Northwest Atlantic Fisheries Organization

Length Based Population Analysis of Sept-Iles Shrimp (Gulf of St. Lawrence)

by

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INTRODUCTION

Our observations of commercial marine stocks are generally length based, principally data from research surveys and commercial fisheries sampling. The models used in population analysis and assessment process are usually age structured. Concepts such as mortality rates and growth coefficients are time (or age) based. Age-length keys and growth models are used to convert length to age. In some cases, and frequently with invertebrate species, age-length keys are difficult or impossible to obtain. We present in this paper, a method which allows the age structured analysis of length based data by constructing age distributions from size distributions and a knowledge of the growth. We call the analysis of these constructed age distributions, the synthetic age population analysis (SAPA).

A model had to be developed to deal simultaneously with length and age distributions of a population. This was done by expanding the concept of partial recruitment from an age basis to an age-length basis. The age based partial recruitment distributes the fishing effort applied on a stock over the ages recruited. Traditionally, the partial recruitment vector is normalized so that its largest value(s) is one, so called fully recruited age(s). The age-length based partial recruitment (PRAL) is now a matrix whose dimensions are the number of age classes recruited by the number of size classes recruited. The distribution of the fishing mortality can be entirely along the age axis, as would be the case for age-structured data, and it may be along the size axis or it may change along both dimensions. The strict size defined partial recruitment would apply to a fishery that was size limited or mesh performance defined only. Because size and age are interrelated, even a strictly age or size defined partial recruitment will, of course, affect both dimensions. Thus, the PRAL is seen to partition the probability of capture for a given age over the size classes of the stock.

When the age determination of samples is practical, the interdependence of size and age are usually defined by an age-length key. The age is determined from a number of samples, either research or commercial, which are representative of the stock. It is applied to length distributions to convert them to representative age structures. The representative requirement is important due to varying year-class strengths which require new keys for each fishing season. In the absence of annual age-length keys, one is faced with a chicken-egg problem. If you knew the age distribution, you could update last year age-length key; if you had an updated key, you could determine the age distribution. Kimura and Chikuni (1987) approached this problem with an iterative technique. We found that the iterative technique had very poor convergence characteristics.

Jones (1974) presented a length based cohort analysis which converts length to age by incorporating a growth model. His method is not designed to follow cohorts and we found it very unreliable when applied to modelled data with variable recruitment. Another technique known as 'cohort slicing' has been used to convert length data to an age basis. This method slices the length distribution at points which separate age classes, which may have been defined by modal analysis or some other means. This method will follow cohorts to a degree and performs much better than Jones's method. However cohort slicing does not deal well with overlapping modes especially when adjacent year-classes are disparate in abundance. Another alternative is to apply an approximate age-length key which is not corrected for changes in year-class strength. Westreim and Ricker (1978) explored the errors in using such an approximation.

A program for simultaneous length and age population analysis was developed and applied to scallop data (Mohn MS 1989). This technique has been refined and will now be used on Sept-Iles (Gulf of St.Lawrence) shrimp data. Figure 1 shows the location of the traditional fishery. Landings and commercial sampling from this fishery are available for the period 1982-1988. These landings and their length distributions were combined with research survey results for 1982, 1984, 1985, 1987 and 1988 to form the input data. The other required inputs are natural mortality and template of the size distributions at each age. The program is a model which runs in the ADAPT (Gavaris 1988) framework.

MATERIALS AND METHODS

Commercial Data.

Shrimp from port sampling were measured to the nearest 0.1 mm (carapace length) and size frequencies were then aggregated into 1 mm groupings from 8 to 32 mm (Figure 2). These were transformed into numbers caught at each length by converting the length classes to weight classes via the allometric relation (Portelance et Fréchette, 1983):

$$W = .00085 \, L^{2.3048}$$

The mean weight of animals for each year was divided into the total catch to give the total number of animals caught which were then distributed over the size frequencies. As the mean weights are in grams and the landings in tons, the numbers in the catch matrix are in millions (Table 1).

