ICLARM

A Draft Guide
to the
Compleat ELEFAN

by

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M. Soriano
and
D. Pauly

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INTERNATIONAL CENTER FOR LIVING AQUATIC RESOURCES MANAGEMENT

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A Draft Guide to the Compleat ELEFAN [a]

by

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ABSTRACT

This draft guide introduces the 10-diskette, graphics-oriented **Compleat ELEFAN** software package (version 1.0, February 1988) for length-based fish stock assessment, implemented for IBM [c] PC and compatible microcomputers with at least 520 Kbytes of memory. Emphasis is given to the description of program operations, and to the linkages between the different routines, which cover most aspects of fish population dynamics (i.e. growth, mortality, gear selection, virtual population, yield-per-recruit analyses, etc). This guide does not - except in cursory manner and for new methods - discuss the models behind the various routines, but references are provided to key articles in the original literature. Readers are invited to provide suggestions towards improving the **Compleat ELEFAN** package and its future detailed documentation.

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INTRODUCTION

The Compleat ELEFAN is a very comprehensive package incorporating numerous, rather sophisticated routines for length-based fish stock assessment – several of them new developments– which most colleagues, we believe will find very useful.

This brief draft guide, on the other hand, presents mainly the sequence of operations involved in running the various routines with little emphasis on the logic or equations behind these.

The reasons for this discrepancy are basically two: (a) while developing this package, from early 1986 to late 1987, we incorporated numerous routines based on new ideas which will still require proper scientific publications and (b) we want to write a self-sufficient, very comprehensive manual, covering all aspects of the program – yet we are aware that "bootleg" copies of the Compleat ELEFAN are already being passed around, and that colleagues are blaming us for not providing documentation for this package.

This guide is thus a mere stopgap. Until a comprehensive manual becomes available, users of the Compleat ELEFAN package are urged to not only read the contents of this document, but also of the papers cited therein, particularly those included in the recently published Proceedings of the Conference/Workshop held on February 1985 in Mazarra del Vallo, Italy, on "Theory and Application of Length-Based Methods in Stock Assessment"[a].

This conference, which marked a crucial stage in the development of length-based methodologies for stock assessment, cannot be reviewed here. With regard to the package presented here, it must be mentioned, however that all suggestions made at the conferences concerning possible improvements of the ELEFAN approach package have been incorporated. Properly used, with well-sampled data, this

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[a] Pauly, D. and G.R. Morgan (eds.) 1987. Length Based Method in Fishery Research. ICLARM Conference Proceedings No. 13, International Center for Living Aquatic Resources Management, Manila and Kuwait Institute for Scientific Research, Safat, Kuwait.

package can thus be used to perform, reliably, most types of assessments for which length-frequency data, or catch-at-length-data are needed.

Some routines or programs which we intend to incorporate into version 2.0 of the package (i.e. the one for which a comprehensive manual will be made available), are among others:

• ELEFAN VI, a program for multispecies yield-per-recruit analysis which explicitly considers gradual mesh selection;

• a routine (to be included into ELEFAN II) for estimation of values of von Bertalanffy parameters L_∞ and K, pertaining to mean <u>age-at-length</u> (rather than to mean length-at-age), as needed e.g. for unbiased estimates of Z through length-converted catch curves; and

• a routine (to be included into ELEFAN I and V) for estimation of an approximate joint confidence region for the von Bertalanffy parameters L_∞ and K from the shape of the response surface of "R_n", our new "goodness-of-fit index".

Because the Compleat ELEFAN package is so large (10 diskettes in all), we will not supply listings of the programs.

Rather, we would appreciate receiving comments from users of this package which will help us improve it, notably by:

• removing bugs, misspelling, computational errors, etc.

• replacing existing routines by more versatile or powerful ones,

• adding new routines and subroutines, or

• making the presentation of routines or scripts neater and/or more understandable.

Also, we would appreciate suggestions as to what should go into the planned manual of version 2.0. To be most useful, comments sent to us should be specific to a given program or routine, and reports of bugs or errors should be supported by the file upon which the results were based, detailed description of the problem, and copies of any relevant printouts. We are looking forward to such comments because they will help us improve this package, so don't hesitate to write us.

All comments shall be considered when we prepare version
2.0, which will be free for all those who have sent us
usable comments and suggestions, and available for a small
upgrade fee to all registered users of version 1.0 and its
immediate successors.

GETTING THE COMPLEAT ELEFAN STARTED

Computer literacy is fast becoming an essential qualification for researchers in fisheries science. As more and more research tasks are supported by computers - from word processing to fisheries stock management decision making - professionals in this field are learning more about the powers and limitation of computers.

The Compleat ELEFAN software package is one of the many designed to alleviate the task of manually processing the data available to fisheries biologists. This document is designed for both beginners and experienced computer users.

Computer hardware refers to the physical entities in a computer system. These are the things that can be seen and touched, and is consists of electrical and electronic circuits, and mechanical devices. The basic configuration of a personal computer consists of a system unit and keyboard (see Fig. 1). The system unit is the central part of the computer and supports a variety of options. The keyboard, on the other hand, is the main input device which is used to send data to the system through a cable. The other pieces of hardware that must (or may) be added are the display (screen), the printer, the plotter, disk drives, etc.
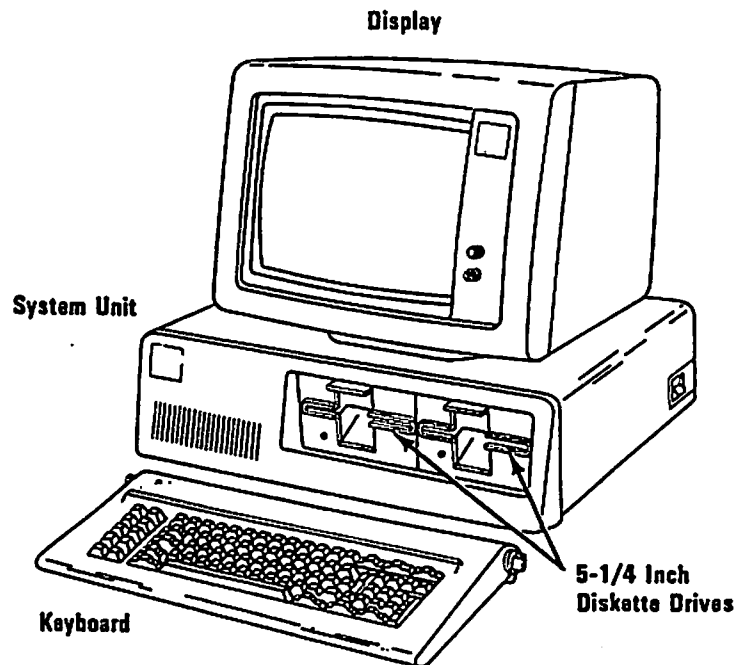

Fig. 1

Hardware requirements of the Compleat ELEFAN

This software was developed for use on IBM PC microcomputers with graphic capabilities and their compatibles. If you are using a computer without this capability, you must add a graphic card (i.e. Hercules monochrome graphic card or color graphic adapter) to be able to run the software (note that a color monitor is not needed).

Except for one program (VPA III), all routines require a minimum of 520 Kbytes of memory. The VPA III program requires 640 Kbytes of on-board memory.

Output of results is generated via the screen and/or printer. Any printer (dot matrix or letter quality) can be used except for graphic outputs, which some printers cannot generate. A plotter can also be used to generate graphic outputs. The software is capable of generating plotter outputs through an IBM plotter (7371 model), but other similar plotters that are using the same GL (Graphic Language) may also be used (e.g. the HP 7470A plotter).

Two 5 1/4" disk drives or one 5 1/4" disk drive and a hard disk are recommended to run the software.

Keyboard and software prompts

The keyboard is used to enter data into the system or to respond to prompts generated internally. It consists of three sections: the typewriter area, the function keys, and the numeric keypad. These keys are "typematic", i.e. they repeat as long as they are held down.

The typewriter area is much, like that found on a conventional typewriter except for some special keys found at the edge of the typewriter area (Fig.2).


```
        |                          !                       |
     Function              Typewriter Area              Numeric
     Keys                                                Keypad
```
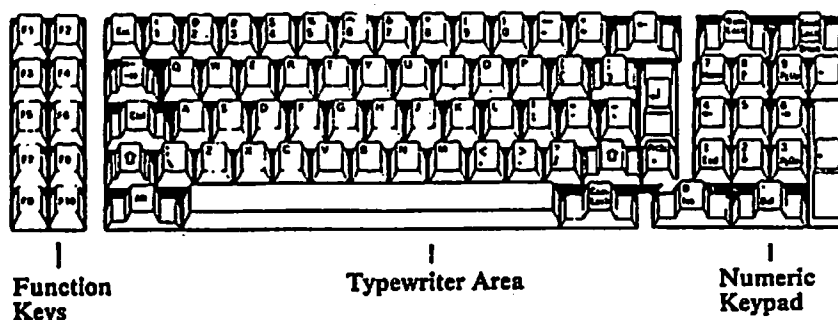
Fig. 2

A prompt is a software request for additional information needed to carry out selected functions. There are three types of prompts which the software uses :

Menu - you are given a choice between several alternative
functions or options, which you select by pressing the
arrow keys to select and the <CR> key to access (<CR> here
expresses "Carriage Return" or <ENTER>).

Line prompts - the software uses this to request a single
item of informations such as e.g. a mortality rate. This
prompt is dealt with by typing the required characters and
terminated by pressing the <CR>. If you realize that you
have made a mistake but have not yet pressed <CR>, use the
<BACKSPACE> key until the offending character is erased,
then retype from there. The <BACKSPACE> key is the only
editing key that can be used at this stage.

Confirmatory prompts - these are very similar to menu
prompts except that you are given two or three options to
choose from. Prompts which are answered with Y for yes and
N for no belong to this category. Choices are given inside
parentheses (e.g. "Proceed (Y/N)").

Selection prompts - these are very similar to the above, but
you are given a list of function keys or number keys (e.g.
<1>) with corresponding function or options.

Throughout the package, the function keys are attributed to
the following functions.

        [F1] - to redo a routine

        [F2] - to move the "turtle" (or pointer) up or to the
               left

        [F3] - to return to the previous menu

        [F4] - to move the "turtle" down or to the right

        [F9] - to proceed to the next routine

        [F10]- to access more help messages (if applicable)

The function keys [F5], [F6], [F7] and [F8] are assigned to
other functions (e.g. to dump graphic, mark points, etc.).
As an alternative to [F2] and [F4], the arrow keys (left and
right, respectively) may be used. [F6] is often used as the
key to mark points for which the <SPACE BAR> may also be
used.

Starting the package

To start the computer, it is advisable to begin with the peripherals connected to the system unit. The switches of the peripherals (screen, printer, etc.) are conveniently located outside of the hardware. There is no need to open any part of the peripherals.

The contrast and brightness of the PC's display can usually be adjusted using control knobs. Keyboards usually have adjustable tilt position for typing comfort. Hold the keyboard when changing position. Firmly push in the foot handles and turn them to the desired level.

Before proceeding, some preliminary operations are necessary and these maybe accessed from DOS or through the menu option called "Utilities" in the main menu of the package (see Fig. 3).

Disk copy : The first thing that you should do when you have unwrapped your set of ELEFAN diskettes is to make working copies. Any disk duplicator program can be used. The most common of these duplicators is the DOS DISKCOPY command. Put the original disks in a safe place and use the copies. If the copies are ever damaged or destroyed, you can make new copies from the original disk. For more informations on how to use the DISKCOPY command, please refer to the DOS manual.

```
NOTE : DO NOT write-protect the working
       copies of the ELEFAN package.
```

The **Compleat ELEFAN** contains a utility to create a backup copy of the diskettes. A minimum of two disk drives is needed for this routine. If you have only one drive, use the DISKCOPY command of MS DOS. Access the routine that will allow you to make a backup copy and have ready ten (10) diskettes for the working copies.

You should have the following diskettes:

DISK #1 : System and Utilities	DISK #6 : ELEFAN II-A
DISK #2 : ELEFAN O	DISK #7 : ELEFAN III
DISK #3 : ELEFAN O-A	DISK #8 : ELEFAN IV
DISK #4 : ELEFAN I	DISK #9 : ELEFAN V
DISK #5 : ELEFAN II	DISK #10 : MPA

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DOS installation for a two-disk drive configuration : The disk operating system (DOS) is not included in the package. The DOS is prerequisite to some utilities and it should be installed only to DISK #1. To copy, insert a disk containing the DOS (note: the Compleat ELEFAN requires MS DOS 2.1 or higher) in A: drive. Boot the computer and wait for the DOS prompt (A>). Carefully insert DISK #1 (of the Compleat ELEFAN) in drive B:. Type SYS B: followed by <CR>. This will copy the DOS to DISK #1.

In addition to the DOS, the following DOS commands are needed by the package :

                    COMMAND.COM
                    GRAFTABL.COM
                    GRAPHICS.COM
                    ASSIGN.COM
                    FORMAT.COM
                    DISKCOPY.COM
                    MODE.COM

To copy these DOS commands, insert a DOS disk containing the files mentioned above in drive A:. With the DISK #1 still in drive B:, type COPY A:XX B: (where XX is the name of the DOS command that needs to be copied, e.g. FORMAT.COM) followed by a <CR>. There is no need to repeat the above procedure for the other disks of the package.

For a computer with a hard disk, boot the computer with either floppy disk drives empty and wait for a DOS prompt (e.g. C>). Carefully insert DISK #1 (of the Compleat ELEFAN) in drive A:. Type SYS A: followed by <CR>. [This can be bypassed if the package is to be installed to a hard disk; see below]

Hard disk installation : A utility (HDINSTAL.EXE) is provided in DISK #1 to properly install the package to your hard disk. Other methods of copying the set of programs to your hard disk may cause problems while using the package. Note also that a minimum of 2.7 megabytes of free storage space is needed.

The DOS path (sometimes called "directory", e.g. C:\DOS) should be known before running this hard disk installation program. The same six MS DOS utilities as listed above are needed to run the package, and this should be accessible through DOS path.

To run, insert DISK #1 in drive A:, then type HDINSTAL followed by <CR>. This utility will initialize any existing "ELEFAN" subdirectory.

Peripheral installation : A utility has been developed to allow the software to run on different system configurations. This utility may either be accessed through

the **INSTALL.EXE** which can be accessed directly from DOS (DISK #1) or through a routine in the utility menu. It will install the following :

    1). the type of graphic card/adapter (CGA or Hercules
        monochrome graphic adapter),
    2). the printer type,
    3). the data drive specification and,
    4). the program drive specification.

Installation is done only once, unless you wish to change peripherals or drive specifications.

Serial port installation : Graphic outputs may also be dumped via plotter; this requires the user to configure the communication ports (COM1:). Please refer to the plotter's manual for communication protocol parameters.

This installation may not be necessary if the plotter can be configured through the dip "switches" found at the back of the peripheral.

Serial printers may also be redirected through this utility. For more technical information on the requirements of this utility, please refer to computer manual, "Guide to Operations".

Formatting a disk : Data disks may either be created using the DOS command "FORMAT" or the utility to format a disk in one of the routines available within the package. Formatting, (1) initializes a disk to a recording format acceptable to DOS, (2) analyzes the entire disk for any defective tracks, and (3) prepares the disk to accept DOS files. For more information regarding the FORMAT command of MS DOS, please refer to the DOS manual.

CAUTION : Please note that formatting destroys all data on the disk. Because of this, you should be very careful before you decide to format a disk, particularly a hard disk.

