

## PROGRESS REPORT ON LENGTH BASED METHODS USING THE 4 DATA SETS DERIVED AT 1993 ICCAT MEETING

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### Introduction

At the 1993 ICCAT meeting in Saint Andrews, Canada, 4 data sets were synthesized to act as test data for length based VPAs. The 'best' set was denoted as HCGM which stands for high contrast, good means. High contrast refers to a large change in fishing mortality over the 15 year simulation and good means have better separation than the bad mean data. In the following study only the high contrast data are investigated. None of the methods proposed during the 1993 meeting performed very well and it was hoped that some progress could be made with these data sets.

Mohn (1993) looked at three methods performance on a simple data set. The methods were cohort slicing, Kimura-Chikuni and one called SP-Key. Because of its poor performance on the simple data the Kimura-Chikuni (1987) method has not been pursued further. Although SP-Key performed well with the data in Mohn (1993), it had trouble with the data produced at the workshop. Recent examinations of the residual patterns from SP-Key showed that the errors were along cohort rather than year or age effects. It was further observed that the definition of the model which was used did not have the power to directly estimate yearclass strengths. A new model was introduced into the SP-Key iterative method which focuses on yearclass strengths. The new model performs much better using the same information. Robustness of the new model to noise has not yet been investigated.

### Methods

Growth template estimated from means and SDs on template data supplied with HCGM and HCBM. SP-Key separates the conversion of CAL to CAA and the SPA functions inside a single iteration. The core of the approach is to estimate an age length key for each year from the growth template. See Mohn (1993) has more details of the method. The input data are catch at length and an abundance index, the size disaggregated catch rate. To start the process an initial conversion to catch at age is done by Cohort Slicing. The resultant

estimates of catches at age are converted into numbers at age by a version of a catch model and an NLLS similar to ADAPT, but any SPA could in theory be used. In the old version, the numbers at age are then used to weight the growth template to form an ALK for each year. In the new version a second optimization is performed. The cohort strengths are adjusted by multiplying the estimate of recruitment at age 1 by a scaling factor and optimising in the Marquardt to the same abundance data as in the SPA step above before applying to the growth template. These numbers at age are only used to weight the ALKs. Then these ALKs convert the catches at length into new estimates of catch at age and the model iterates until convergence. The process stops when the average change in a catch at age is less than 2% or after 10 iterations.

The model is tuned against the catch rate at age for ages 1 - 4. Ages 1 - 6 in the terminal year are estimated in the NLLS and the rest of the survivors of the cohorts are estimated using the model assumption that the fish are fully recruited after age 3.

A couple of technical changes have also been incorporated. Using a suggestion from V. Restrepo, the catch at length data can be truncated to exclude the very large fish that are difficult to assign to ages. In the following the entire size frequencies are used (100 - 350 cm in 5 cm groups) and in some cases the data are truncated to 100 - 300 cm. Another minor change is that the calibration coefficients are now calculated algebraically instead of being estimated in the NLLS.

The performance at each iteration is compared to the true catch and numbers at age data. Three indices are presented, the sum square residual of the estimated catch at age, the sum square residual of the numbers at age and the residual sum of squares from the tuning.

## Results.

Table 1 contains the results for four different trials, the high contrast good mean and bad mean data using the entire length frequencies and truncating to 300 cm. The first iteration in each case is the sliced data. In Table 1.a the method converged after 6 iterations. The sum square residuals for catch and numbers at age are about 5 times smaller after the iteration process than the sliced data. Most of the improvement takes place however after 2 iterations. Figure 1 shows the true recruitment, the sliced estimate and the SP-Key estimates in the upper plot. The lower plot contains the average F for ages 3-8 for both methods and the true results. SP-Key estimates the recruitment pulses very well but over estimates the other years by about 40 %. This over estimation is reflected in the lower plot where the average F's are consistently underestimated.

The truncated HCGM data results are in Table 1.b and Figure 2. The 2% convergence in successive catch at age estimates was never attained and the method converged towards the true catch and population values up to step 5 or 6 and then started to slowly diverge. The RSS followed the same pattern and perhaps a second criteria of converge should be incorporated into the algorithm based on the RSS. Figure 2 shows a much better fit to the non-peak recruitments and to the average F's than Figure 1, but the peaks are not as well estimated.