Research Data.

Five research surveys were conducted over the period from 1982 to 1988, with 1983 and 1986 not being available. As was done for the commercial data, the size frequencies from 8 to 32 mm were re-scaled to correspond to survey biomass indices (Table 2, Figure 3). The 1982 survey was conducted with a Yankee 36 shrimp trawl and was corrected by a factor of 1.5 to make it comparable to the others which used a Western 2A. The results were multiplied by 1000 so that they would have a similar scale to the catch data. But it must be noted that unlike the catch data, these values are in arbitrary units.

Length at age template.

Modes in the length frequencies distributions (LFD's) were subjectively defined at six sizes. The male modes were at 12, 17 and 20.5 mm. The fourth mode at 23.5 mm contained either males or primiparous females. The last two modes of multiparous females were centered at 26 and 27 mm. It was assumed that all the modes had standard deviations of 1 mm.. The resultant template is given in Table 3. The age-length template has two uses: first, to act as a basis for an age-length key to convert catch at length into catch at age in the cohort slicing analysis, and second, in the simultaneous length-age cohort program, to manipulate the synthetic age population. A test run was also carried out with an age-length template having standard deviations of 2mm.

Program overview.

Both cohort slicing and the synthetic age population analyses are based on the cohort equation which finds the numbers at age in year y and age a from the catch of that year and age and the numbers surviving at the next oldest

age (Pope, 1972). In the cohort slicing analysis, the catch at length data are converted into approximate catch at age by slicing the 7 years catch distributions (Figure 4). The catch at age is then converted to numbers and fishing mortality at age by using traditional cohort analysis. Also, as with most cohort analyses, estimate of natural mortality and starting estimates of the partial recruitment and exploitation rates on the oldest ages of each cohort were needed. The cohort analysis was not extensively tuned as is usually done because the output was only used to derive starting numbers for SAPA.

The synthetic age population analysis uses a non-linear least squares (nlls) technique to optimally fit the population model to the data (Figure 5). The parameters to be fit are the starting F (F last year) value which is used internally in SAPA, and a series of research catchability coefficients (q's) which link the population abundance estimated from the catch data to the research abundance estimates. The version of the model reported herein requires four catchablilities (q) to be fit, one each for ages 2, 3 and 4 and a single value for ages 5, 6 and 7 which are all assumed to be fully recruited to the research gear. A starting selectivity pattern is also required for the most recent year. A terminal F (F oldest ages) pattern is required as well as a value of the natural mortality. These values (M, selectivity, F oldest ages) are fixed while the parameters (q, F last year) are being determined.

Instead of working with single numbers at each age and year, the simultaneous analysis works on length distributions at each age and year. The catch at length is distributed into age classes using the age-length key constructed from the age-length template and an estimate of the total numbers of animals at each age and year. The catch at age and length is then passed through the simultaneous cohort equation which produces new estimates of the numbers at age and length. These are then used to weight the age-length template producing a new age-length key and the process is repeated. After the process converges and the parameters have been optimally fit to the data, the assumed starting selectivity or terminal F may be updated and the process repeated.

RESULTS

Table 4 contains the catch-, numbers-, and F-at-age from the preliminary cohort slicing analysis. The catch-at-age is the result of slicing the length distributions in Table 1 at the mid-points of the assumed age modes and is in units of millions of animals. The cohort analysis was begun using a starting F (F last year) value of 0.5 as well as a terminal F (F oldest ages) of 0.5. The natural mortality was assumed to be 0.3 and the selectivity values were 0.05, 0.1, 0.3, 0.8, 1.0 and 1.0. This analysis suggests a strong recruitment in recent years, especially the two year olds in 1987.