For problems or deviations from the above, please refer to the manual (Guide to Operations) or ask an experienced user.

After installing the package properly, type **ELEFAN** after the DOS prompt (e.g. A>), then press <CR>.

Once the software package is accessed, the system menu will be loaded and executed (see Fig. 3). You may use the arrow keys (up and down) or function keys [F2] and [F4] respectively. To access a routine, position the highlighted

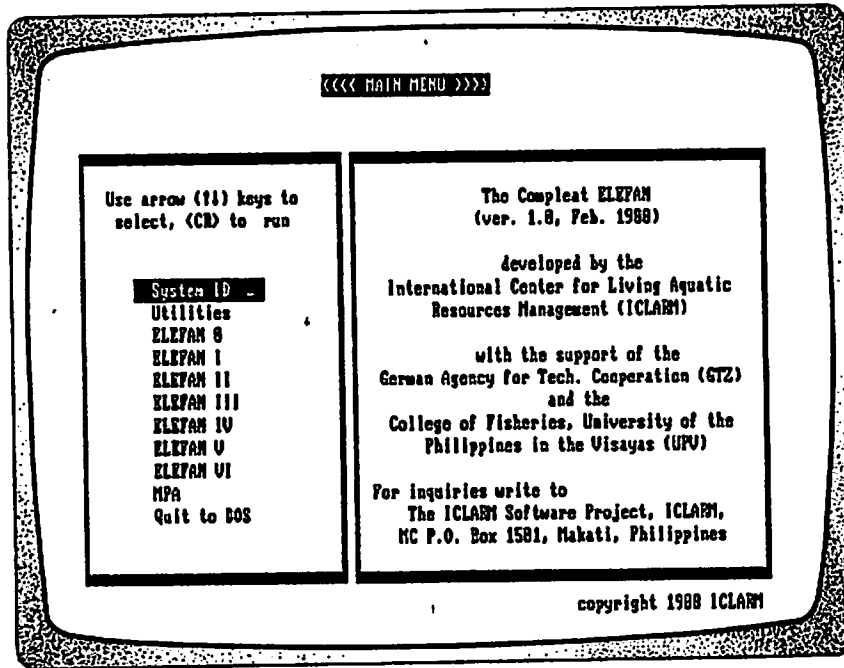area (by using an arrow key) to the desired routine, then
press <CR>.

Fig. 3

WORKING WITH ELEFAN O

Introduction

The Data Entry and File Management Routine referred to as ELEFAN O allows entry of data sets such as length-frequency data, weight-frequency data, commercial shrimp tail counts, tagging/recapture and/or length-at-age data and stores them in a format accessible to other ELEFAN routines.

The ELEFAN O menu contains nine routines appearing on computer screen as follows:
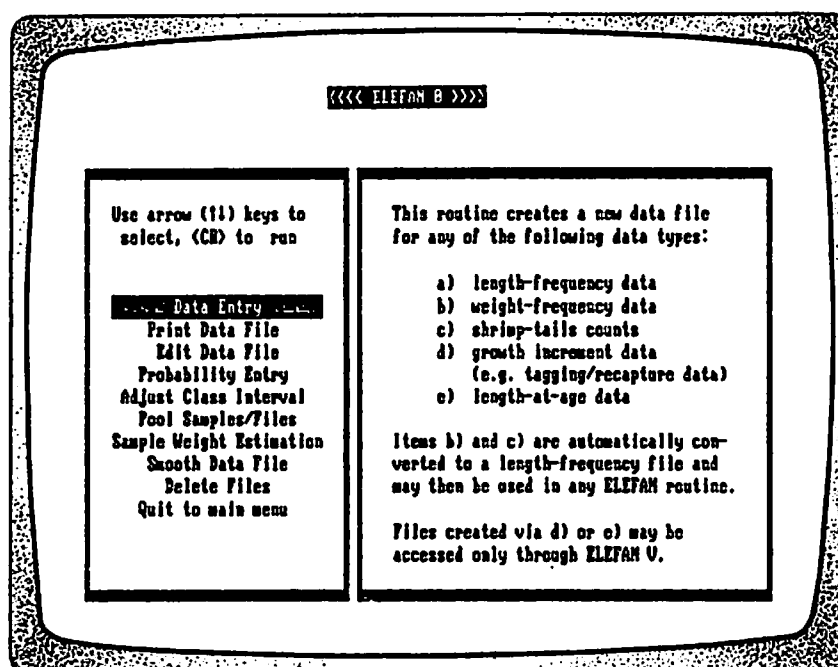

Fig. 4

Before going into the details of each of these routines, it is important to mention here the general screen layout of ELEFAN O. The first four lines on the screen are reserved for the routine title, lines 5 to 18 are for the body of the routine and two separate boxes on the lower part of the screen are reserved for instructions (left box) and function keys (right box).

TITLE

BODY

INSTRUCTION BOX

DATA ENTRY ROUTINE - FILE SPECIFICATION

Please supply the following:

Species name   :Upeneus moluccensis
Other file identifiers   :RAGAY GULF 1981
Number of sampling dates   :
Smallest recorded midlength   :
Largest recorded midlength   :
Class interval   :
Unit of measurement   :

[F3]-quit to ELEFAN 0 menu

Fig. 5

Attention should be given to the instruction box which is intended to guide the user. Attention should also be given to the function key box, which provides other options ensuring flexibility while a routine is being used. The function keys [F2] and [F4], which are not shown on the function key box, are assigned to move to previous field and next field, respectively.

Data entry

Unless foreign files are transferred to the ELEFAN system, the world of ELEFAN begins here. This routine allows for the entry of the following types of data sets:

    1.   Length-frequency data
    2.   Growth increment data
    3.   Length-at-age data

The length-frequency data may be accessed any time using any ELEFAN routine. Growth increment (e.g. tagging/recapture) data and length-at-age data once entered may only be accessed by ELEFAN 0, e.g. for editing, and by ELEFAN V for analysis.

The next version of the package will, additionally, allow weight-frequency and commercial shrimp tail count data to be stored on disk and analyzed.

Basically, the data entry routine is made up of three screens, arranged as follows:

File specification screen :
This screen requires input providing a general description of the file such as the species name, number of samples, smallest and largest midlengths/ midweights, class interval and unit of measurement used.

Data entry screen : The data entry screen requires input of the date of sampling (month, day and year) and frequency number for each class length or weight. (Tagging/recapture and length-at-age requires actual lengths). The lower right corner of the screen labelled "SUM" keeps track of the total frequencies entered. The data entry screen appears n times depending to the number of sampling dates entered in the file specification. Each sampling date is checked for duplicates and is used to sort the entries.

Save data file screen : This last screen requires input of a unique filename to save the data set onto a diskette. This filename is the only link to access a particular data set in any ELEFAN routine.

Printing of data

As needed, by using this routine, hard copies of any ELEFAN data file may be outputted to a printer. The only information required of the user is the filename where the data set is stored. Everything else follows.

Editing a file

Alteration of an existing ELEFAN data files is done using this routine. It has the same screen flow as that of Data Entry. The class interval of the file specification screen is the only field that can not be altered, (please refer to the Adjust Class Interval routine instead).

All fields may be edited and, in particular, a sample may be deleted by entering 99 for the month. Each sample appear on screen in chronological order. To select the desired sample for editing, simply enter its corresponding sample number while you are on the "SAMPLE" field or use function keys [F6] or [F9] to move from one step to another.

The "save edited file" screen allows the user to save the edited data set to a new filename or overwrite the old data set by using its old filename.

Edit routine screens :

The "Edit Routine" may be invoked to RENAME a data set, by accessing an old file and saving it without alteration under a new filename. The old file may then be deleted using the "Delete Routine".

The "Edit Routine" may also be used to COPY an ELEFAN data file from one diskette to another by using function key [F9] - change data diskette, while on the save file screen.

Probability entry

This routine allows for the entry of probabilities of capture for each class length of a given data set. These probabilities may come from ELEFAN II (Catch Curve Routine), or previous studies of the species in question.

Each length frequency in the file is then divided (by length class) by its corresponding probability of capture to obtain the relative abundance for each class.

Adjusting class interval

Class intervals are altered using this routine, which was developed for the purpose of merging files with different class intervals. Basically it slices up the whole length data into the class interval the user desires.

The filename of the data set to be sliced-up is selected from the library and the desired change of class interval is entered. Succeeding screens will give a view of the sliced-up data file.

Note that a new class interval need not be a whole number, nor a whole multiple of the old class interval, i.e. data originally grouped into say 1 cm intervals may be regrouped into a 1.5 cm interval using this routine.

Pooling of sample/files

Pooling of samples or merging of two files is another data manipulation feature of the ELEFAN system. Two samples of one data set may be pooled together or samples of two files may be merged by any of the following options:

(1) <u>Addition of frequencies</u> : this option simply adds up frequencies of two or more samples and stores them under one sampling date.

(2) <u>Weighting by the square root of sample size</u> : this pooling option is a modification of (3) and is recommended for low frequency samples; the mathematical equation is as follows:

$$f'ij = wij \cdot fij$$

where $f'ij$ = pooled frequency for sample i, class j
fij = frequency number for sample i, class j
wij = $fij / \sqrt{Ti}$ where Ti is total frequency for sample i.

(3) <u>Weighting by percentage</u> : weighting of samples by percentage gives each sampling date an equal weight, whatever its initial size.

Mathematically, .

$$f'ij = wij \cdot fij$$

where f'ij = pooled frequency for sample i, class j
       fij = frequency number for sample i, class j
       wij = fij/Ti, where Ti is total frequency for
             sample i.

Estimation of sample weight

The sample weight of a given file is estimated using the length- weight relationship (W=a*L^b). Mean weight in each length class and of each sample are computed. The estimation of the mean weight of the fish of a given class is computed as suggested by Beyer (1987).

Smoothing of L/F data

This routine makes use of a running average over 3 or 5 classes to smooth the available length frequency data, as suggested by Laurec and Mesnil (1987) for cases where data are irregular.

Deleting a file

This routine deletes an ELEFAN data file not only from the diskette but also from the ELEFAN disk library. The user is cautioned from deleting an ELEFAN data file using the DOS utility primarily because this latter routine would not update the ELEFAN disk library.

WORKING WITH ELEFAN I

Introduction

ELEFAN I is a program which uses length frequency data to estimate the parameters K, Loo, C and WP of the von Bertalanffy equation, modified to express seasonal growth in length of fish or aquatic invertebrates (Pauly and David, 1981).

The program's key assumptions are:

- samples used are representative of the population;

- length differences can largely be attributed to differences in age;

- growth is similar from one year to the next, i.e. there are no factors inducing any strong changes in growth between years; and

- the seasonally oscillating von Bertalanffy growth equation provides an appropriate approximation to the growth of fish and aquatic invertebrates.

Although ELEFAN I could in principle be used in conjunction with any type of growth curve, only one growth curve was incorporated into this version. It is the seasonally oscillating version of the von Bertalanffy Growth Function (VBGF) proposed by Pauly and Gaschütz (1979), which has the form

$$L_t = L_\infty(1-e^{-[K(t-t_0) + \frac{CK}{2\pi} \sin (2\pi (t-t_s))]})$$

where ts=WP+.05 and all parameters are as defined in Pauly (1984)

There are three (3) routines available in the ELEFAN I program to help the user estimate growth parameters :

- Curve fitting by eye : allows a user to fit a growth curve through a (restructured) length-frequency data set, given a set of parameters;

- Response surface analysis : allows a user to vary two growth parameters in a 11 by 11 matrix. The 10+ points providing the best fit to the data are identified, allowing the user to locate combinations of parameters that are better than others; and

. Direct search for optimum parameter combination: allows the user to let the computer search for the "optimum" combination of growth parameter values , given a set of seeded parameters and step sizes by which the program can modify the seeded values.

These three routines use "Rn" as goodness-of-fit index; this index ("new R") is computed from $Rn=10^{\wedge}(ESP/ASP)/10$, with ESP/ASP being as defined in earlier versions of ELEFAN I (the use of Rn prevent the occurrence of negative values of goodness-of-fit).

A fourth routine is included which allows the user to output the results in graphic form through a printer and/or a plotter.

Data file access/restructuring

Immediately after ELEFAN I has been accessed from the main menu, as in any of the programs to be discussed later, the program will first search for the disk library created during data entry and manipulation.

Fig. 6

If no length-frequency file or data disk is found in the data drive, the computer will prompt for a change of data disk or offer the option to quit to the main menu by pressing [F3]. Once the disk library has been accessed, a file may be selected by moving the cursor, i.e. by pressing an arrow key followed by <CR>. The file accessed may still be replaced after the file parameters have been displayed (see Fig. 6).

Restructuring of data will commence immediately after confirmation, i.e. by pressing [F9]. Depending on the size of your file and the speed of the computer, this routine may take a minute or so.

An option to output the restructured data via the installed printer will also be given.

Submenu

This program has four subroutines (see Fig. 7) to analyze a given length-frequency file.
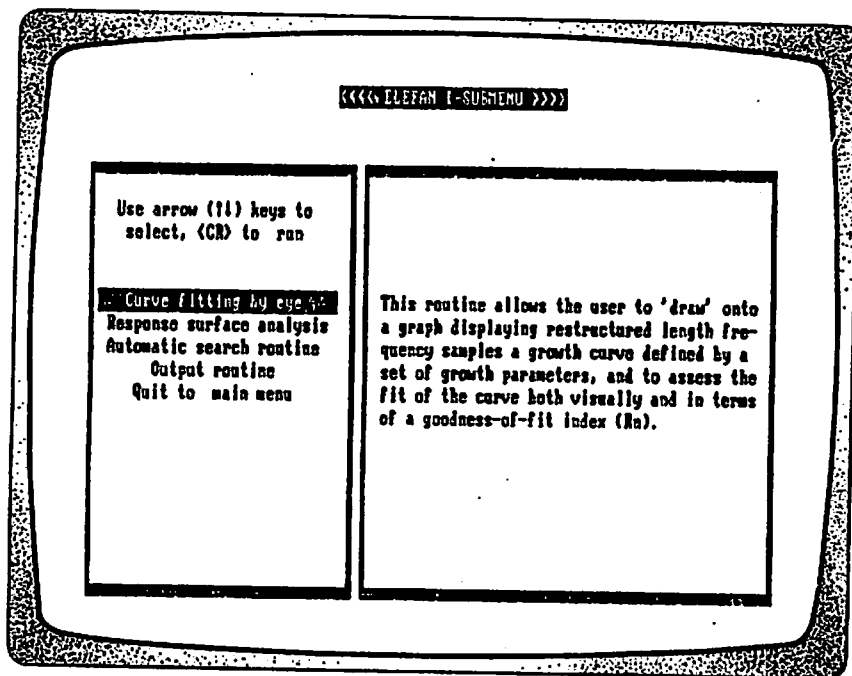
Fig. 7

Response surface analysis

The limits (lower and upper) for each of the four growth parameter will be required by the program. To leave a parameter constant, press <CR> when the program prompts for the upper limit for this parameter (see Fig. 8).

Two growth parameters have to be left variable; otherwise the limits for each of the parameters have to be re-entered.

Fig. 8

Default values for the starting points are provided. When all parameters have been entered, a prompt on whether or not a printer output is desired will appear. After answering the prompts, the user will be given the opportunity to change whatever needs changing before the computer starts generating the response surface.

In the final output, the best 10+ points will be boxed for easier identification of the best combination of parameters. (see Fig. 9). At any time, a user may abandon the routine by pressing [F3] or [F7]. to rerun the response surface generator with another set of entries.

