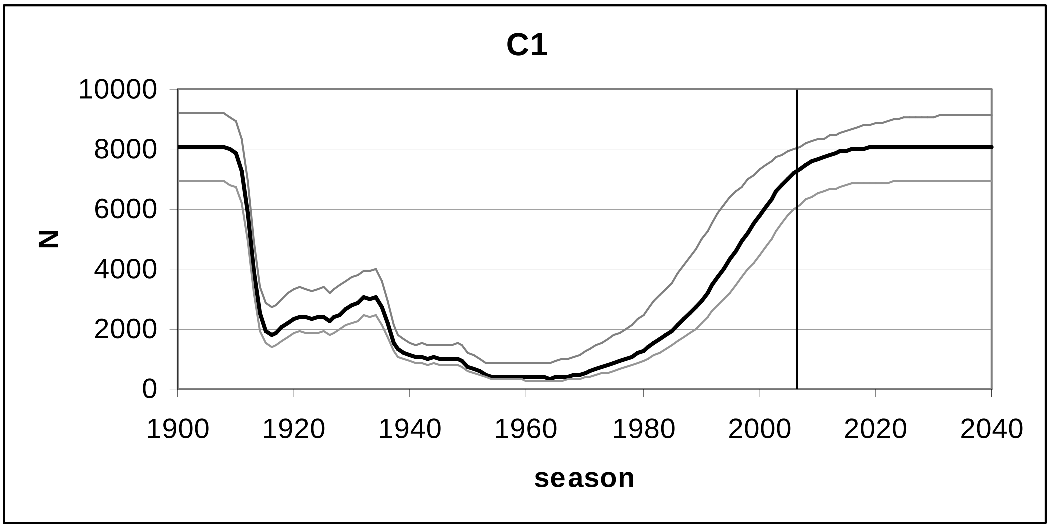


Figure 4a: Sabbatical model trajectories of is the Bayesian posterior median values of η_y^{C3}, the whales in the C3 breeding grounds. The vertical line shows 2006. The squares show the upper and lower abundance estimates from Cerchio (2008a) for comparative purposes – these estimates are not used in fitting the model because the capture-recapture data underlying them are used instead.

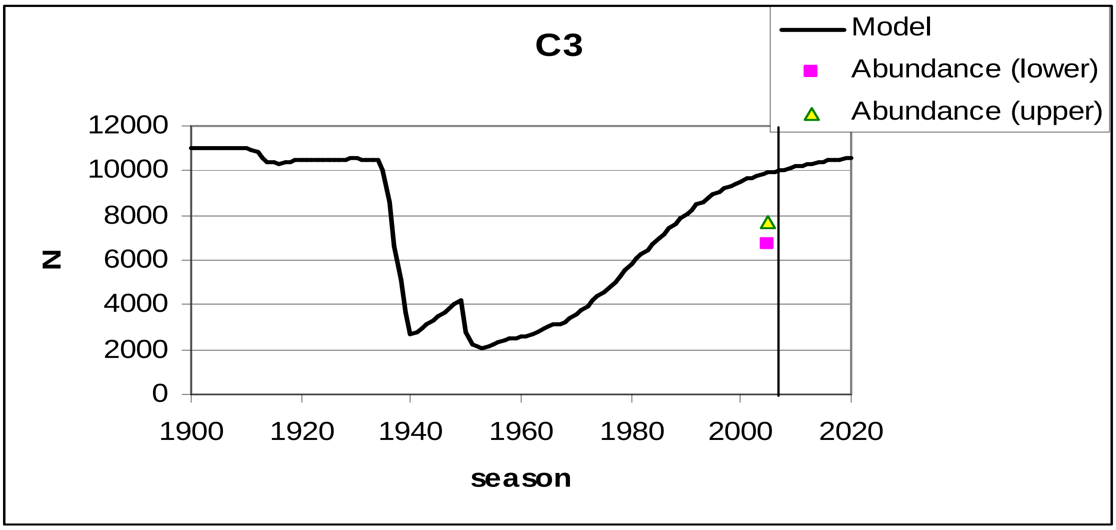


Figure 4b: Sabbatical model C3 population (N_y^{C3}) trajectories, showing the median and 95% probability envelopes. The vertical line shows 2006.