The trial run of the cohort slicing analysis could have been used as an input for the SAPA. The usual practice derived from simulated data is to initialize the synthetic age population analysis from time slicing output. However, for the shrimp data, the SAPA was initialized by setting all ages and lengths to 1 instead of using the output from the cohort slicing analysis. This was done because the homogeneous synthetic population had a better fit to the data than the synthetic population derived from the cohort slicing analysis. It was later discovered that this was due to setting the initial estimates of the research catchabilities (q's) too high. The initial estimate of the synthetic population does not significantly affect the final values, but it does affect the convergence time. The same terminal F's and selectivity pattern were carried over. The initial estimates for the q's and starting F's to be fit in SAPA were 0.8 and 0.5 respectively.

After the optimization program converged, the results were used to estimate a new selectivity pattern and terminal F's. This was done by averaging the 1986 and 1987 F-at-age to produce a new selectivity and by averaging (weighted by population size estimates) the F-at-age from ages 5 and 6 to produce a new terminal F pattern. These values are 0.02, 0.48, 0.40, 0.73, 0.81 and 1.0 for the selectivity and 0.31, 0.29, 0.31, 0.43, 0.45, 0.78 and 0.63 for the terminal F. The non-linear least squares routine was rerun and the final results are shown in Table 5. The research catchabilities are 0.047, 0.172, 0.289, for ages 2, 3 and 4, and 0.290 for ages 5, 6 and 7 which are constrained by the model to be equal. These results suggest that the research gear is about one sixth as efficient at capturing 2 year olds and one half at 3 year olds compared to the older animals. These results show a relatively strong 1984 year class and relatively weak (less than half the size) 1986 year class.

A second set of runs were made using an age-length template which had twice the standard deviation of lengths at age compared to Table 3. The results tended to make strong year classes stronger and reduce or remove weaker year classes. For example, the 1986 recruiting year class was entirely removed instead of the 1161 million animals given in Table 5.

DISCUSSION

A new method has been presented for the population analysis of length based data. It uses an age-length template from which trial age-length keys and a synthetic age-length population are constructed. The method requires a non-linear estimation of parameters which in the present version link the research abundance-at-length to the synthetic population. This technique is essentially asking what population can be constructed which best fits the observed catch and survey length distributions and the age-length template, which we call the synthetic age population.

Care has been made to distinguish between the age-length template and an age-length key. The former is the pattern of sizes for each age. The age-length key has the same distributions but they are weighted by the relative year-class strengths so that the key will be representative of the population. In this study, normal distributions were used but any distribution might have been tried. For example, one with shorter tails might be more realistic. We fixed a single template for the 7 year time period of the data. This is not required and if it were known or believed that the growth of a population were changing in time or in a density dependent manner the SAPA program can accommodate this.

The number of parameters that are fit in SAPA have been kept to minimum. One reason is that the time for the program to converge depends on the number of parameters and the present program is already somewhat large. Applications on microcomputers may take hours to converge. Also, in simulation studies, models with a larger number of parameters had a greater tendency to converge before true values were reached. Another technical note is that the tuning by adjusting the terminal F pattern and the selectivity are not automatic and require input from the scientist. This is somewhat a matter of personal preference and versions exist where this is done automatically. Again the speed of convergence is a factor.

The final results of the SAPA are seen to vary considerably from the cohort slicing results. If one compares the catch-at-age estimates for ages 2 and 3, it is seen that the SAPA estimates suggest relatively more three year olds than the cohort slicing estimates. This is because the cohort slicing cannot distinguish between small three olds and large two year olds of the same size. The SAPA apportions these animals to best fit the overall distributions through out the life of the cohort. Cohort slicing estimates that the 1985 year class (12.4 billion of animals in 1987) is the largest in the 7 year period with the 1986 year class being second. The SAPA estimates show these two year classes to be modest and poor respectively (viz, 2342 and 1161 million compared to an average recruitment of 2030 million). Our results also suggest that fishing mortality has shown an increasing trend over the 7 year period. Catch and effort data from this fishery showed that standardized fishing effort had increased since 1982, from 52,000 hours to 76,300 hours in 1988 (Savard, 1989).

The SAPA procedure is still under development. It has been checked with simulated data but needs to be applied to more fisheries data to test its usefulness. It is versatile and should be applicable to a wide range of data.