<(RESPONSE SURFACE (Rn X 1888) : Upeneus moluccensis >)

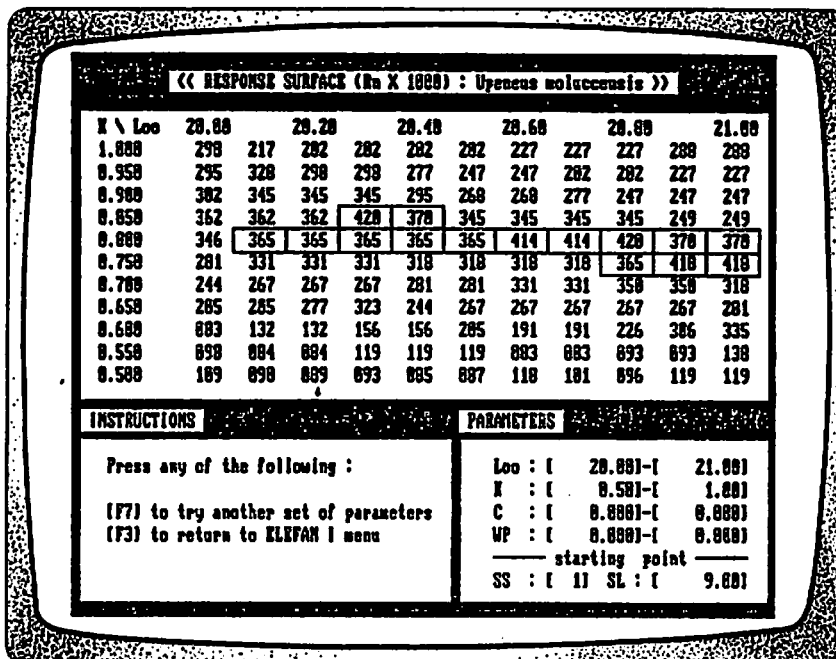| X \ Loo	20.88		20.28		20.48		20.68		20.88		21.88
1.888	298	217	282	282	282	282	227	227	227	288	288
0.958	295	328	298	298	277	247	247	282	282	227	227
0.988	382	345	345	345	295	268	268	277	247	247	247
0.858	362	362	362	428	378	345	345	345	345	249	249
0.888	346	365	365	365	365	365	414	414	428	378	378
0.758	281	331	331	331	318	318	318	318	365	418	418
0.788	244	267	267	267	281	281	331	331	358	358	318
0.658	285	285	277	323	244	267	267	267	267	267	281
0.688	883	132	132	156	156	285	191	191	226	386	335
0.558	898	884	884	119	119	119	883	883	893	893	138
0.588	189	898	889	893	895	887	118	181	896	119	119

INSTRUCTIONS

Press any of the following :

[F7] to try another set of parameters
[F3] to return to ELEFAN I menu

PARAMETERS

Loo : [20.88]-[21.88]
K : [8.58]-[1.88]
C : [8.888]-[8.888]
WP : [8.888]-[8.888]
------ starting point ------
SS : [1] SL : [9.88]

Fig. 9

Curve fitting by eye

Given a set of parameters (i.e. Loo, K, C and WP), this routine will fit the curve over the restructured data plotted on screen. Aside from the response surface, a user will find this routine particularly helpful in defining, at least approximately, the values of these parameters and identifying a good starting point.

The starting point (starting sample and starting length, i.e. the coordinates of a point through which the curve must pass) will also be asked (see Fig. 10).
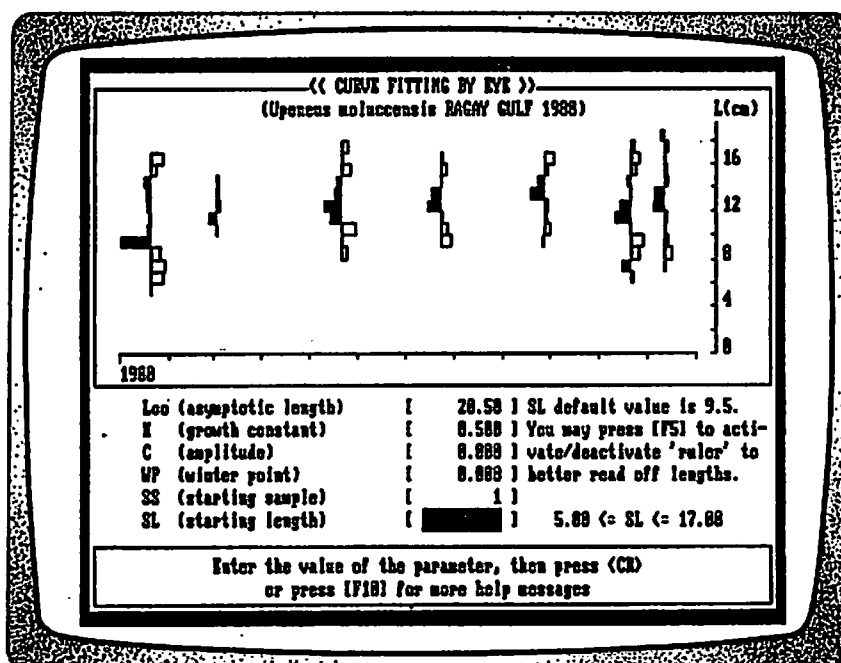
Fig. 10

A ruler may be activated using [F5] to ease identification
of a starting length (default is the class with the highest
peak) once the starting length is prompted for input. Use
the arrow keys to move the ruler to a desired location.
Pressing the <CR> will change the default value of the
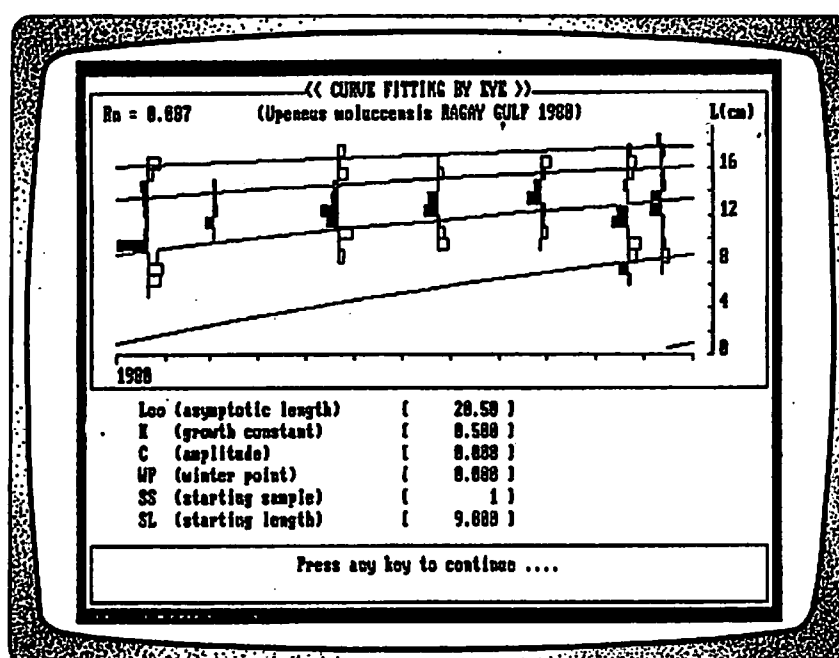starting length.

Fig. 11

The values entered before a curve is drawn will be used as the next default value, i.e. a user may simply press <CR> if a former entry is to be kept unchanged.

Search for optimum base point

This routine will allow a user to "seed" growth parameter values (i.e. to enter first guesses) and the step size by which the guesses will vary. The program will vary the parameters up to 6 steps at a time. That is, if for example you entered a seeded value of Loo of 21, and a step size of .1, it will first vary the value for Loo to 21.1 and compute for any improvements in the Rn value. If the computed Rn value is equal or less than the previous value, it will check the Rn value for Loo equal to 20.9, then 21.2, then 20.8, and so on. It will continue to vary the parameter until a value is reached which leads to a higher Rn value, and this combination of parameters will be used as the new input values. The search will continue until no further improvement is reached.

Once the "seed" parameter values and step sizes have been entered (see Fig. 12), the user will be given the option, via [F5], to let the computer search for the coordinates of the best starting point given the seeded parameters entered earlier. Depending on the size of the file, this may take some time.

If [F6] is pressed, the starting point (i.e. starting length and starting sample) will have to be provided. Default values are available (i.e. the coordinates of the class with the highest "restructured" point value).

Optimal step size ranging from about 3-6% of a parameter value for the initial searches to 1% or less may be used to better identify a good set of parameter combinations. Depending on the size of your file, searching can be a long process.

The computed growth curve will be plotted over the restructured sample everytime a new base point is identified.

<< SEARCH FOR OPTIMUM COMBINATION >>

FILE PARAMETERS   PARAMETER INPUT

Filename
▶ MUMORZ   Seeded values Step sizes
Species name
▶ Upeneus moluccensis   Loo : [........] [+/-   ]
Other labels   K : [   ] [+/-   ]
▶ RAGAY GULF 1981   C : [   ] [+/-   ]
No. of samples   WP : [   ] [+/-   ]
▶ 7
Class interval
▶ 1
Range of length observations
▶ 5 - 19 cm

INSTRUCTIONS

Enter the Loo (asymptotic length) to be used (Loo)≥5)
NOTE : Press [F10] for more help messages.

Fig. 12

It is recommended to re-initiate a search several times, from different seed values before accepting an "optimum" as such.

Graphic outputs

After an optimum of growth parameters has been identified, this routine will allow users to output the results through either a plotter or a printer.

If a growth curve is desired, the parameters (see Fig. 13) will be required and the computer will compute the corresponding Rn value. Also available is an option to output the points of the growth curve on every 15th of the month. A sample plotter output is given in Fig.14.
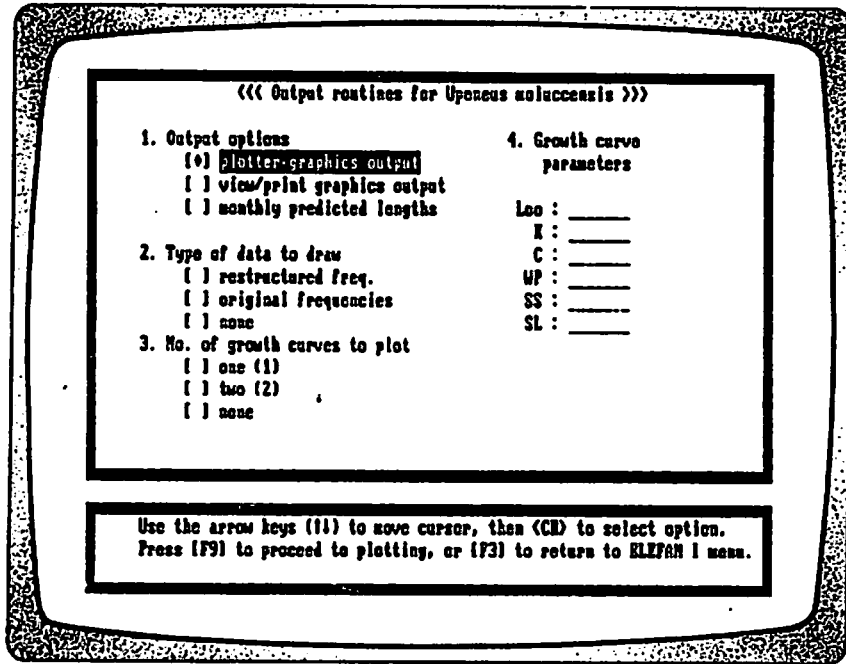
Fig. 13
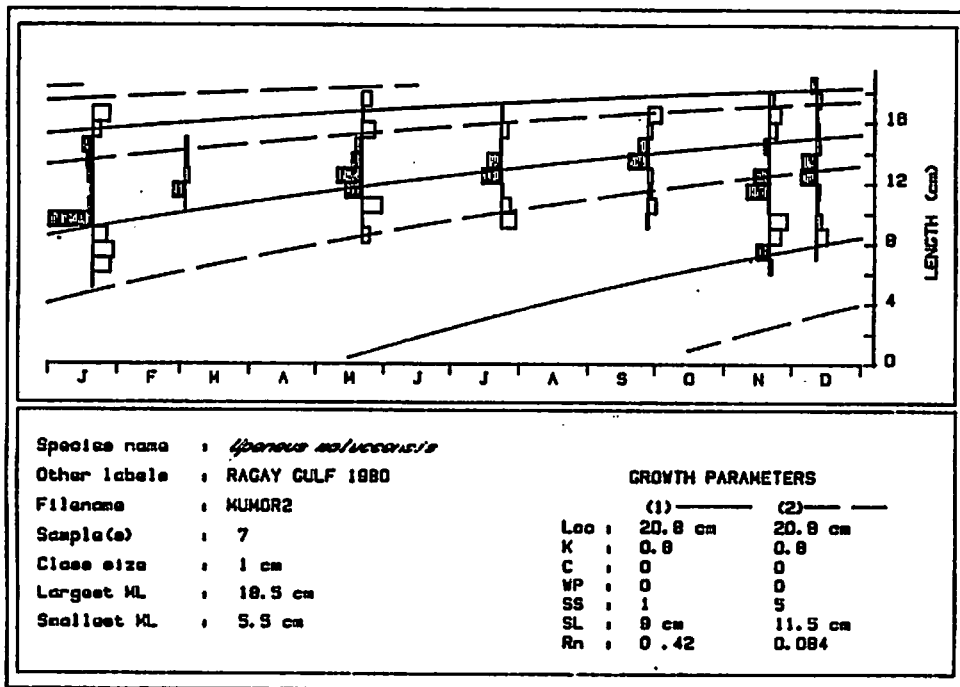
Fig. 14

WORKING WITH ELEFAN II

Introduction

ELEFAN II is a collection of auxiliary routines and a sequel
to ELEFAN I. It covers major topics as follows:

1. Estimation of total mortality from a catch curve
   using VBGF parameters estimated by ELEFAN I or
   known from an independent source;

2. Smoothing of selection pattern given the
   probability of capture for each length class using
   a logistic transformation;

3. Estimation of Loo and Z/K using a modified version
   of the Wetherall method;

4. Derivation of seasonal patterns of recruitment;
   and

5. Relative yield and biomass per recruit analysis.

Below (Fig. 15) is a layout of ELEFAN II main menu.

Fig. 15

Catch curve and resultant curves

Catch curves are constructed for the investigation of total
mortality (Z) within a fish population. The catch curve
routine requires the filename of the ELEFAN data set for
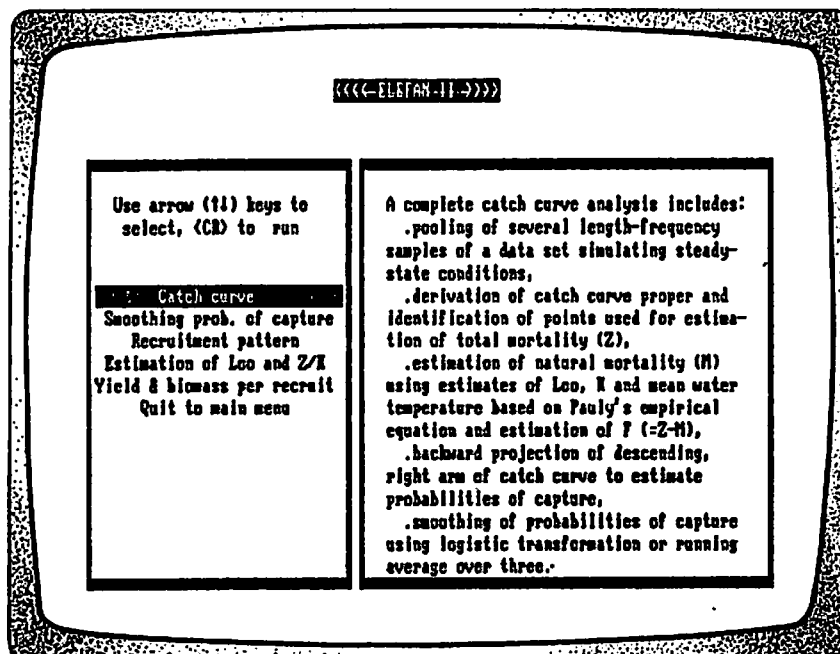analysis and growth parameters (Loo and K) to be entered
through the keyboard.