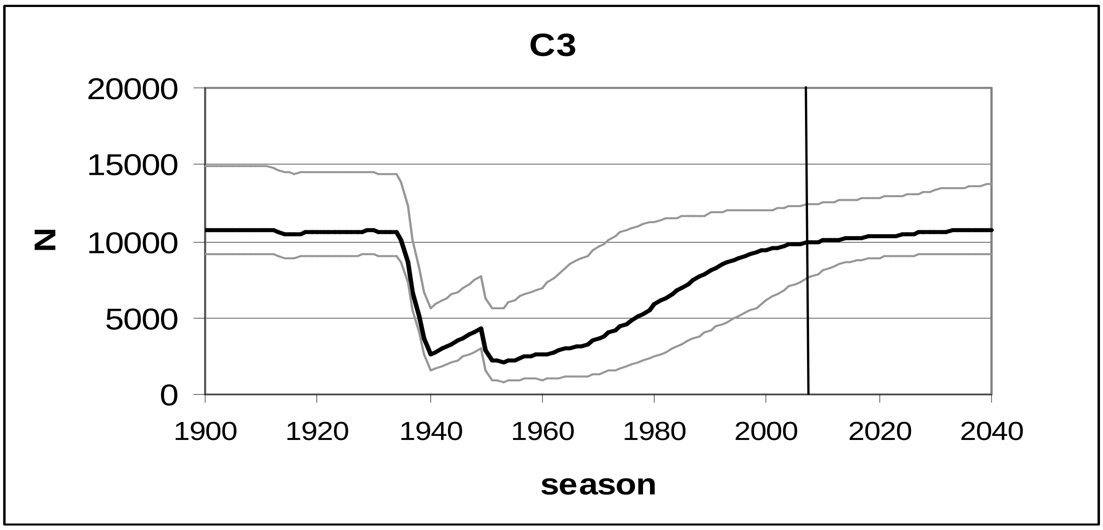


Figure 5a: Comparison between the sabbatical and resident model fits of C1 population trajectories (the Bayesian medians of N_y^{C1} are shown).

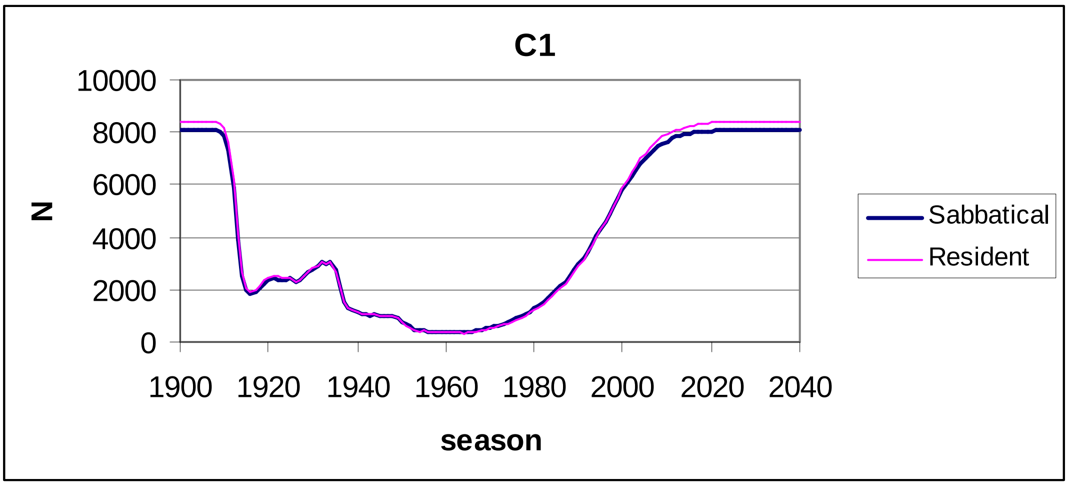


Figure 5b: Comparison between the sabbatical and resident model fits of C3 population trajectories (the Bayesian medians of N_y^{C3} are shown).