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Table 1.   Catch-at-length data in 1 mm groupings in millions of animals.

	1982	1983	1984	1985	1986	1987	1988
8	.30	.13	.00	.12	.53	.00	.09
9	.59	.00	.00	.42	1.87	.15	.00
10	2.90	1.23	.23	.97	2.07	2.45	.18
11	3.50	.85	.62	1.95	1.94	1.61	.57
12	9.49	1.69	2.09	1.40	3.54	4.66	2.20
13	15.24	7.80	6.67	4.92	11.68	15.13	12.50
14	22.30	22.72	15.91	12.17	30.89	30.20	38.16
15	30.60	51.22	30.62	18.62	65.05	55.57	80.10
16	49.22	96.00	48.11	25.01	93.20	75.83	110.85
17	62.04	121.10	47.42	37.61	65.40	82.48	93.67
18	52.31	91.30	31.93	57.50	28.96	59.01	76.70
19	40.38	33.63	43.86	77.15	19.01	41.90	86.30
20	29.25	21.22	57.68	57.50	17.96	31.19	89.66
21	27.40	19.09	50.72	29.21	20.21	31.73	74.20
22	22.42	21.30	30.57	39.12	33.23	30.03	50.66
23	28.29	17.73	23.77	46.49	47.91	41.12	46.56
24	44.13	17.21	26.49	49.89	65.19	63.37	47.00
25	57.30	28.94	28.70	51.23	67.39	69.02	48.70
26	53.02	44.21	34.53	38.64	51.52	67.42	47.70
27	30.42	33.50	41.31	32.25	21.81	41.74	30.81
28	9.49	14.02	31.87	19.83	11.08	14.53	12.50
29	2.38	3.19	10.80	5.48	5.14	4.13	3.73
30	.00	.38	1.81	.91	.93	.85	1.33
31	.00	.00	.29	.00	.67	.23	.18

Table 2. Abundance-at-length data in 1 mm groupings.

	1982	1983	1984	1985	1986	1987	1988
8	.00	-	.00	.09	-	.67	.00
9	.00	-	.16	.17	-	5.04	.94
10	1.78	-	1.18	1.22	-	18.03	3.16
11	18.37	-	3.08	5.83	-	22.18	2.46
12	76.57	-	3.40	18.88	-	11.43	.70
13	133.58	-	3.16	27.32	-	9.86	3.74
14	84.15	-	14.93	18.88	-	27.67	24.92
15	36.86	-	48.34	24.80	-	64.07	68.09
16	39.23	-	81.60	37.94	-	104.95	114.65
17	63.17	-	77.73	42.81	-	127.47	112.43
18	73.72	-	46.84	50.91	-	116.83	81.89
19	73.25	-	46.13	78.49	-	82.22	87.27
20	50.37	-	70.07	112.34	-	67.32	126.35
21	53.22	-	83.89	67.61	-	74.15	121.20
22	45.87	-	56.80	50.30	-	65.86	72.65
23	48.48	-	34.12	61.26	-	60.26	61.42
24	51.08	-	36.73	68.40	-	63.40	81.77
25	70.17	-	46.05	77.62	-	74.26	85.17
26	112.95	-	46.84	58.39	-	68.55	63.52
27	96.36	-	46.13	35.33	-	37.52	39.78
28	42.43	-	31.12	21.06	-	14.23	14.51
29	11.62	-	9.95	8.61	-	3.36	3.16
30	1.42	-	1.66	1.74	-	.56	.23
31	.36	-	.08	.00	-	.11	.00

Table 3. Age-length template used to construct synthetic age population.
Lengths are carapace lengths in mm. Only values greater than .001
are printed, but full precision is used in calculations.