The user is given the option to select particular samples to
use in estimating Z; some transformation of the data set are
allowed. Transformation options are as follows :

1.   No transformation (original data),
2.   Using the square root of sample total as weighting
     factor; and
3.   Transforming all samples into % samples before
     pooling.

The selected/transformed samples are then added up by length
class and each cumulated frequency ($\%N_i$) is divided by the
time needed for the fish to grow from the lower to the upper
limit of its length class (Δt_i).

The ln ($\%N_i/\Delta t_i$) values are then plotted vs age on the
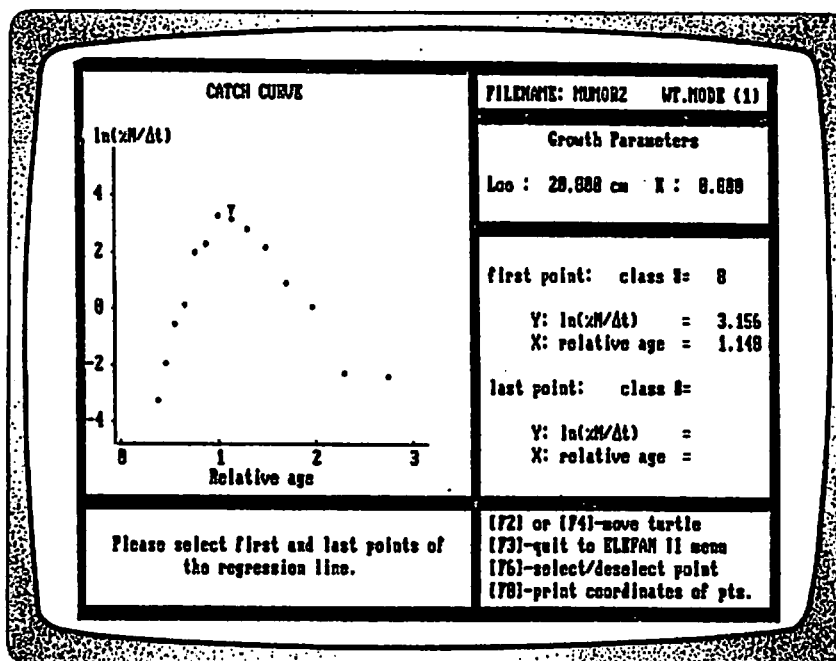screen, as shown in Fig. 16.

Fig. 16

The "turtle" (or pointer) on the graph requires the user to select points to use in estimating total mortality. The turtle may be moved from one point to the other using function keys ([F2] or [F4]) or arrow keys (left or right).

The points selected must include only fish which are fully recruited and vulnerable to the gear employed. A generally applicable rule is to use as a first point the one immediately to the right of the highest point of the catch curve.

Often, one or two points corresponding to very high "ages" must be excluded from the computation of Z because they pertain to length values very close to Loo, affecting Z dramatically. Jones (1987) and Laurec and Mesnil (1987) provided rules as to which of these points should be excluded from the computation.

A preliminary estimate of Z is made using the linear regression :

$$Ln(\%N/\Delta t) = a+b*t, \text{ where } t = \text{relative age}$$

An iteration procedure (P.Sparre, per.comm. to Pauly 1984, Chapter 5) corrects the Z=-b of the regression line for the non-linearity of the growth model and for the fact that some mortality occurs within each length class. The iteration equation is :

$$\log(N_i/(1-\exp(-Z_i*\Delta t_i))) = a-Z_i* \Delta t_i \; ;$$

then natural mortality (M) is estimated from the empirical relationship :

$$\log_{10} (M) = -0.0066 - 0.279 \log_{10} (Loo) + 0.6543$$
$$\log_{10} (K) + 0.4634 \log_{10} (T)$$

where T is temperature in °Centigrade (Pauly 1980).

The user is not compelled to use the computer-estimated Z and M values, and the values for Z and M to be used must in fact be entered by the user.

Given Z and M, a resultant curve may be derived from the left, ascending arm of the catch curve. The fishing mortality (F=Z-M) ranges between M (=mortality in the highest length class not caught at all) and Z (=mortality from the first selected point of the catch curve). Thus,

$Z_i=M+F_i$, where Z_i and F_i are the total mortality and fishing mortality for class i, respectively. The number of available fish in the population is then estimated using :

$$N_i=N_{i+1} * exp(Z_i*\Delta t) * \frac{(1-exp(Z_{i-1}*t_{i-1}))}{(1-exp(Z_i*t_i))}$$

The screen plot of the catch curve with estimates for Z, M and N_i's is shown in Fig. 17.

The probability of selection P_i is N_i(caught)/N_i(available). The resultant curve is fitted using a logistic transformation (x=log(p/q)) or moving average over on the selection probabilities. Fig. 18 shows an example of a resultant curve.
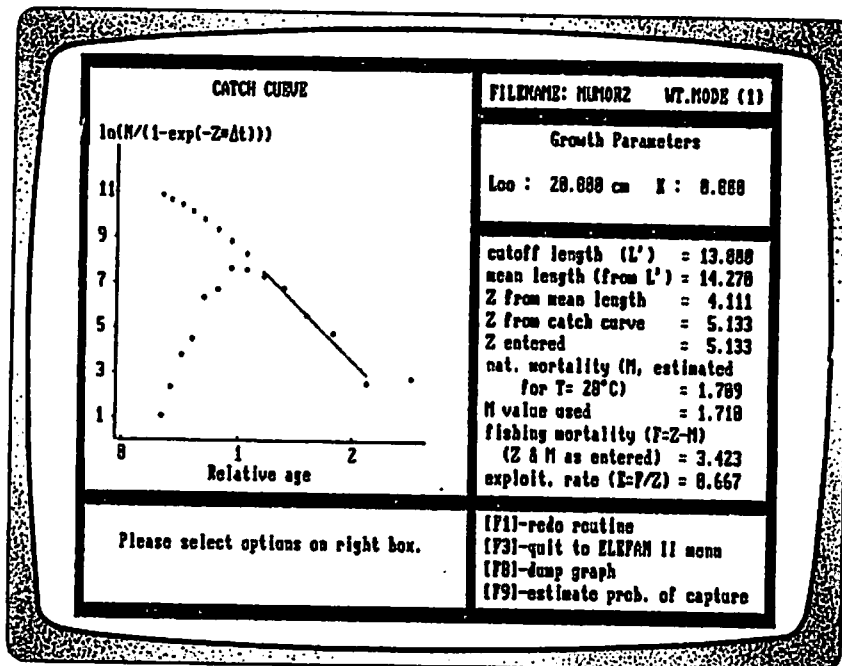
Fig. 17

Fitting of probability of capture

This routine estimates L_{25}, L_{50} and L_{75} given a set of probability of capture over different length classes. This is one of the few routines in the ELEFAN package that may be used without the need to access an ELEFAN data file. The basic information needed to run this routine are the smallest midlength, largest midlength, class interval and the probability of capture for each length class. The algorithm and screen output is similar to the resultant curve section of the catch curve routine.
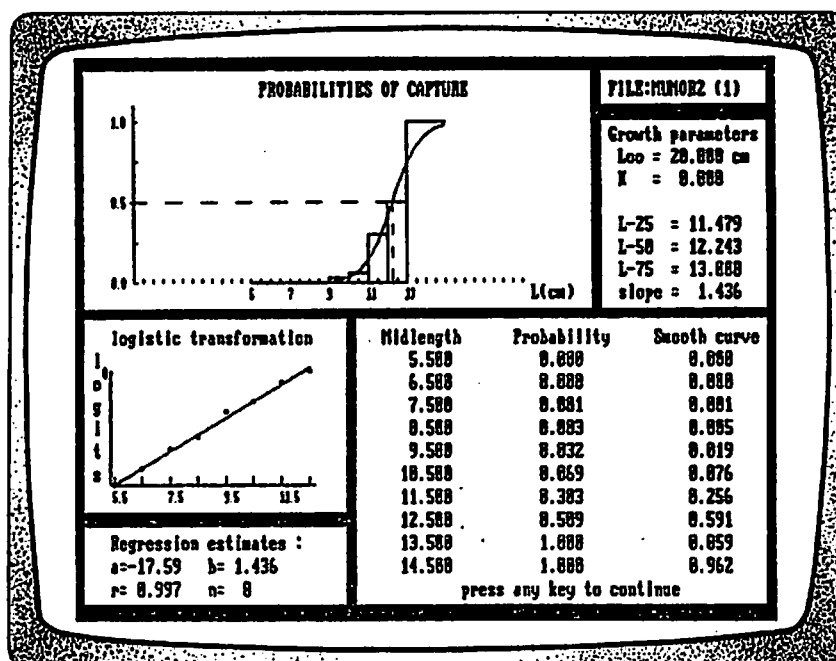
Fig. 18

Recruitment pattern

A recruitment pattern is obtained by projecting a set of length-frequency data backward onto a one-year time axis. Recruitment patterns can be used to infer the number of recruitment pulses occurring per year (see Fig. 19). However, when the parameter t_0 is not given, the exact time of recruitment can not be determined.

A routine (Soriano 1987) is built into the program which automatically fits a recruitment' pattern with one or two normal distributors when the recruitment explained by one or two normal curves ranges between 90% and 110% of the observed annual recruitment.

In the same manner as in the catch curve routine, an ELEFAN data file and its growth parameters (Loo, K,C, and WP) must be provided. The user is also given the option to select samples for analysis and the type of data transformation to use for computation.
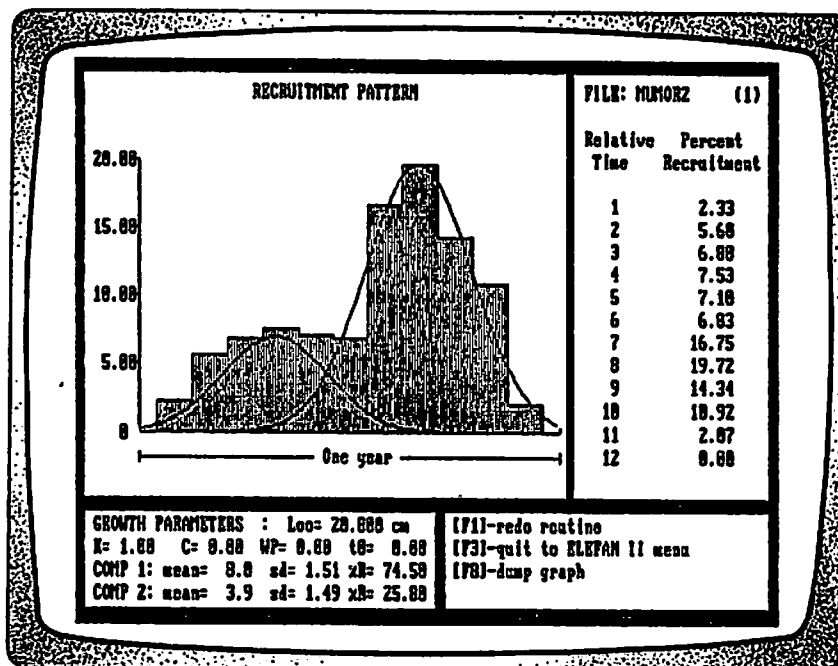
Fig. 19

Estimation of Loo and Z/K

This routine estimates Loo and Z/K using the method of Wetherall (1986), as modified by Pauly (1986).

In the same manner as with the catch curve and recruitment pattern routines, the user has the option to select samples and transform the available length-frequency data before pooling.

The transformed samples are then cumulated by length class and plotted on the left box of the screen (see Fig. 20) with midlength on the X-axis. The right box gives a plot of $(L_i(mean)-L'_i)$ vs L'_i.

The user is then required, using the plot on the left box, to select a point representative of animals fully selected and recruited, from which Loo and Z/K will be estimated.

A regression line is then fitted to the points with each point weighted by its cumulative frequency. The Loo and Z/K estimates are given by (Pauly 1986):

$$(Yi-Xi)*Ni = a+b*Xi*Ni$$
$$Loo = a/-b$$
$$Z/K = (1+b)/-b$$

```
FILENAME: MUMOR2    WT.MODE (1)          MODIFIED WETHERALL PLOT

frequency                                L(mean)-L'
1200                •  +                   8 .
                                           7  .
1000               .                       6    .
                                           5      .
 800             .                         4        .
                                           3          .
 600           .                           2            .
                                           1              .  .
 400         .                             0
                                              5   8   11  14  17
 200       .              .                      cutoff length (L';cm)
          .            .  .
   0  . . .  .  .
      5    8   11  14  17
          midlength

[F1]-choose new point           REGRESSION EQUATION:
[F2]-print results         Y = 4.65 + (-0.21 )*X ,  r=-0.943
[F3]-quit to ELEFAN II menu      Estimate of Loo = 19.286 cm
[F8]-dump graph                  Estimate of Z/K = 3.762
```
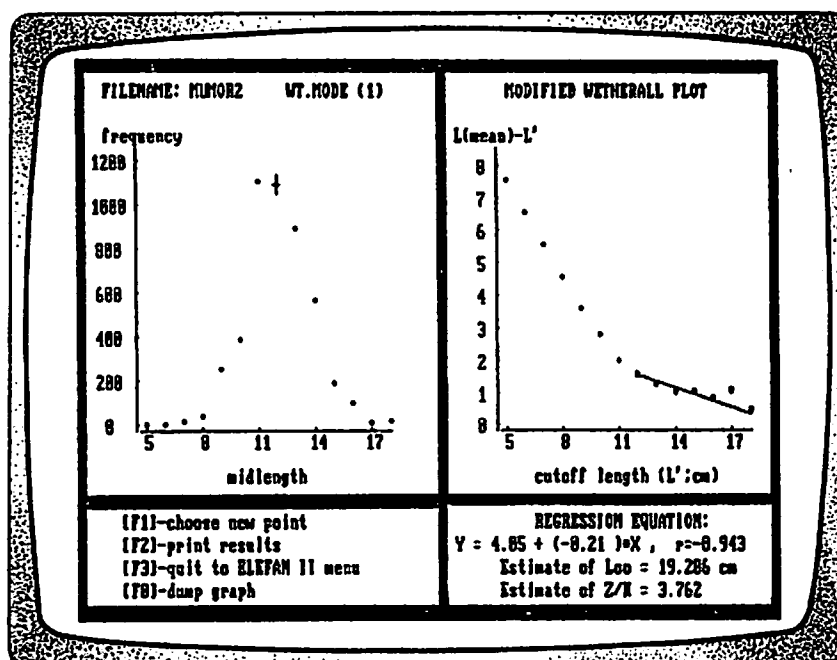
Fig. 20

Yield/recruit and Biomass/recruit

This routine estimates the optimum level of exploitation
rate (E) using the relative yield/recruit (Y'/R) model of
Beverton and Holt (1964) as modified by Pauly and Soriano
(1986). This routine may be accessed without using an ELEFAN
data file. Y'/R may be computed in two different manners :

    1. assuming knife-edge: wherein Y'/R is a function of
         selection   M/K, E and c (mean length at
                          first capture/Loo), as in
                          Beverton and Holt (1964).