Tables 1.c and d are for the more difficult HCBM data and show similar patterns although all indices of fit are worse and the improvement of SP-Key over slicing is closer to a factor of 3 than the factor of 5 seen above.

## Discussion.

This version of the SP-Key method shows significant improvements over cohort slicing when applied to the ICCAT simulated data. The second optimization which has been added to the algorithm was introduced after an examination of the pattern of residuals which showed a strongly diagonal. The previous model could not correct for yearclass strength errors. One model that was formulated just to address the diagonal residuals, was tried and discarded. It was parameterized so that the survivors from every yearclass were estimated.

Many other models could, and should, be tried within the SP-Key iterative structure. The method is still being developed and would greatly benefit from application to other data, collaboration with other investigators, and usage in other laboratories.

## Bibliography.

- Kimura, D.K. and S. Chikuni. 1987. Mixtures of empirical distributions: an iterative application of the age-length key. *Biometrics* 43: 25-35.
- Mohn, R. 1993. A comparison of three methods to convert catch at length data into catch at age. ICCAT SCRS/93/56

Table 1. Summary of errors during iterations. Iteration 1 is sliced catch and research data. If the procedure converged to the 2% tolerance in catch at age, iterations were terminated.

### 1.a Full HCGM

Iteration #	SSR Catch	SSR Numbers	RSS - NLLS
1	968	347728	9.87
2	279	151263	4.46
3	179	85948	2.42
4	159	75908	1.86
5	157	76070	1.70
6	157	75153	1.64
7			
8			
9			
10			

### 1.b. HCGM truncated to 300 cm

Iteration #	SSR Catch	SSR Numbers	RSS - NLLS
1	909	201086	3.47
2	325	96131	2.04
3	233	67060	1.69
4	204	55723	1.49
5	198	51458	1.40
6	200	50365	1.38
7	205	50523	1.40
8	210	51047	1.42
9	216	51599	1.44
10	220	52084	1.46

### 1.d Full HCBM

Iteration #	SSR Catch	SSR Numbers	RSS - NLLS
1	2057	1165283	18.43
2	934	356652	6.31
3	794	251005	3.41
4	765	235465	2.67
5	761	232354	2.49
6	761	232622	2.45
7	762	233020	2.44
8			
9			
10			

### 1.d HCBM truncated to 300 cm

Iteration #	SSR Catch	SSR Numbers	RSS - NLLS
1	1849	290807	4.14
2	1016	162608	2.06
3	900	132827	1.70
4	849	120824	1.50
5	826	115503	1.41
6	816	110792	1.38
7	813	110195	1.39
8	817	111146	1.45
9	823	109679	1.54
10	829	111432	1.64

Figure 1. Recruit estimates and average Fs from HCGM data using slicing and key methods.

