Notes on the performance stock structure hypotheses III and IV used in the RMP implementation for fin whales in EG + WI subareas

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Abstract

In 2010 a draft proposal for further research on the stock structure hypotheses for North Atlantic - fin whales was submitted to the Scientific Committee of the IWC. This document provides an addendum to that proposal based on the recommendations of the Scientific Committee. It studies the acceptability of various mixing rates and provides a maximum likelihood estimate of the mixing rate. In addition a tag-recapture experiment is simulated for stock structure hypotheses III and IV.

Introduction

At the Scientific Committee meeting in 2010 (SC62) a proposal for further research on the feasibility of management variant 2 (V2) for North - Atlantic fin whales was submitted by Iceland [Gunnlaugsson et al., 2010]. In the resulting discussion it was recommended that further work on the proposal should broadly be based on the following points:

- Use the setup from the Implementation Simulation Trials to determine the appropriate mixing, that is overlap on the feeding grounds, that would allow V2 to be considered acceptable. Use that mixing percentage to base the power analysis.

- Do further analysis along the lines described in Appendix 3 of Gunnlaugsson et al. [2010]. There tag recaptures in the WI area are analysed.

On the basis of these recommendations of the Scientific Committee further analysis of stock structure hypothesis IV (HIV) is presented here. It details of the analysis of said hypothesis and all steps are described. The document is organised as follows:

- Problem statement where HIV is contrasted to the other stock structure hypotheses.

- Analysis of mixing rates. The maximum likelihood score conditioned on the mixing rate was calculated. Furthermore maximum likelihood estimate of the mixing is obtained and the residuals of historicals tag-recaptures in the WI subarea studied.

- Simulation of a tagging experiment based on stock structure hypothesis III (HIII) and IV and compare.

The stock structure hypotheses

The basic dynamics of the models used in the IST, description of stock structure hypotheses and management variants are described in detail in Annex B of IWC [2009] and in Punt [1999]. What follows here is a recap of the relevant characteristics that are studied in this document.

In the IST for NA-fin whales the management variants were tested with seven general stock structure hypotheses. For management areas EG, WI and EI only one of these hypotheses, HIV, differs significantly from the other six. In HIV it is assumed that the fin whales in the waters around Iceland originate from three separate breeding (central) stocks with no dispersion on the breeding grounds. All other hypotheses assume that there is some degree of dispersion, for the central stocks, on the breeding grounds.

In HIV it is assumed that the central stocks, even though separate on the breeding grounds, overlap on the feeding grounds. The feeding grounds have been split up into three distinct subareas. The subareas represent the main feeding ground for each of the central stocks. While 90% of the stocks individuals migrate to their own feeding ground, regardless of where they were last year, 5% migrate to each of the areas adjacent to their native feeding ground.

In contrast HIII (and others) the central stocks, $C1$, $C2$ and $C2$, disperse on the breeding ground according the following schema:

Straying from	%
C1 to C2	5%
C2 to C3	30%

and straying the reverse direction is then defined and estimated in order to to maintain equilibrium in the stocks sizes.

The mixing matrix

One of the questions raised in last years meeting was the determination of the lowest mixing rate that would allow V2 to pass the IST. In HIV the mixing rates between sub-areas are defined by the following matrix:

$$\begin{pmatrix} \gamma & \alpha\gamma & 0 & 0 & 0 & 0 \\ 1-\gamma & \alpha\gamma & 0 & 0 & 0 & 0 \\ 0 & 1-2\alpha & \alpha & 0 & 0 & 0 \\ 0 & \alpha & 1-2\alpha & \alpha & 0 & 0 \\ 0 & 0 & \alpha & 1-2\alpha & 0 & 0 \\ 0 & 0 & 0 & \alpha & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix} \tag{1}$$

where the columns represent the breeding stocks and the rows feeding areas. In the standard HIV $\alpha = 0.05$ and γ is estimated in the IST. To answer the questions set out by the Scientific Commitee the mixing parameter α was varied between 0.05 and 0.3 for MSY rates of $1\%, 2.5\%$ and 4%. The negative log-likelihood conditioned on the mixing and MSY rate is minimized. Acceptance with respect to V2 was tested for each set of the parameters obtained from the conditioned minimisations. In addition to acceptability tests, maximum likelihood estimates (MLE) of α conditioned on the MSYR was obtained along with the corresponding 95% confidence interval.