    2. using probabilities : the input required here are
         of capture that   the smallest midlength,
         are gradually   largest midlength, class
         changing   interval, Loo, M/K and the
                          probability of capture for
                          each midlength (a maximum of
                          five data sets can be
                          entered at a time).

Also included in this routine is a plot of relative biomass/recruit (B'/R) vs exploitation rate (E). Fig. 21 is a sample screen output of Y'/R and B'/R with logistic selection.
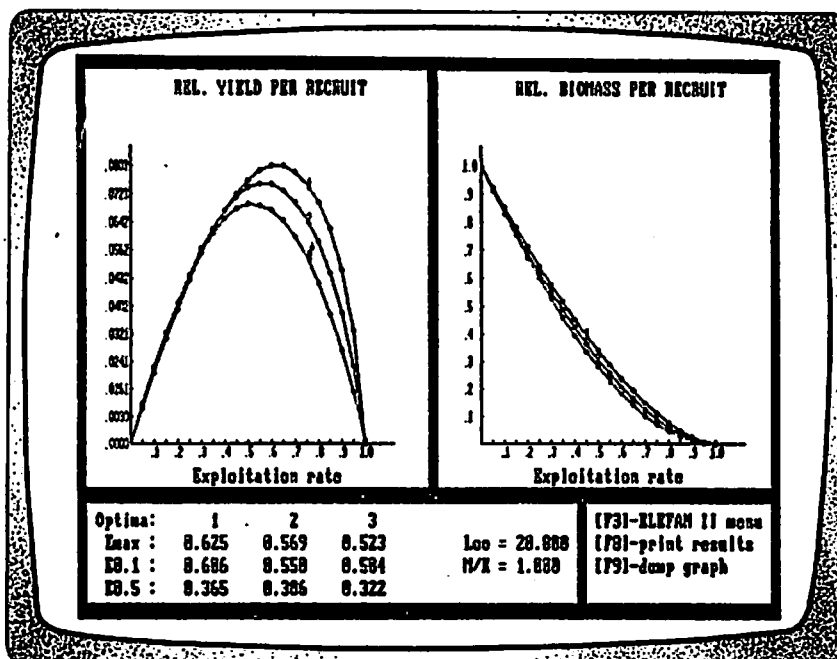

Fig. 21

WORKING WITH ELEFAN III

Introduction

ELEFAN III differs from ELEFAN I and II in that more is needed to run the program than just length-frequency data. The added data which ELEFAN III requires are catch data usually by month. Also, as is characteristic of most approaches based on Virtual Population Analysis (VPA), it is the entire catch from the whole stock which must be used, not only a part thereof.

ELEFAN III incorporates three types of VPA, i.e. VPA I, VPA II, and VPA III.

VPA I estimates for any given cohort, the standing stock (in numbers) and fishing mortalities by time interval (month, quarter, year, etc.). VPA II is used to estimate mean standing stock for a stable-age distribution, as can be simulated by combining data for several years. VPA III provides estimates of standing stock and fishing mortality by month and by length, which is achieved by "slicing" (pseudo-) cohorts through catch-at-length data by means of a set of growth parameters. This approach assumes that little exchange occurs between the monthly "cohorts", which applies mainly in short-lived animals, such as anchovies or penaeid shrimps, for which the VPA III routine has been specifically designed.

Beverton and Holt (1957) showed that the catch (C_i) from a population during a unit time period (i) is equal to the product of the population size at the beginning of the time period (N_i) times the fraction of the deaths caused by fishing, times the fraction of total deaths, or

$$C_i = \frac{F_i}{Z_i} (1 - e^{-Z_i}) \, N_i \qquad (1)$$

where F_i is the fishing mortality in the ith period,
  $Z_i = F_i + M$, and M is the natural mortality, generally
  assumed constant for all period,

The version of Beverton and Holt's catch equation which has become most widely used for stock assessment purposes, however, is

$$\frac{N_{i+1}}{C_i} = \frac{Z_i \cdot e^{-Z_i}}{F_i (1 - e^{-Z_i})} \qquad (2)$$

also written

$$\frac{C_i}{N_{i+1}} = \frac{F_i}{Z_i}(e^{Z_i} - 1) \qquad (3)$$

which is the equation in Gulland's (1965) Virtual Population Analysis and which can be derived from (1) by substituting for N_i the relationship

$$N_i = N_{i+1} \cdot e^{Z_i} \qquad (4)$$

Equation (2) is used with catch-at-age data from the whole of a fishery, and covering most of the life span of a given cohort (thus VPA is used to estimate retroactively the size of a past cohort), an estimate of M and a (guessed) value of the fishing mortality that affected the oldest age group of a given cohort (F_t). Terminal fishing mortality (F_t) and the terminal catch (C_t) are used to estimate the size of the terminal population (N_t), either from

$$N_t = \frac{C_t \cdot Z_t}{F_t(1 - e^{-Z_t})} \qquad (5)$$

or from

$$N_t = C_t \cdot Z_t / F_t \qquad (6)$$

Generally, equation (5) is used when the cohort is not extinct past N_t (and C_t), while equation (6) is used when C_t includes the last remnants of a cohort (ELEFAN III incorporates equation 5). Then, using N_t as initial value of N_{i+1}, F_i and N_i values are estimated sequentially from older to younger age group be repeatedly solving equations (2) and (4), respectively.

The discussion that follows is limited to the principles behind these various routines and the reasons they were incorporated into ELEFAN III.

VPA I : The principle behind VPA hinges around the concept of the "cohort", i.e., a group of fish or invertebrates born or hatched and recruited at more or less the same time and sharing throughout their lives a common pattern of exploitation by their predators and a fishery.

In most applications of VPA I, the "exploitation" by predators is expressed by a single value of the rate of natural mortality M, which is assumed to apply throughout most of the life of the cohort (i.e., from the time the animals enter the fishery to the time the cohort is decimated).

VPA, then, is a method to reconstruct a cohort (i.e., to estimate the number of animals that were present at each age (of a cohort's life) by using a value of M and the catch by the fishery (in terms of numbers) of each group in the cohort. The cohort is always reconstructed backward in time, starting with the last caught animals of a cohort (the "terminal catch"), which is used to obtain an approximation of the "terminal population" using a guessed value of the "terminal fishing mortality" exerted upon the "terminal population". Then, successive estimates of the population sizes are obtained for each age group by adding the catch of the fishery to a previous estimate of population size, to which the number of fish caught by predators has also been "added".

The method, which was formulated by Gulland (1965) has been reviewed by Pope (1972), Mesnil (1980) and Pauly (1984). It is incorporated in ELEFAN III as "VPA I" to allow users of the Compleat ELEFAN system to acquaint themselves with VPA in its original form and to perform age-structured VPAs whenever the data for such analyses are available to them.

VPA II : Catch-at-length data differs from catch-at-age data (such as used in age-structured VPA or VPA I) in that they do not pertain - nor can readily be made to pertain - to a given cohort as defined above.

Still, versions of VPA can be run with catch-at-length data. Two very different versions of 'VPA are incorporated in ELEFAN III which uses catch-at-length data. The first of these (VPA II) is conceived such that while it is not meant to help in reconstructing any given cohort, it can, given catch data covering the life span of several cohort, reconstruct an average cohort. Thus, the results of VPA II are not structured in time; instead the population sizes and fishing mortalities which are typical outputs of VPAs are related to sizes. These results, therefore cannot be used to manage a fishery in real time, nor to study temporal fluctuations of recruitment.

VPA III : VPA III was devised to combine the advantages of both VPA I and II, to allow use of catch-at-length data as inputs and still to run an "age"-structured VPA, and thus to obtain results that are structured both in size and in time (see Fig. 22 and 23).
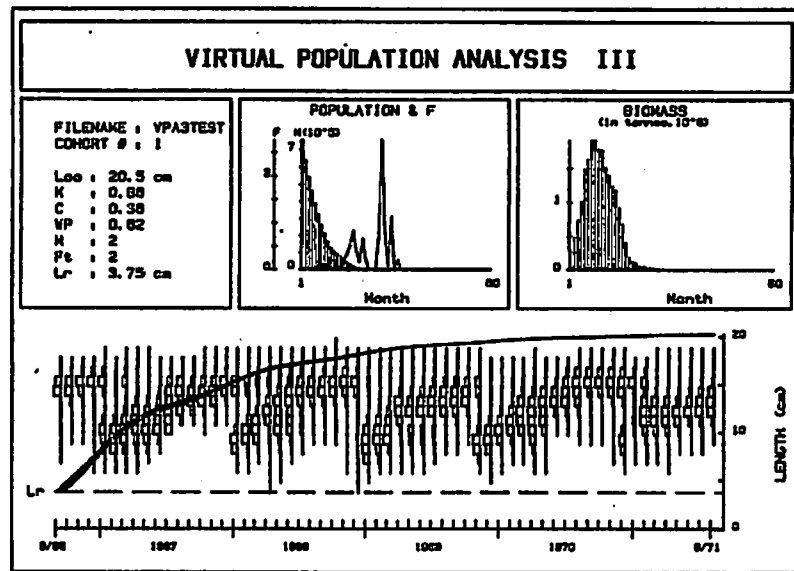
Fig. 22. Fascimile of an ELEFAN III output (via plotter) showing catch-at-length data (not to scale) and one of the many monthly cohorts which can be superimposed on these data. The upper two panels show the population and fishing mortality estimates pertaining to this cohort, along with its biomass (rightmost panel). The population estimate pertaining to month 1 is an expression of recruitment of fish of length Lr.
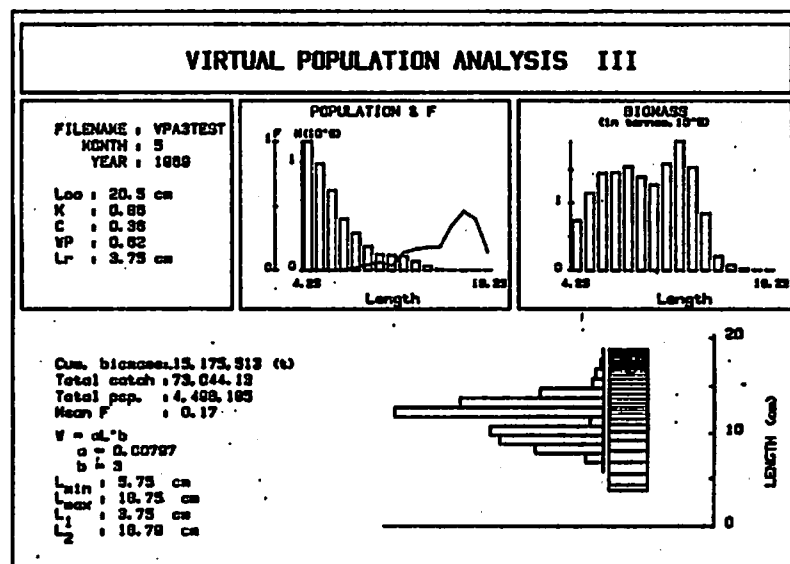

Fig. 23. Showing the summary result of a VPA III pertaining to a given month (here May 1969), and showing the catch data, the cohort "passing through that month (box with narrowing lines), the size structure of the population and other statistics.

This was achieved by assuming that all fish in the population under investigation have the same growth parameters, as is also assumed in the other ELEFAN programs.

In reality, not all fish in a given cohort have the same growth parameters, however, and it can be expected that some fish will "leave their cohort" because they grow either faster or slower than predicted by the mean cohort growth curve. Such differences in growth rate here have the effect of artificially increasing the autocorrelation between monthly estimates of recruitment.

Preparing catch data

A routine is available to allow users to store monthly catches and coefficients of the length-weight relationship. For managing the data, three routines are available;(a) data entry, (b) data editing, and (c) viewing or printing of data (see Fig.24).
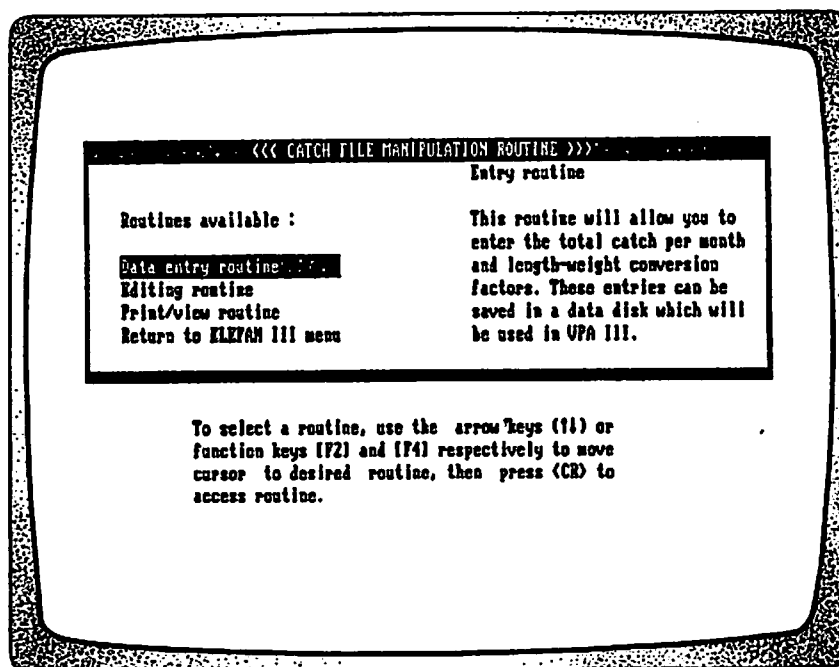

Fig. 24

Data entry. This subroutine will allow monthly catch data (in tonnes) and the constants of the length-weight relationship to be stored onto the data disk.

Monthly catches (always in metric tonnes), and the 'a' and the 'b' constants in the length-weight relationship will be asked sequentially. Note that the "a" value must link length to weight in grams (g). The values of the previous entry

will serve as a default value for the coefficients (a and b). However, the monthly catches will not have a default value. To go back to a previous entry (date), press [F2] (see Fig. 25).

Fig. 25

Editing routine. This routine will allow a catch file saved earlier to be edited. To edit, a user may either go through

Fig. 26

the file sequentially or in any order by entering the date (MM/YY) to go to a particular record. To save the edited file, press [F9]; otherwise, press [F3] to return to the previous menu without changing the file (see Fig. 26).

Print/View routine. This subroutine will allow data stored and/or edited to be displayed on screen or printed. Once a file has been accessed, pressing [F9] will print results to printer, while [F8] will only display results in the screen (see Fig. 27).


```
        <<<< PRINT/VIEW ROUTINE FOR STORED CATCH DATA >>>>

FILE PARAMETERS
                                    DATE  CATCH (in tonnes)   a      b

                                    1/53    172,325.88   8.88662 3.88888
  Filename                          2/53    199,136.88   8.88645 3.88888
  > ANCHOV                          3/53     92,571.88   8.88638 3.88888
                                    4/53    154,261.88   8.88641 3.88888
  Beginning period (MM/YY)          5/53    152,967.88   8.88668 3.88888
  > 1 / 53                          6/53    186,928.88   8.88676 3.88888
                                    7/53    137,938.88   8.88678 3.88888
  Ending period (MM/YY)             8/53    118,142.88   8.88686 3.88888
  > 12 / 82                         9/53    153,313.88   8.88694 3.88888
                                   18/53    212,868.88   8.88688 3.88888


INSTRUCTIONS

                        Press any key for more
```

Fig. 27

VPA I

The following input is necessary to run this program : (1) a file identifier independent of the files stored in disk; (2) the number of periods for which catches are available; (3) M and F_t estimates (on an anual basis); and (4) catches by ages starting with the youngest fish (see Fig. 28).