Age Length	2	3	4	5	6	7
8	.001	-	-	-	-	-
9	.021	-	-	-	-	-
10	.136	-	-	-	-	-
11	.341	-	-	-	-	-
12	.341	-	-	-	-	-
13	.136	.001	-	-	-	-
14	.021	.021	-	-	-	-
15	.001	.136	-	-	-	-
16	-	.341	-	-	-	-
17	-	.341	.006	-	-	-
18	-	.136	.061	-	-	-
19	-	.021	.242	-	-	-
20	-	.001	.383	.006	-	-
21	-	-	.242	.061	-	-
22	-	-	.061	.242	.001	-
23	-	-	.006	.383	.021	.001
24	-	-	-	.242	.136	.021
25	-	-	-	.061	.341	.136
26	-	-	-	.006	.341	.341
27	-	-	-	-	.136	.341
28	-	-	-	-	.021	.136
29	-	-	-	-	.001	.021
30	-	-	-	-	-	.001
31	-	-	-	-	-	-

Table 4. Output from the cohort slicing analysis.

	1982	1983	1984	1985	1986	1987	1988
Catch-at-age							
2	70	60	41	31	85	82	94
3	209	359	176	187	234	277	386
4	89	70	150	145	76	103	236
5	115	57	72	135	164	156	130
6	83	68	62	68	79	106	75
7	27	34	65	42	29	41	33
Numbers-at-age							
2	2181	1959	1675	1735	4094	12446	4392
3	975	1556	1399	1206	1258	2960	9150
4	627	542	844	886	732	731	1955
5	587	388	341	496	531	477	452
6	231	336	239	191	251	253	219
7	79	100	190	123	83	118	96
Fishing mortality-at-age							
2	.04	.04	.03	.02	.02	.01	.03
3	.29	.31	.16	.20	.24	.11	.05
4	.18	.16	.23	.21	.13	.18	.15
5	.26	.19	.28	.38	.44	.48	.40
6	.54	.27	.36	.53	.46	.66	.50
7	.50	.50	.50	.50	.50	.50	.50

Table 5. Output from the synthetic age population analysis.

	1982	1983	1984	1985	1986	1987	1988
Catch-at-age							
2	32	13	9	10	25	24.	15
3	215	366	177	140	277	308	391
4	91	91	141	182	59	98	271
5	113	48	86	116	150	122	126
6	66	93	47	97	83	151	82
7	77	38	105	64	73	61	69
Numbers-at-age							
2	2140	2437	1482	1613	3036	2342	1161
3	1619	1558	1794	1090	1186	2228	1715
4	799	1015	839	1176	687	640	1385
5	1104	514	674	500	715	459	390
6	305	721	339	425	271	400	235
7	333	170	454	211	231	129	167
Fishing mortality-at-age							
2	.02	.01	.01	.01	.01	.01	.01
3	.17	.32	.12	.16	.32	.18	.30
4	.14	.11	.22	.20	.10	.20	.26
5	.13	.12	.16	.31	.28	.37	.46
6	.29	.16	.17	.31	.44	.57	.51
7	.31	.29	.31	.43	.45	.78	.63
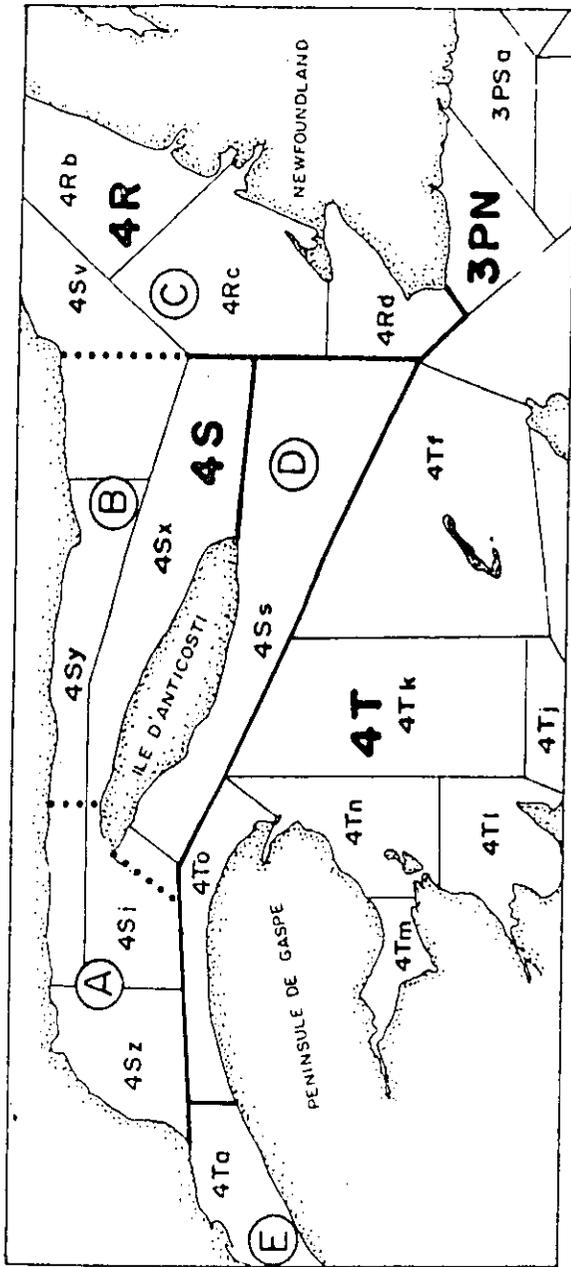
Figure 1. Location of the Sept-Iles fishery in the Gulf of St.Lawrence.