Tagging experiment in the EG subarea

To compare HIV to HIII a tagging experiment could be devised. In Appendix 5 of SC62/RMP1 a simulation study of different stock structure hypotheses is presented. Here stock structure hypotheses III and IV were simulated for ten years. A tag release of 100 to 1500 animals is made in the EG subarea. The tagged individuals are recaptured in WI, where an annual harvest of 150 whales is made.

The stock dynamics in the simulations was the same as in the IST and used the parameter values obtained from likelihood run for HIII and HIV conditioned on MSYR of 1%. The recaptures were considered, as in the IST, to be distributed according to

$$\prod_t \frac{\Gamma(U_t + \hat{U}_t)}{\Gamma(\hat{U}_t + 1)\Gamma(U_t)} \left(\frac{\lambda}{1+\lambda}\right)^{U_t} \left(\frac{1}{1+\lambda}\right)^{\hat{U}_t}$$

that is a negative binomial distribution with a dispersion parameter U_t defined to be the predicted number of animals recaptured in subarea WI that were tagged in area EG t years ago. The detection parameter λ was set equal to 2.

There were two types of tagging experiments, a direct, e.g. discovery type,tagging experiment and genetic tag obtained from a skin sample. To compare the two hypotheses using direct tagging a negative binomial regression model for a time trend in the dispersion parameter was fitted. The resulting model was compared using a likelihood ratio test with a model with no time trend in dispersion. The the rejection interval was set such that the type I error, i.e. the rejection probability when HIV is the true stock structure, was either 5% or 10%.

In genetic tagging such as described in Skaug et al. [2001] a skin sample from a single whale can effectively tag up to 2.3 other whales, as shown in Gunnlaugsson [2011 (submitted]. For a genetic tag the number of caught tagged whales, that is effectively tagged whales, was compared with the number of pairs in the catch by calculating the ratio

$$\rho = \frac{\sum_{i \in \mathfrak{C}} T_i}{\sum_{i \in \mathfrak{C}} R_c} \tag{2}$$

where $\mathfrak{C}$ denotes the different sub stocks, C_1, C_2 and C_3, T_i is number of tagged whales of the sub stock i that are caught in the WI small area and R_i is the number of the relatedness detected in the catch which is expected to be:

$$R_i = \frac{c_i(c_i - 1)}{2n_i} \tag{3}$$

where it is assumed one genetic relation can be detected per individual, c_i is the total catch and n_i is the total size of sub stock i. The catches, c_i, are assumed to multinomially distributed according to the proportions of each stock in the WI subarea. Note that the R_i tends to be smaller as the total stock sizes are larger or there are fewer isolated breeding stocks in the WI area.

Results

Maximum likelihood

The conditioning trials were run on a cluster consisting of 42 nodes located at the University of Iceland. In all 75 trials were run, 25 different values of α and 3 MSY rates. The minimum negative log-likelihood conditioned α is shown in figure 1. The figure shows that the fit is significantly worse when assuming MSYR of 1% than for the other MSYR. The difference between MSYR of 2.5% and 4% is, however, insignificant. In table 1 the MLE of α is shown along with the confindence interval. Note that for MSYR of 1%, 5% mixing rate is rejected but not for other MSYR. According to figure 1 the likelihood value for 5%, 1% mixing and MYSR respectively may not be the true conditioned minima. In figure 2 the model residuals for historical tag-recaptures in WI subarea are shown. None of the stock structure hypotheses (I - VII) managed to fit this tag experiment well.

MSYR	Min. value	$\hat{\alpha}$	95% conf. interval
0.01	247.49	0.08	0.08 - 0.11
0.025	242.97	0.08	0.05 - 0.11
0.04	242.74	0.10	0.05 - 0.11