Given the necessary input (above), the results generated by this routine will be displayed graphically (see Fig. 29) and an option of either printing the results to a printer or dumping the graphic result via a plotter or a printer is also given. The user also has the option to repeat the procedure (changing the values of M and/or F_t).
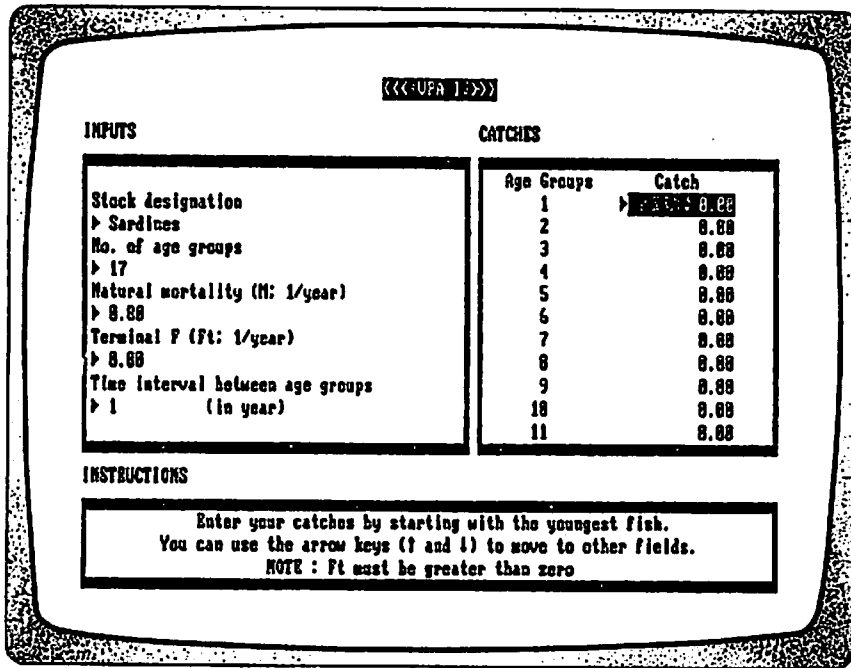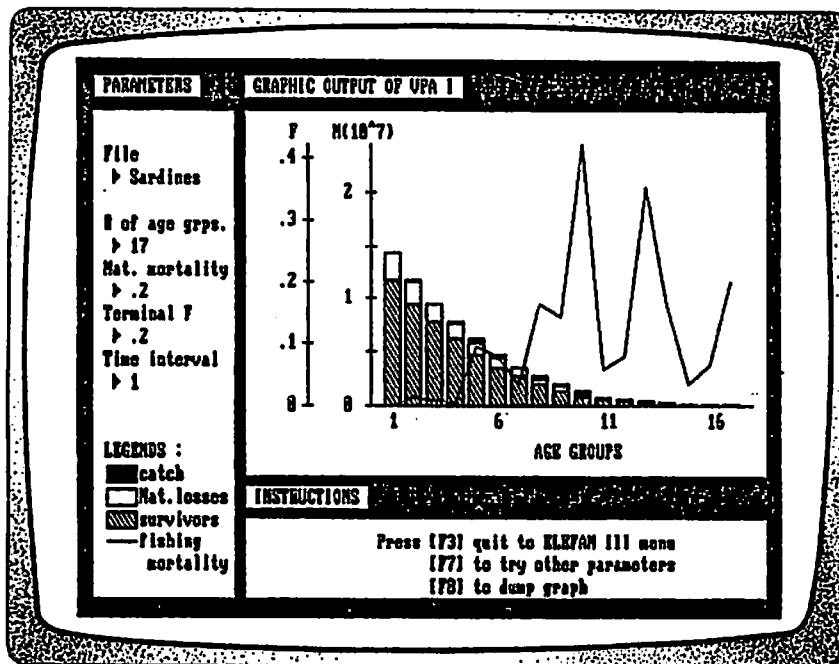
Fig. 28

Fig. 29

VPA II

VPA II makes use of either catch-at-length data or length-frequency data saved on disk through ELEFAN 0. In either type of data, the mean annual catch data (in tonnes) represented by the samples and the constants for the length-weight relationship will be required by the program. For length-frequency data, in addition to the input requirements mentioned earlier, monthly catch (in tonnes) will be asked to allow conversion of the data from length-frequency to catch-at-length type of data. The growth parameters (Loo and K), as well as natural and terminal fishing mortalities will also have to entered (see Fig. 30) to complete the neccessary inputs before a length-structured VPA can be performed.

Fig. 30

After the requirements for VPA II have been satisfied, the computer will estimate the steady-state biomass for each length class. These results may be output via a printer. The other VPA II results (estimated F_i, catches and population) may be displayed graphically on screen. As with VPA I the user has the option to print the numerical results or dump the graphic results via the printer or plotter (see Fig. 31).

VPA III

VPA III, as mentioned earlier, incorporates the features of
both VPA I and II. A rather comprehensive set of monthly
length- frequency and catch data is needed to successfully
apply the routine. Data that were stored as a "length-
frequency" data file may be transformed to a catch-at-length
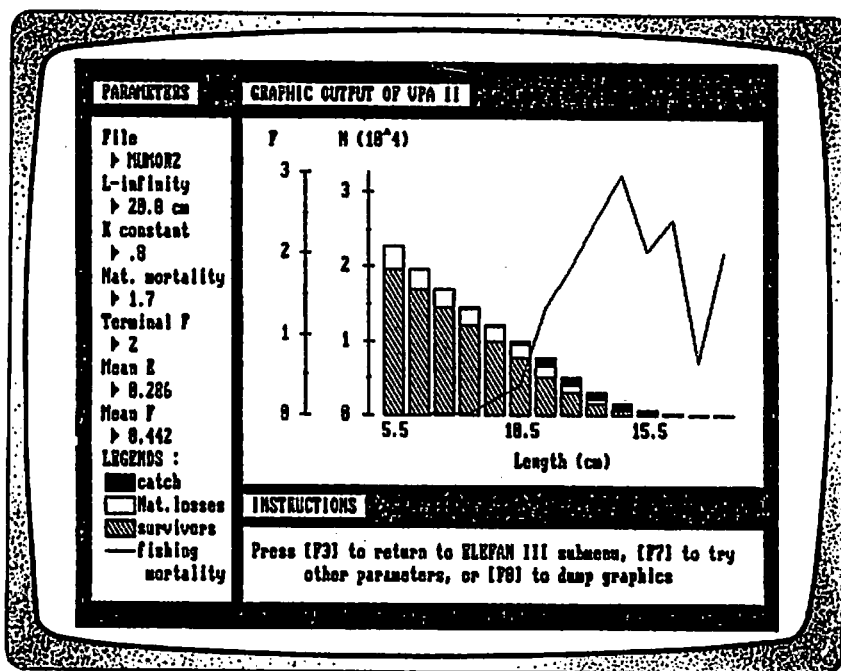data file using a file of monthly catches in tonnes (see
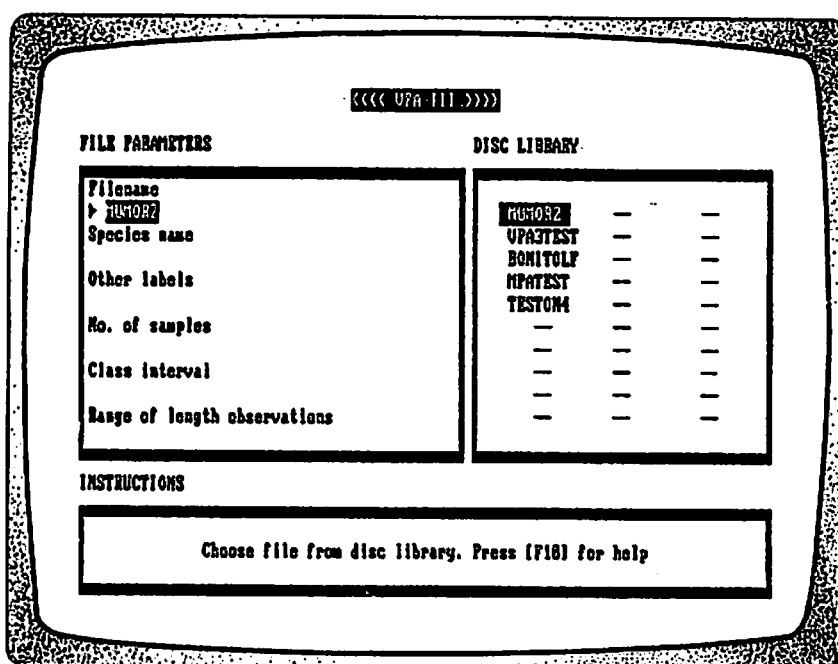

Fig. 31

Fig. 32

above). The user will be asked to select a file from the library (see Fig. 32) of catch files. The catch-at-length data file may be printed to a printer. Because of the way this routine is programmed, continuous computer paper is needed for printing.

The user is also given the opportunity to smooth the computed catch-at-length data. The growth parameters (Loo, K, C and WP), the natural fishing mortality and the terminal fishing mortality are required input. This routine may take up to 10 minutes, depending on the size of the file and the processing speed of the available computer. Using the parameters given, it will also initialize the array that stores the results for computed monthly summaries (see Fig. 34).

Once the above routine has been completed, the user will be given the opportunity to reanalyze separate cohorts, one after the other (see Fig. 33). The results generated in each cohort analysis will update the array that stores the monthly summaries. Computed results will be shown graphically and these results may either be printed or dumped to a plotter or printer (see Fig. 22). To proceed to the monthly summary routine, enter [F9] when a cohort number is prompted.
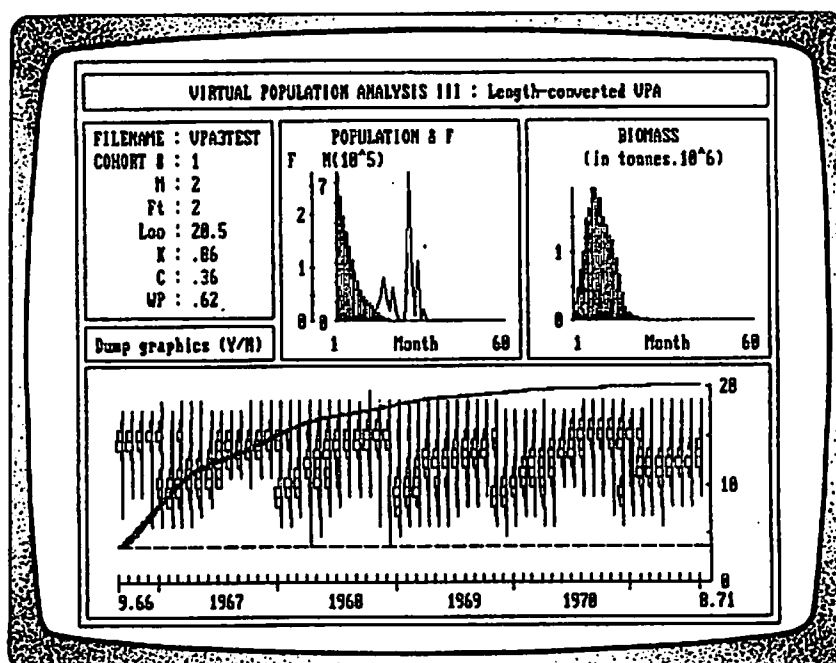

Fig. 33

For the monthly summaries, only the date (MM/YY) will be asked. The summaries will be shown graphically. These results, as in the case of the above routine, may either be printed to a printer or plotted via a plotter and/or printer (see Fig. 34 and Fig 23).
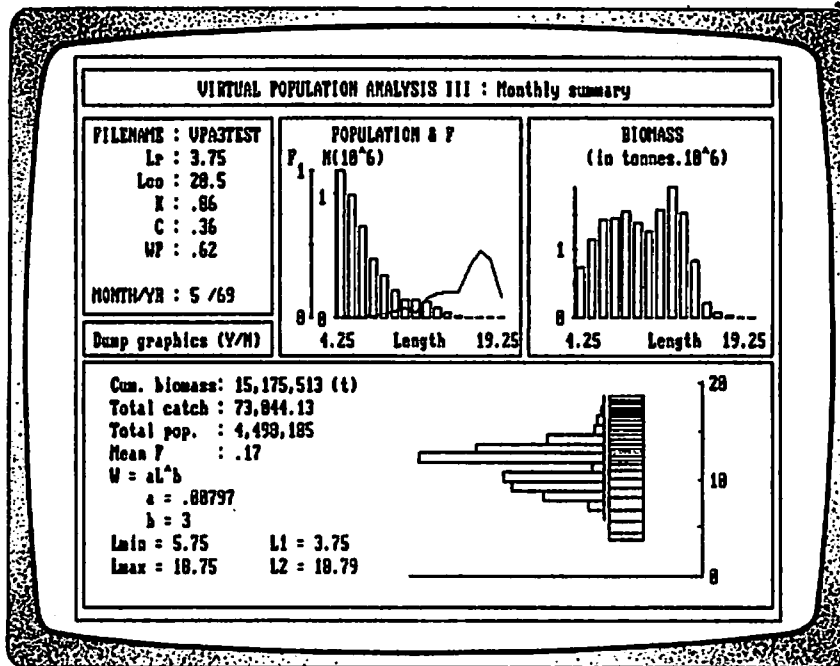

Fig. 34

WORKING WITH ELEFAN IV

Introduction (adapted from Munro 1984).

In conventional catch curves, the logarithms of the relative abundances of successive age groups are plotted against age, in order to obtain an estimate of the total instantaneous mortality rate, Z, from the slope of the descending right arm of the plot. Values of the left of the descending arm of the graph, reflecting catches of incompletely retained fishes are ignored.

Pauly (1982, 1983) has described how length-frequency distributions can be converted to age-structured catch curves in which the observed frequencies in successive length groups are divided by the time required for a fish to grow through each length group and plotted against the estimated ages of the mid-points of successive length groups. From the slope of the resulting length-converted catch curve, an estimate of Z is derived. This value is composed of the fishing mortality rate (F) generated by the gear in question plus the natural mortality rate (M). Usually, this method is applied only to length groups which are larger than the size (L') at which the fishes become fully retainable by the gear and is inapplicable to gillnets and other gears which exhibit a bell-shaped selection curve or to length groups which are within the selection ogive of gear such as trawls.

The method now proposed is based around the premise that for any fishing gear, the catch (N) of each successive catch is a function of the probability of retention (P) of that size group in the fishing gear and the relative abundance (A) of that size group in the population. Also, the total mortality coefficient (Z) observable between successive length groups in an exploited stock is the sum of the natural mortality coefficient plus the product of the probability of retention, P_i, and the prevailing fishing mortality coefficient (F).

Thus, for the ith length group

$$Z_i = M + P_i F$$

Thus, a regression of estimates of Z_i, against P_i should yield a regression of slope F and Y-axis intercept equal to M.