A. Sept-Iles
B. Nord-Anticosti
C. Esquiman

D. Sud-Anticosti
E. Estuaire
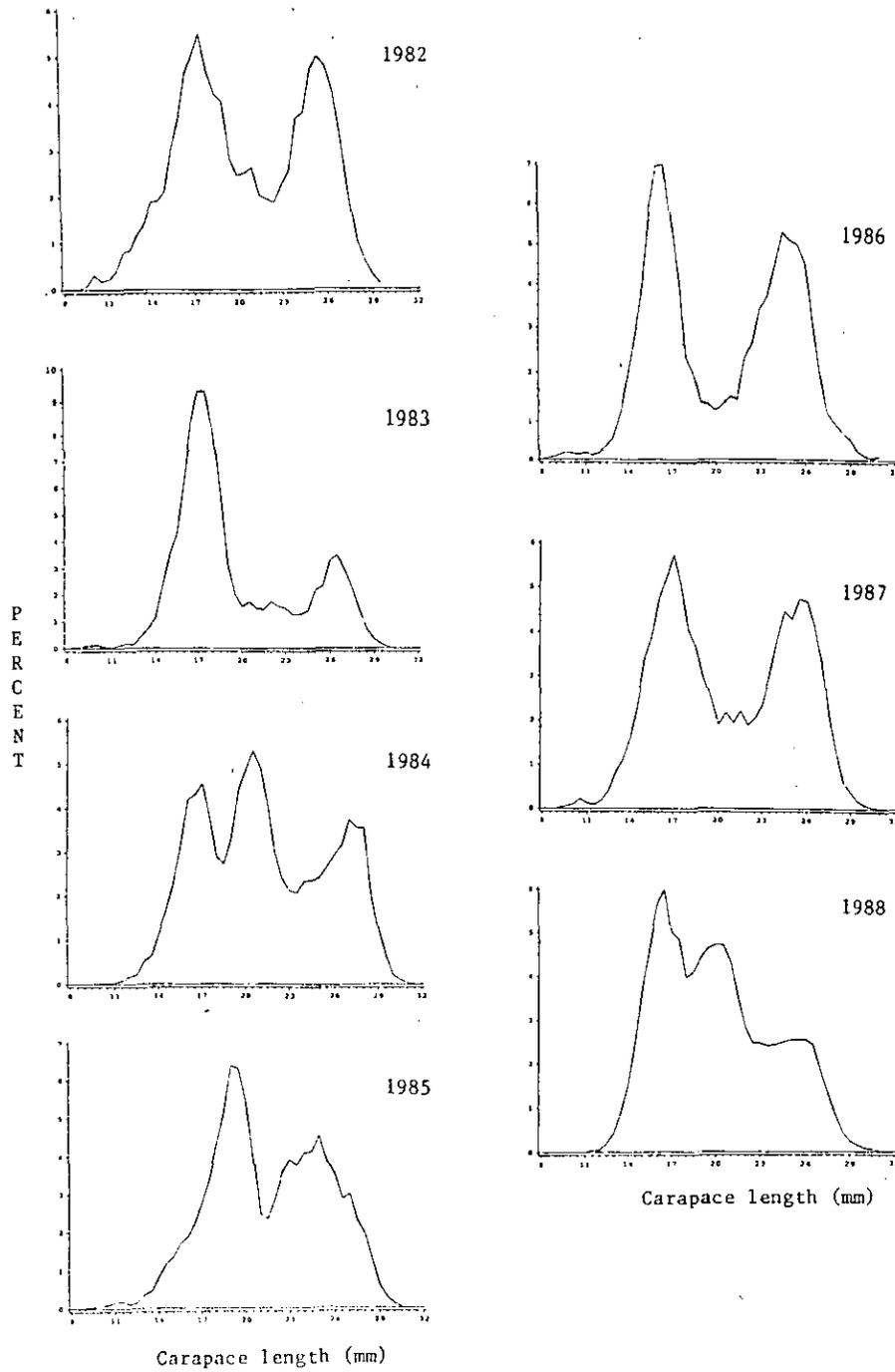
Figure 2. Length frequency