Table 1: MLE estimate of α, $\hat{\alpha}$, with its corresponding minimum negative log-likelihood value, 95%-confidence interval and MSYR.
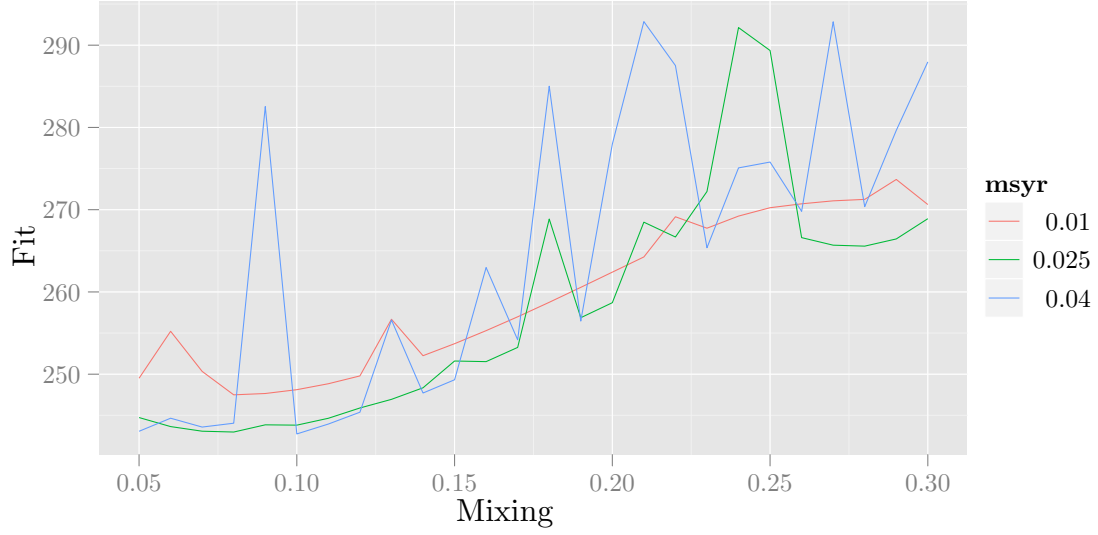
Figure 1: The log-likelihood function used in IST as a function of the mixing percentage, α. The likelihood function was minimized for each value of α. The unusual discontinuities in the log-likelihood function could be due to
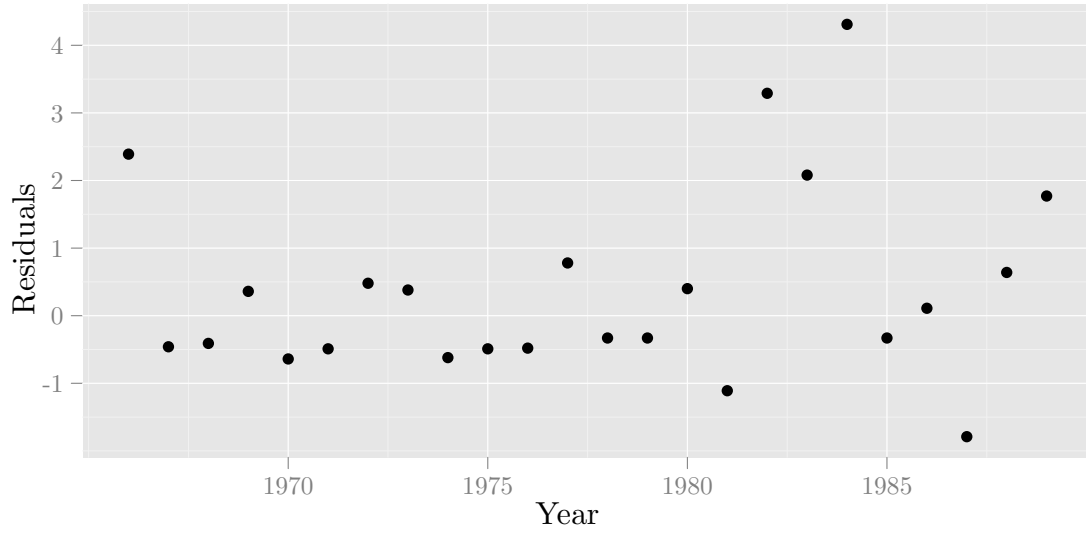

Figure 2: A residual plot for the fitted tag-recapture experiments for whales caught in WI before 1989. Note the unusually high recapture in 1982 - 1984, that are connected to whales tagged 1981 in WI and subsequently recaptured in the same area.

Optimization concerns

The results from the optimization raises questions regarding the performance of the minimizer used in the optimization. In figure 1 we see that the objective function exhibits strange discontinuities for random values of α. The minimization, which is setup in the same way as in the IST, could possibly be stuck in a local minima or the convergence critera is misspecified. In any case this needs to be studied further.

Acceptability

Tables 2, 3 and 4 show the results from the acceptability calculations. Differences in numbers and results, even though the same seed was used in the conditioning trials, could be attributed to compiler/operating system differences. Deducing from table 2 it is clear that a mixing rate of 22% is required to get borderline performance for V2 for MSYR of 1%. For all other MSYR the performance is acceptable.