Methodology

The requirements for implementing the method are as follows:

a. Unbiased estimates of the length composition of the catch averaged over a year which will be entered through ELEFAN 0 and can readily be accessed through the displayed disk library once ELEFAN IV is accessed through the main menu of the package;

b. Estimates of parameters of the von Bertalanffy growth function (Loo and K); and

c. Estimates of the probability of retention (P) at successive lengths (L), acquired independently of the estimates of the mean annual length composition. (See Hamley (1975) and Pope (1975) for reviews of various methods for estimating selection curves).
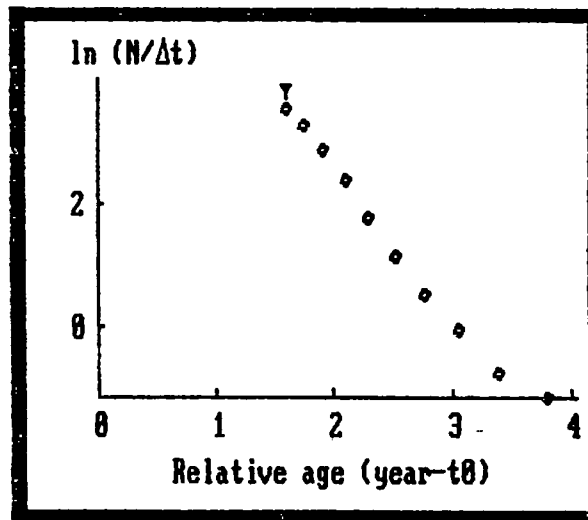

Fig. 35. Length-converted catch curve for fishes exploited by a single size of gill net in which values of log. R_m = A_m/t_{i+i} are plotted against the relative ages (t_m - t_o) attained at the mid-points of successive length groups. Note the changes in slope resulting from mesh selectivity. Data from Table 1.
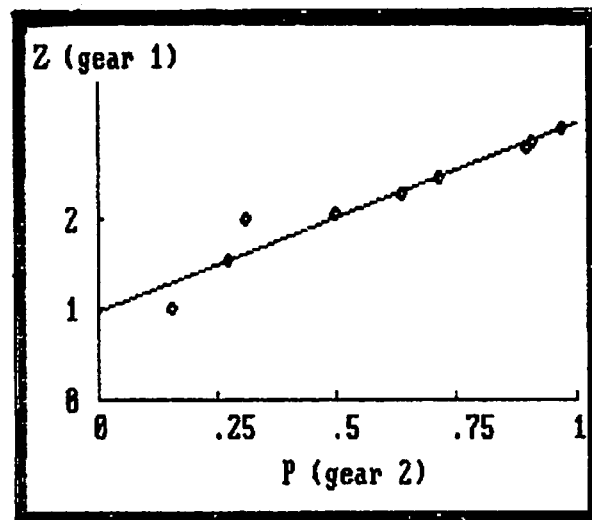
Fig. 36. Regression of coefficients of mortality, Z_i between successive length groups against the probabilities of retention, P_i, at the median points between those successive length groups. Data from Table 1.

Table 1. Hypothetical example (K = 0.5, L_∞ = 30, M = 1.00, F = 2.00) showing steps in derivation of estimates of total mortality rate (Z_i) from catches (N_m) in successive length groups (L_m) by calculating apparent abundance (A_m = C_m/P_m) and true relative abundance (R_m = $A_m/\Delta t_{i,i+1}$). Survival rate S_i = R_{m+1}/R_m and Z_i = $\log_e S_i/\Delta t_{m,m+1}$. See text for details. The ages, t, of successive lengths are the relative ages which are calculated by assigning a zero value to the parameter, t_0, of the von Bertalanffy growth function. The subscripts i and m refer to the beginning and midpoint of a length group.

L_m	L_i	P	N_m	A_m	t a) (yr)	$\Delta t_{i,i+1}$ (yr)	R_m	S_i	$\Delta t_{m,m+1}$ (yr)	Z_i
	16.0	.04			1.524					
16.5		.12	89	742	(1.597)	.148	5,004			
	17.0	.28			1.672			.790	.154	1.53
17.5		.43	272	633	(1.751)	.160	3,951			
	18.0	.62			1.833			.684	.167	2.27
18.5		.85	400	471	(1.918)	.174	2,704			
	19.0	.90			2.007			.598	.182	2.83
19.5		.97	299	308	(2.100)	.191	1,617			
	20.0	1.00			2.197			.551	.200	2.98
20.5		.97	182	188	(2.300)	.211	890			
	21.0	.90			2.408			.541	.222	2.76
21.5		.82	93	113	(2.522)	.236	481			
	22.0	.71			2.644			.544	.250	2.43
22.5		.60	42	70	(2.773)	.267	262			
	23.0	.50			2.911			.557	.286	2.05
23.5		.40	18	45	(3.059)	.308	146			
	24.0	.31			3.219			.521	.334	2.00
24.5		.22	6	27	(3.393)	.365	75			
	25.0	.15			3.584			.666	.401	1.01
25.5		.09	2	22	(3.794)	.446	50			
	26.0	.04			4.030					

a) values in brackets are t_m's

The analytical procedure is illustrated in Table 1 and Figs. 35 and 36 and by a hypothetical example from a gill net fishery. The procedure is as follows:

a. Tabulate the annual average length frequencies (N_m) of the catch and the probabilities of retention (P_m) of successive length groups (L_m) (the subscript m refers to the mid-point of a length group);

b. Calculate the apparent relative abundances (A) of successive length groups within the selection curve as $A_m = N_m/P$;

c. Calculate the ages (in years) at the start (t_i), mid-point (t_m) and end (t_{i+1}) of successive length groups and the time required ($t_{i,i+1}$) for a fish to grow through each length group;

d. Divide A_m by $t_{i,i+1}$ to get the true relative abundance (R_m) of the fish in each length group (Fig. 1 shows a length-converted catch curve in which log_e R_m is plotted against relative age (t-t_o). Note the sigmoid shape generated by mesh selectivity);

e. Calculate the survival rate between successive length groups, $S = R_{m+i}/R_m$ and the annual coefficients of total mortality, $Z_i = log_e$ S_i $t_{m,m+i}$ between successive midlengths; and

f. Plot Z_i, against P_i, to obtain estimates of F and M, using the equation $Z_i = P_i(F+M)$, and obtain an estimate of M (Fig. 36).

Computational options and variations

A variation of the above is implemented in this package wherein it is assumed that the values of N_m, A_m and R_m are derived from sampling gear (Gear 1) with a retention range smaller than is used commercially, and where the Z_i's are computed from the above values and are plotted against the probabilities of retention, P_i, of successive lengths, L_i, in the commercial gear (Gear 2). In such a case, estimates of Z_i pertaining to lengths below the retention range of the commercial year (where $P_i=0$) are direct estimates of natural mortality (M). In other words: the probabilities of capture of Gear 1 are used to compute the Z_i values, which are then plotted againts the probabilities of capture of Gear 2 to estimate M as the Y-intercept of the regression.

Putting the foregoing in a different form, if estimates of R_m, and thus Z_i, can be obtained for length groups outside of (usually smaller than) the retention range of the commercially utilized fishing gear, estimates of the natural mortality rate, M, of the unexploited size groups can be obtained from the sample length-frequency distributions.

Probability of capture for Gear 1 may be entered and saved through ELEFAN 0.

Another computational option as suggested by J. Moreau (pers. comm.) is to interpolate the computed values of Z_i and to plot these values againts the values of P entered (Gear 2). This would differ from the methodology suggested by J. Munro (1984) in which, Z_i between successive length groups is plotted against P_i values interpolated between successive length groups.
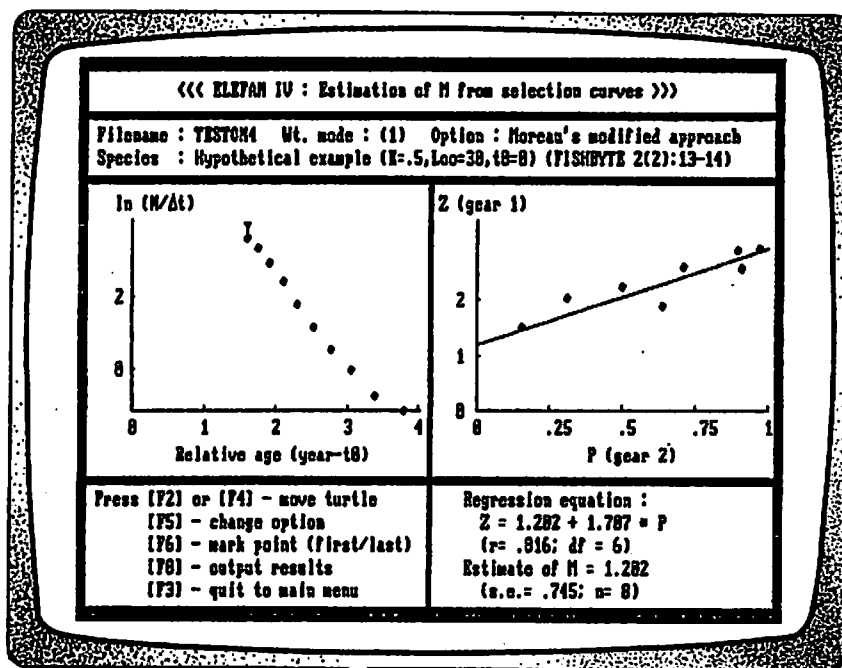

Fig. 37. J. Moreau's modified approach. Data from Table 1.

For either of the two options, the regression equation and standard error is estimated.

WORKING WITH ELEFAN V

Introduction

ELEFAN V is based on an approach suggested by Morgan (1987), and is used to estimate growth parameters through simultaneously analyzing length-frequency and growth increment data.

Growth increment data can be of three different types :

- tagging/recapture data;
- growth increments derived from length-at-age data; or
- growth increments obtained from model class progression analysis (MPA).

The approach used in ELEFAN V for the simultaneous analysis of length-frequency data and growth increment data involves presentation of a mean goodness-of-fit index (Rm) for different data types in the form of a response surface.

This programs contains two major routines :

1. Response surface for analysis of length-frequency and growth increment data and
2. Growth parameters estimation from growth increment data alone.

Response surface for length-frequency and growth increment data

The response surface presents the goodness-of-fit index (Rn) for the length-frequency data, computed as :

$$Rn=(10^{**p/**p})/10$$

and of the coefficient of determination (r^2) of the actual and predicted lengths at the end of the growth increments; thus, $Rm=(Rn+r^2)/2$.

The response surface is a two-way table with one growth parameter varying on the X-axis and another parameter on the Y-axis. More particularly, for two parameters K and Loo (leaving C and WP constant), the response surface provides Rm (x1000) values (see Fig. 38).

Fig. 38

This routine also provides an assessment of the compatibility of length-frequency to growth increment data (see Fig. 39)

Growth parameters estimation from growth increment data

The estimation of growth parameters from growth increment data begins with a Gulland and Holt plot ($\Delta L/\Delta t$ vs L, see Gulland and Holt 1959) giving the user a preliminary view of the data structure. Using the G-H plot allows the user to detect and delete outliers.
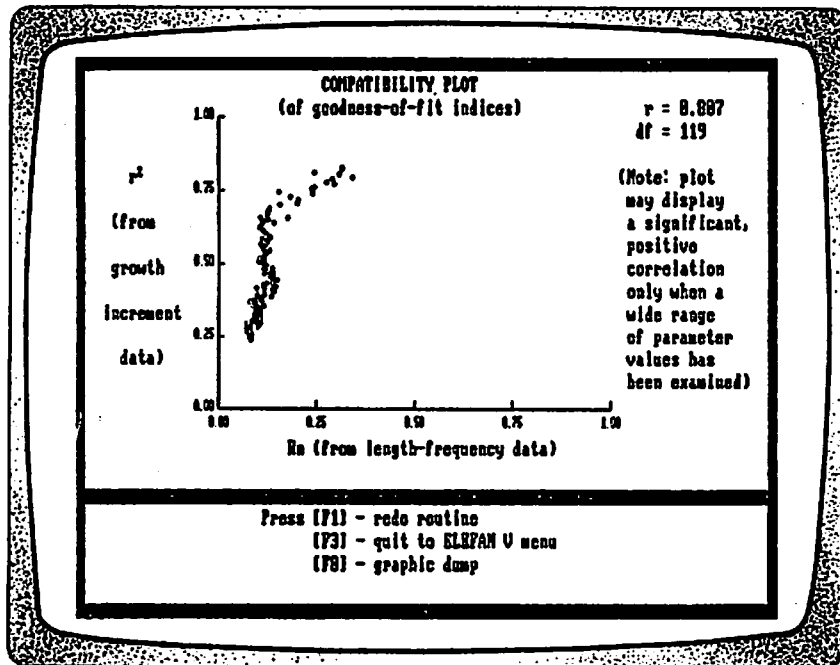
Fig. 39

After samples have been selected, a regression line is
fitted on the data for preliminary estimates for K and Loo.
The plot of deviations from the line over time is used to
identify seasonal patterns in the data, and provides initial
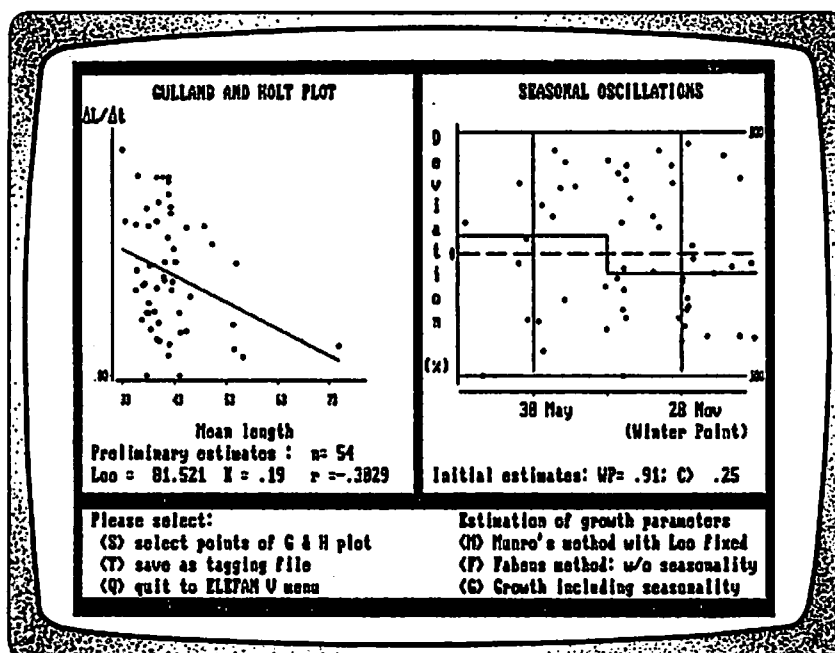estimates of C and WP (see Fig. 40).

Fig. 40

The preliminary estimates of Loo and K from the G-H plot may be improved using either of three methods:

1. Munro's method (Munro 1982);
2. Fabens' method (Fabens 1965); or
3. A newly developed method for the analysis of seasonally oscillating growth using increment data (see below).

The selected points may then be saved in another file to be analyzed jointly with length-frequency data. It is recommended to try to estimate growth parameters from available growth increment data (and to identify which part of the available data can be used for such purpose) before proceeding to the simultaneous analysis of L/F and growth increment data.