distributions from commercial sampling.
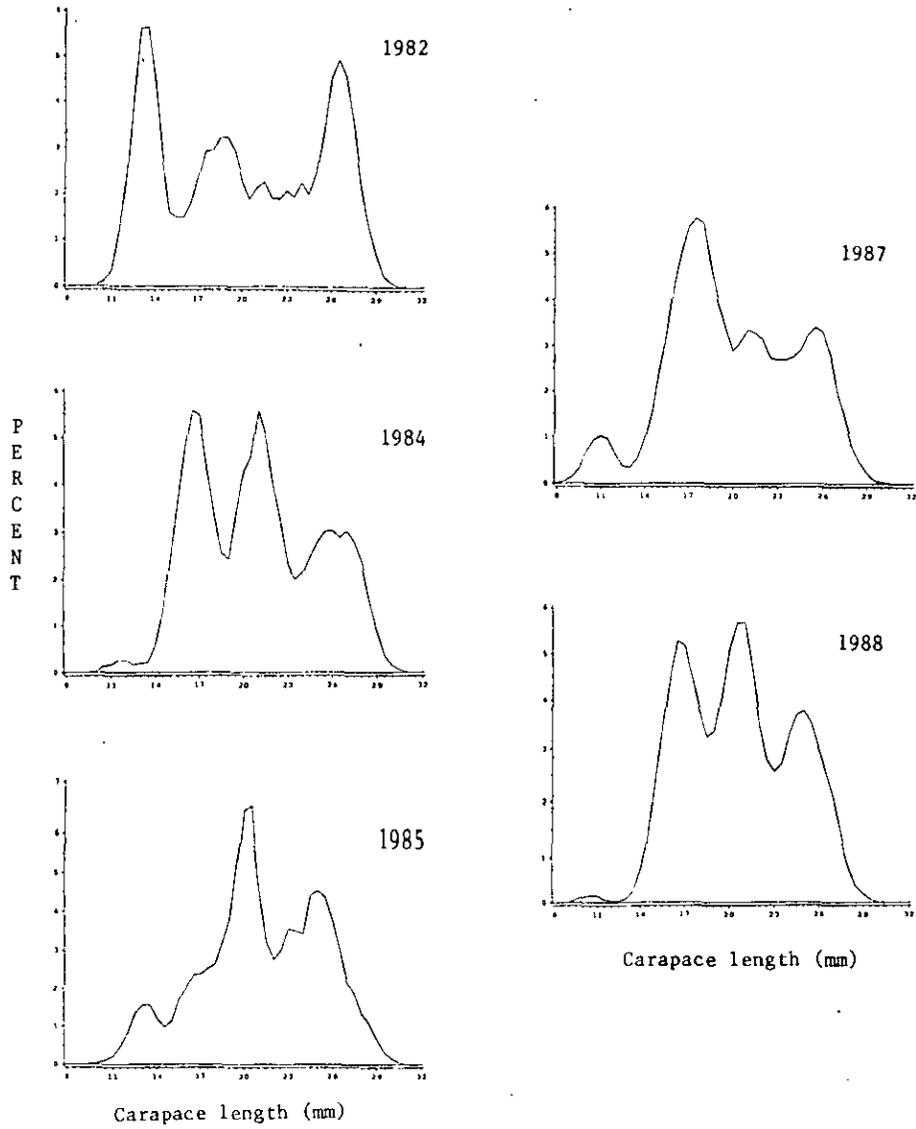
Figure 3. Length frequency distributions from research surveys sampling.