Tagging

The tag-recapture experiment was simulated a 1000 times for each number of tags. In table 5 it is shown in order to get a power of 80% with a chance of Type I error of 5% a little over a thousand direct tags are needed. If, however, the requirement on type I error is loosened to 10% the the required number of tags to get a power of 80% is 700.

When studying the genetic tags the number of required tags is significantly less, as shown in table 6, or a 100 effective tags. Comparing this to the results in Appendix 5 of Gunnlaugsson et al. [2010], it is noteworthy that the power of the test is much greater in this trial than in the previous analysis. This could be due to a number of reasons, one being that the dispersion between the central stock was set up differently. Another possibility is that the stock sizes were different resulting in different estimate of R_i from equation 3.

References

International Whaling Commission. Report of the 2nd intersessional workshop of the north atlantic fin whale implementation. *J.Cetacean Res. Manage.*, 11 (Suppl. 2):587–627, June 2009.

Th. Gunnlaugsson. Relatedness between samples quantifed and an optimal criterion for match detection approximated. *J.Cetacean Res. Manage.*, 11 (Suppl. 2)(587-627), 2011 (submitted).

Th. Gunnlaugsson, G.A. Víkingsson, C. Pampoulie, and B.T. Elvarsson. Research programme on North Atlantic fin whales in relation to RMP Variant 2 and stock structure hypothesis IV. Paper submitted to the Scientific Committee of the IWC, SC/62/RMP1, 22 pp

AE Punt. A full description of the standard baleen ii model and some variants thereof. *J. Cetacean Res. Manage*, 1:267–276, 1999.

Skaug et al. Allele-sharing methods for estimation of population size. *Biometrics*, 57(3):750–756, 2001.

Table 2: The acceptability of V2 for different values of the mixing parameter.

Mixing	MSYR	Annual Catch Total Median	Annual Catch First 10 years 5%	med.	95%	Final Depletion stock 1	2	3	4	5	6	Minimum Depletion Ratio stock 1	2	3	4	5	6	Combined stock 1	2	3	4	5	6	Overall
5%	1%	61	87	87	87	A	A	U	U	B	A	A	A	U	A	A	A	A	A	U	A	A	A	U
6%	1%	61	87	87	87	A	A	U	U	B	A	A	A	U	A	A	A	A	A	U	A	A	A	U
7%	1%	61	87	87	87	A	A	U	U	B	A	A	A	U	A	A	A	A	A	U	A	A	A	U
8%	1%	61	87	87	87	A	A	U	U	B	A	A	A	U	A	A	A	A	A	U	A	A	A	U
9%	1%	61	87	87	87	A	A	U	U	U	A	A	A	U	A	A	A	A	A	U	A	A	A	U
10%	1%	61	87	87	87	A	A	U	U	U	A	A	A	U	A	A	A	A	A	U	A	A	A	U
11%	1%	63	87	87	87	A	A	U	U	B	A	A	A	U	A	A	A	A	A	U	A	A	A	U
12%	1%	63	87	87	87	A	A	U	U	B	A	A	A	U	A	A	A	A	A	U	A	A	A	U
13%	1%	70	87	87	87	A	A	U	U	U	A	A	A	U	A	A	A	A	A	U	A	A	A	U
14%	1%	64	87	87	87	A	A	U	U	U	A	A	A	U	B	A	A	A	A	U	B	A	A	U
15%	1%	65	87	87	87	A	A	U	U	U	A	A	A	U	B	A	A	A	A	U	B	A	A	U
16%	1%	66	87	87	87	A	A	U	U	U	A	A	A	U	B	A	A	A	A	U	B	A	A	U
17%	1%	66	87	87	87	A	A	U	U	U	A	A	A	U	B	A	A	A	A	U	B	A	A	U
18%	1%	67	87	87	87	A	A	U	U	U	A	A	A	U	B	A	A	A	A	U	B	A	A	U
19%	1%	67	87	87	87	A	A	U	U	B	A	A	A	U	B	A	A	A	A	U	B	A	A	U
20%	1%	69	87	87	87	A	A	U	U	B	A	A	A	U	B	A	A	A	A	U	B	A	A	U
21%	1%	69	87	87	87	A	A	U	U	B	A	A	A	U	B	A	A	A	A	U	B	A	A	U
22%	1%	71	87	87	87	A	A	U	U	U	A	A	A	B	B	A	A	A	A	B	B	A	A	B
23%	1%	71	87	87	87	A	A	U	U	B	A	A	A	B	B	A	A	A	A	B	B	A	A	B
24%	1%	68	87	87	87	A	A	U	U	U	A	A	A	B	B	A	A	A	A	B	B	A	A	B
25%	1%	71	87	87	87	A	A	U	U	B	A	A	A	B	B	A	A	A	A	B	B	A	A	B
26%	1%	71	87	87	87	A	A	U	U	B	A	A	A	B	B	A	A	A	A	B	B	A	A	B
27%	1%	72	87	87	87	A	A	U	U	U	A	A	A	B	B	A	A	A	A	B	B	A	A	B
28%	1%	74	87	87	87	A	A	B	U	B	A	A	A	B	B	A	A	A	A	B	B	A	A	B
29%	1%	71	87	87	87	A	A	B	U	B	A	A	A	B	B	A	A	A	A	B	B	A	A	B
30%	1%	73	87	87	87	A	A	B	U	B	A	A	A	B	B	A	A	A	A	B	B	A	A	B