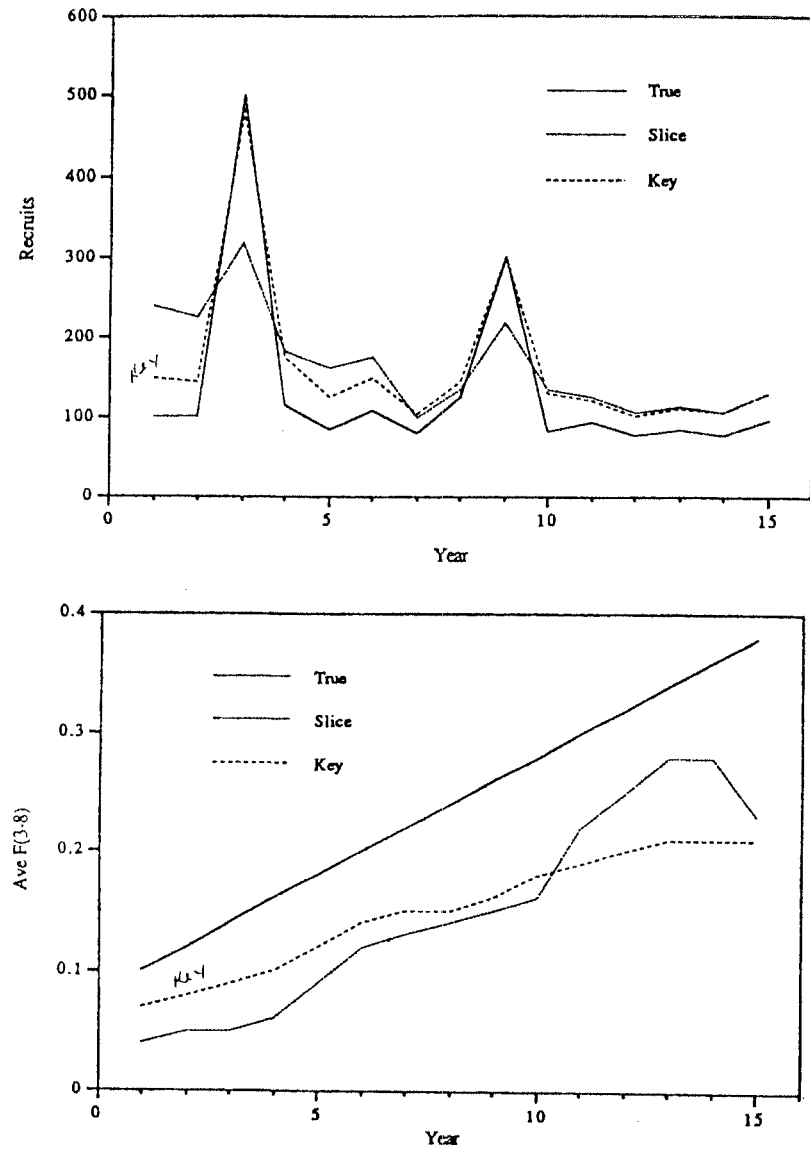


Figure 2. HCGM with data truncated at 300 cm.