commercial sampling

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          ┌─────────┐
          │  LFD's  │
          └─────────┘

          landings
          LW equation

   ┌───────────────────────┐
   │   CATCH-AT-LENGTH     │
   └───────────────────────┘

          mean L at age
               sd

      ┌─────────────────┐
      │  CATCH-AT-AGE   │
      └─────────────────┘

          cohort equation


       M  ─────────────
  Selectivity ─────────
F oldest ages ─────────
  F last year ─────────

      ┌─────────────────┐
      │  CATCH-AT-AGE   │
      │ NUMBERS-AT-AGE  │
      │    F-AT-AGE     │
      └─────────────────┘


               SAPA
```
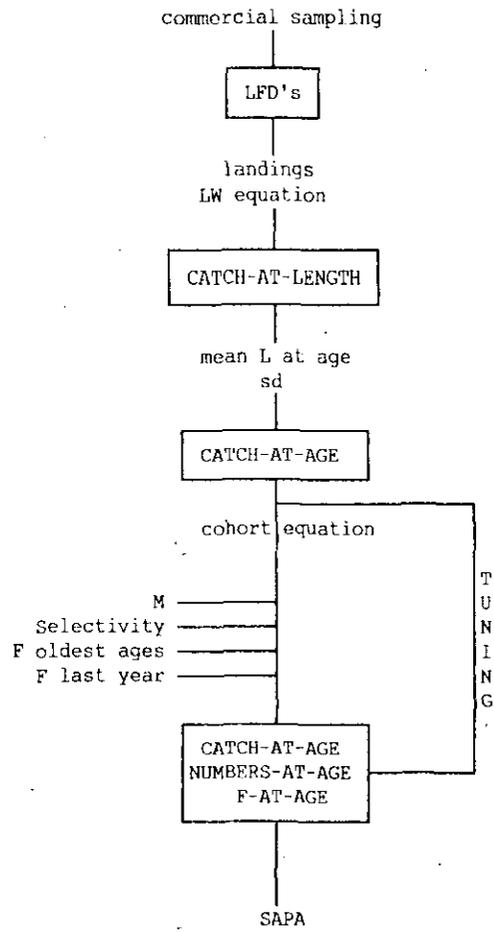
Figure 4.   Schematic diagram of cohort slicing analysis.

commercial sampling

LFD's

landings
LW equation

CATCH AT LENGTH   growth pattern

NUMBERS AT AGE ——age-length key—— AGE-LENGTH TEMPLATE

CATCH AT AGE-LENGTH

simultaneous cohort equation

N

Selectivity
F oldest ages

T
U
N
I
N   F last year   research sampling
G

LFD's

NUMBERS AT AGE-LENGTH   abundance estimates
LW equation

NUMBERS   q ——— nlls ——— ABUNDANCE
AT   fit   AT
LENGTH   LENGTH

converges?
no   yes

NUMBERS AT AGE

NUMBERS AT AGE
CATCH AT AGE
F AT AGE

update

Figure 5.   Schematic diagram of synthetic age population analysis.