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Table 3: The acceptability of V2 for different values of the mixing parameter.

Mixing	MSYR	Annual Catch Total Median	First 10 years 5%	First 10 years med.	First 10 years 95%	Final Depletion stock 1	2	3	4	5	6	Minimum Depletion Ratio stock 1	2	3	4	5	6	Combined stock 1	2	3	4	5	6	Overall
5%	2.5%	78	87	87	87	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A
6%	2.5%	88	87	87	87	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A
7%	2.5%	90	87	87	87	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A
8%	2.5%	90	87	87	87	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A
9%	2.5%	89	87	87	87	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A
10%	2.5%	89	87	87	87	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A
11%	2.5%	88	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
12%	2.5%	89	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
13%	2.5%	89	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
14%	2.5%	90	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
15%	2.5%	90	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
16%	2.5%	91	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
17%	2.5%	91	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
18%	2.5%	91	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
19%	2.5%	91	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
20%	2.5%	92	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
21%	2.5%	91	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
22%	2.5%	92	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
23%	2.5%	87	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
24%	2.5%	93	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
25%	2.5%	90	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
26%	2.5%	100	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
27%	2.5%	105	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
28%	2.5%	103	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
29%	2.5%	102	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
30%	2.5%	98	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A

Table 4: The acceptability of V2 for different values of the mixing parameter.

Mixing	MSYR	Annual Catch				Final Depletion						Minimum Depletion Ratio						Combined						Overall
		Total	First 10 years			stock						stock						stock						
		Median	5%	med.	95%	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	
5%	4%	87	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
6%	4%	78	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
7%	4%	86	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
8%	4%	87	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
9%	4%	122	87	87	87	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A
10%	4%	84	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
11%	4%	85	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
12%	4%	84	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
13%	4%	71	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
14%	4%	84	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
15%	4%	84	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
16%	4%	80	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
17%	4%	84	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
18%	4%	85	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
19%	4%	82	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
20%	4%	73	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
21%	4%	83	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
22%	4%	70	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
23%	4%	97	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
24%	4%	103	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
25%	4%	105	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
26%	4%	100	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
27%	4%	96	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
28%	4%	100	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A
29%	4%	107	87	87	87	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
30%	4%	106	87	87	87	A	A	A	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A

Table 5: The probability of rejecting HIV conditioned on the stock hypytheses using a direct tag-recapture experiment. The rejection interval was chosen such that the probability of type I error was either 5% or 10%.

Stock-Hypo.	Number of tags							
	100	200	300	400	500	600	700	800
HIV	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
HIII	0.47	0.56	0.62	0.66	0.74	0.74	0.81	0.85
HIV	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
HIII	0.40	0.48	0.49	0.54	0.64	0.62	0.72	0.75

	Number of tags						
	900	1000	1100	1200	1300	1400	1500
HIV	0.10	0.10	0.10	0.10	0.10	0.10	0.10
HIII	0.86	0.88	0.92	0.94	0.93	0.94	0.96
HIV	0.05	0.05	0.05	0.05	0.05	0.05	0.05
HIII	0.75	0.79	0.86	0.86	0.82	0.88	0.92

Table 6: The probability of rejecting HIV conditioned on the stock hypytheses using a genetic tag-recapture experiment. The rejection interval was chosen such that the probability of type I error was 5%.

Stock hypo.	Effective number of tags				
	100	200	300	400	500
HIV	0.05	0.05	0.05	0.05	0.05
HIII	0.94	0.99	1.00	1.00	1.00