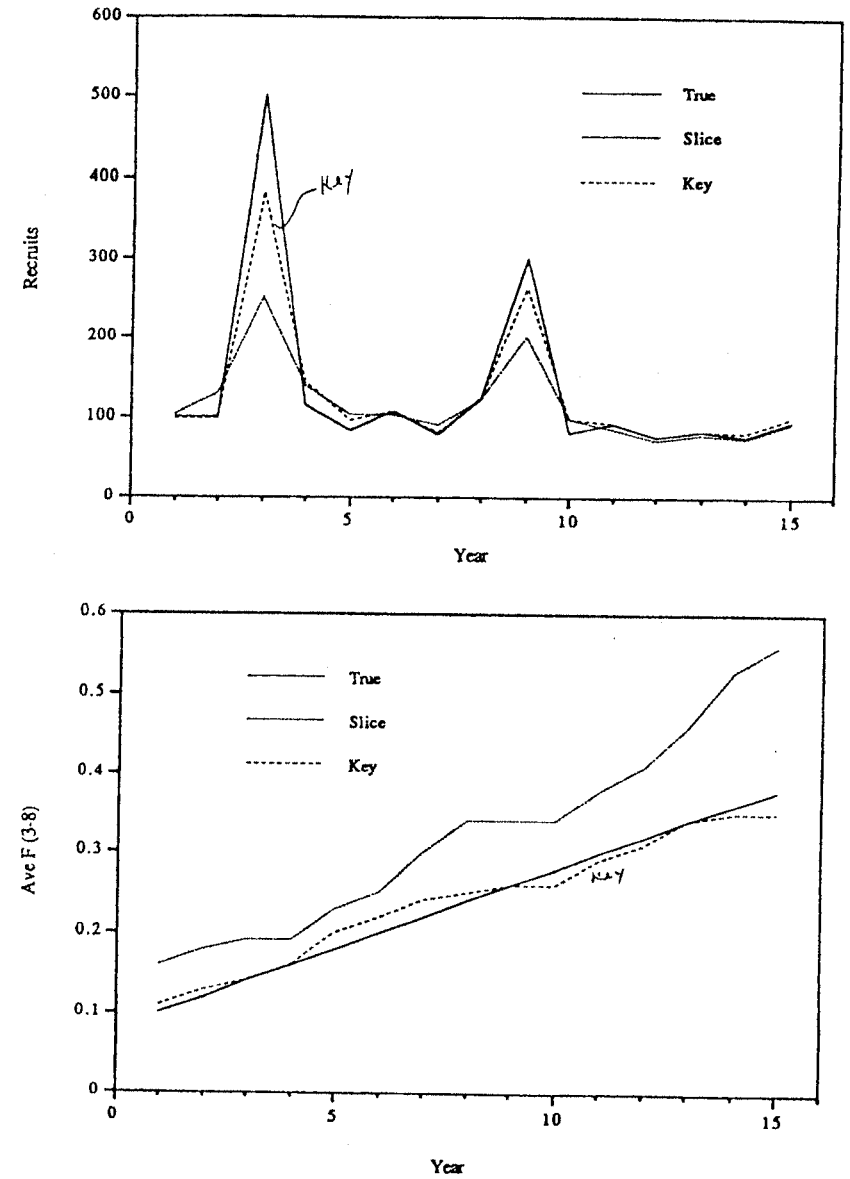


Figure 3. Recruit estimates and average Fs from HCBM data using slicing and key methods.

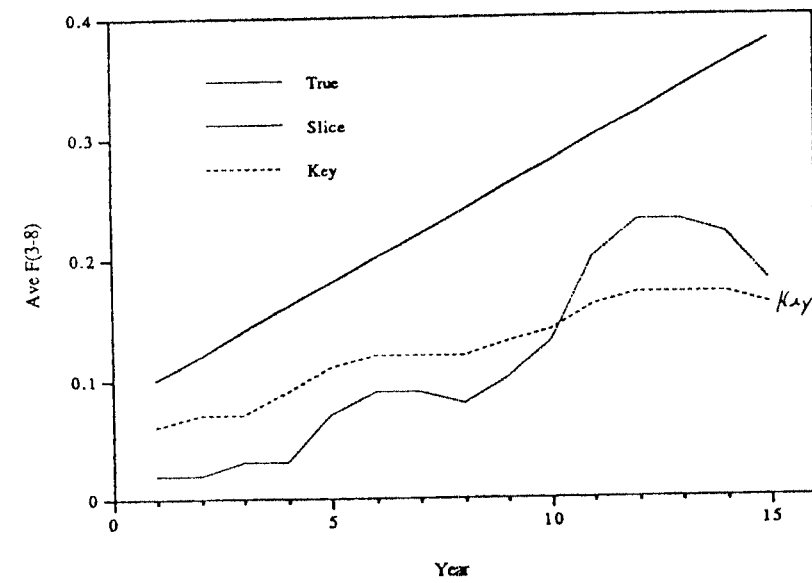
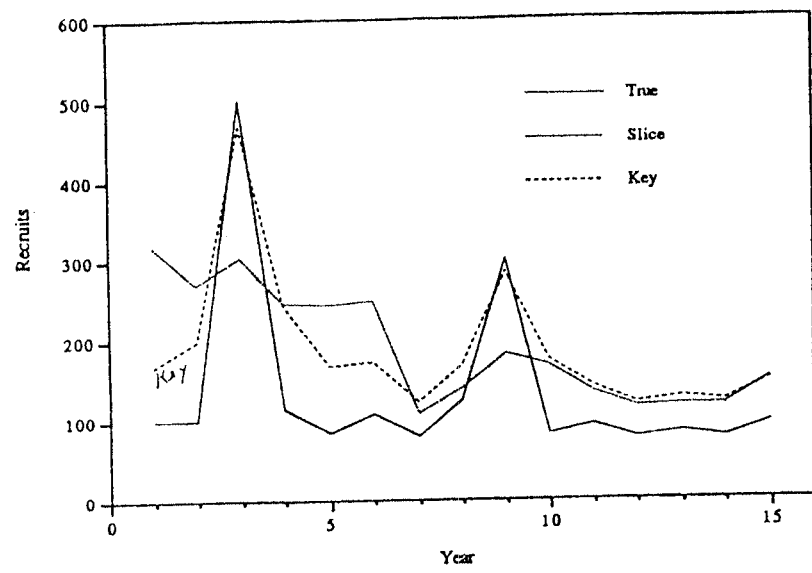


Figure 4. Recruit estimates and average Fs from HCBM truncated at 300 cm.