A new method for estimating the parameters of a seasonally oscillating growth curve from growth increment data

When growth increments are available, each of which has an initial date (t_1) and length (L_1) and a final date (t_2) and length (L_2), the growth parameters Loo, K, ts, and C of a seasonally oscillating version of the VBGF can be computed using a multiple regression derived as a further development of the model of Appeldoorn (1987), of the form :

$$Y = -Kd + b_1(\sin 2\pi t_1 - \sin 2\pi t_2) + b_2(\cos 2\pi t_2 - \cos 2\pi t_1)$$

where $Y = \log_e \dfrac{(L_{oo}-L_2)}{(L_{oo}-L_1)}$

$$b_1 = \frac{CK \cos 2\pi t_s}{2\pi}$$

$$b_2 = \frac{CK \sin 2\pi t_s}{2\pi}$$

$$t_s = \tan^{-1}(b_3/b_2)/2\pi$$

and $\quad d = t_2 - t_1$

Thus, one can compute R^2 values for different values of Loo until R^2 is maximized. Therefore, estimating the four parameters needed (Loo, K, ts and C) involves searching in only one dimension.

[Note that "t_s" is related to the Winter point (WP) used in the ELEFAN programs through $t_s + 0.5 = WP$]

WORKING WITH MODAL CLASS PROGRESSION ANALYSIS (MPA)

Introduction

Prior to the discovery of daily and seasonal rings in fish otoliths and scales, the detailed analysis of length-frequency data was, besides marking-recapture studies and direct observation of captive fish, the only method available to draw inferences on the growth of tropical fishes, and indeed the only method that could be applied routinely (Pauly 1987).

A great deal of confused terminology surrounds the use of length-frequency data in growth analysis and before discussing Modal Class Progression (MPA), it is necessary to clarify the terms we shall use.

We believe the term "Petersen's method", which is often very loosely used, should be restricted to the analysis of one length-frequency sample at a time. This analysis usually consists of identification of class modes or means in the sample in question using either a purely visual approach, graphical techniques, or computer-based methods of class separation. The next step in Petersen's technique is the subjective attribution of relative ages to the class modal or mean lengths thus identified. This then enables the estimation of growth parameters using the identified size groups, and the relative ages attributed to them.

Petersen's method for length frequency analysis is illustrated in Fig. 41 below, which also illustrates what happens if the subjective attribution of relative ages goes wrong (which happens quite frequently, and is behind many statements that the VBGF is not suitable as a model for growth of this or that fish).
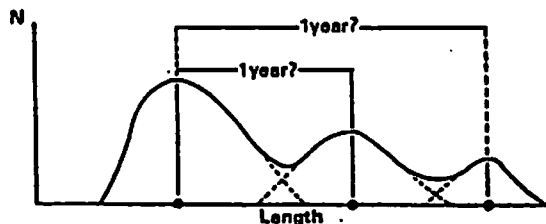

Fig. 41. Application of the 'Petersen Method' (*sensus stricto*) to a hypothetical length-frequency sample. Note that the time separating various peaks must be assumed, a difficult task in animals which may, or may not, spawn several times a year.

We shall use the term "Modal Progression Analysis" (MPA) for the method in which several length-frequency samples are plotted sequentially, and where the apparent shift of modes is used to infer growth. In MPA, the identification of class modal or mean lengths is done as in Petersen's method, after which subjective identification of modes perceived to belong to the same cohort of fish enables the tracing of growth curves, or computation of growth increments between modes. Thus, in MPA, the critical issue is not the attribution of "ages" to the various groups - as in the Petersen method - but the linking of means perceived to belong to a same cohort (see Fig. 42).
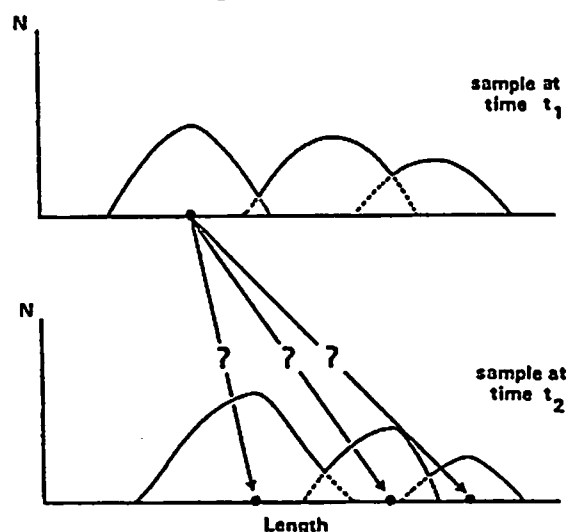

Fig. 42. Application of 'modal progression analysis' to a set of two samples obtained at known times (t_1, t_2). Note that the problem here is the proper identification of peaks to be inter-connected, and not the question as to how the much time separates the peaks (as was the case in Fig. 41).

The subjective judgement required in the second step of both of these methods and the large potential errors thus induced have prompted a search for ways of reformulating these two traditional methods so that improved solutions are obtained.

This was achieved in this package in two ways:

1. by constraining possible solutions through the use of pre-selected growth functions, usually the VBGF and especially its seasonally oscillating formulation (ELEFAN I); and

2. by combining the length-frequency data with other information, such as growth increment data from tagging-recapture experiments or length-at-age data obtained, e.g., from otolith analysis (ELEFAN V).

However, many researchers prefer to stick to modal progression analysis (MPA) despite its shortcomings. For these, we have included here a computerized version of MPA as part of the Compleat ELEFAN package.

This routine is subdivided into four parts: (a) separation of length-frequency samples into normal distributions using the method of Bhattacharya (1967) or entry of means (and standard deviations if available), (b) linking of the means, (c) computation of the C.V. of Loo and (d) saving of the linked means (which represent growth increment data, having the same characteristic as tagging/recapture data) which can then be analyzed using ELEFAN V.

Data files and sample access

As in the case of other routines of the Compleat ELEFAN, the computer will first search for a disk library in the data disk when this routine is accessed. Once the library is read, the directory will be shown in the right portion of the screen. The user will be asked to select a file from the list displayed.

Once a file has been read, its parameters will be shown in the display. The computer will read the samples after [F9] has been pressed. Next, the computer will ask for the number of the sample to work with (a value entered that is greater than the total number of samples or less than 1 will not be accepted). Once the sample is accessed, the program will chain to Part I of MPA, which is the separation of normal distribution using the Bhattacharya method.

Bhattacharya method

There are four boxes in the left side of the screen (Fig. 43). The first box contains the filename and sample number accessed. The next box contains the parameter of the turtle, i.e., the coordinates for the X and Y axes (after transformation) and the population (N). The third box contains the parameters of a normally distributed component that has been identified, and the last box is for the messages. In this particular instance (see Fig. 43) the user is asked to mark the first point by moving the turtle using the arrow keys and then pressing the [F6] or <SPACE BAR> when the turtle is properly positioned. Later the user will be asked to identify the second point.

[F10], [F3] and [F8] are interrupt keys whose functions (help, quit to main menu and graphic printer dump respectively) may be accessed at any time, as needed.

The population in each normally distributed component will be computed and the regression line and the normal curve will be drawn (see Fig. 44). The user will be given the opportunity to select new points if the computed parameters of the component generated is not satisfactory.

The estimated population of the defined component will be subtracted from the sample and a display of the new transformation will be displayed.
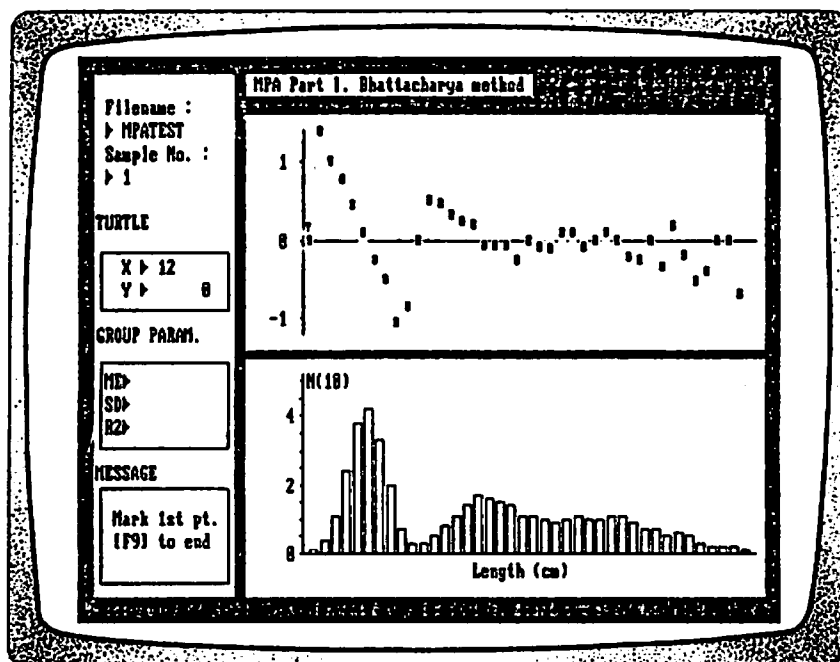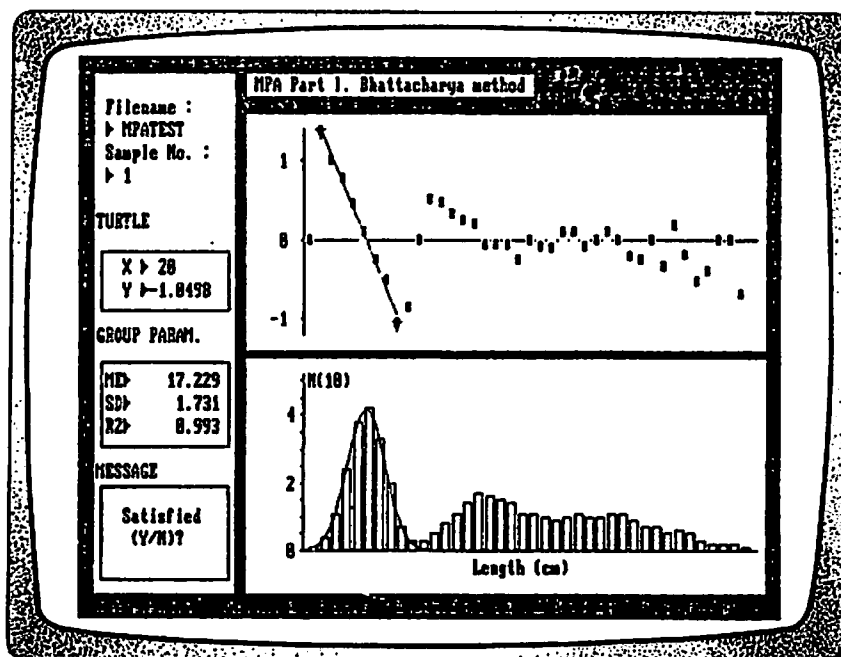

Fig. 43

Fig. 44

The procedure is repeated until most or all visible
components are separated, in which case a user can press
[F9] to end. A summary of results will be displayed and may
be printed.

The program will then compute expected frequencies for the
whole sample (see Fig. 45); when sufficient degrees of
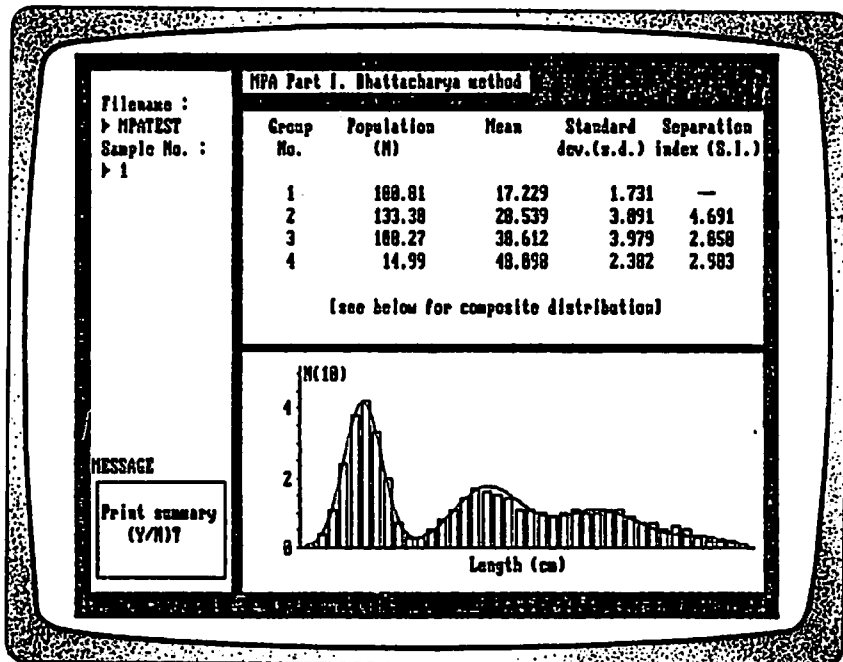freedom are available, a chi-square test will be performed,

Fig. 45

indicating how well the expected frequencies fit the
observed frequencies. These results may be plotted on a per-
sample basis on a plotter (see Fig. 46). The program will
automatically store the computed means for later analysis.
These means, may however, be lost if you immediately return
to the main menu (by pressing [F3]) and it will also be
overwritten if the same sample is reanalyzed.

Linking of the means

When all (or enough) samples have been analyzed, enter Q to
proceed to the routine allowing linking of the mean lengths
(i.e. derivation of growth increment data). This routine
uses the four arrow keys to move the turtle (see Fig. 47).

Position the turtle at a point representing the start of a
growth increment, and mark this point by pressing [F6] or
<SPACE BAR>, then move the turtle to a point representing
the end of the growth increment in question and mark it
(note that negative growth increments will be accepted).

Continue until all points representing end points of growth increments have been marked.
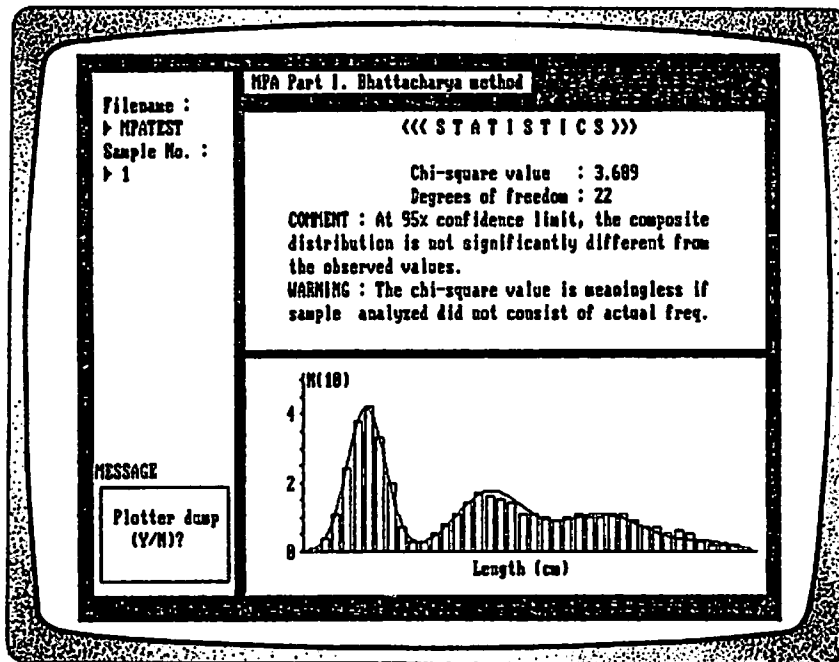

Fig. 46

Press [F7] to redo the routine. The C.V.'s, means and $\Delta L/\Delta t$ value for each pair of means are saved for later analysis.
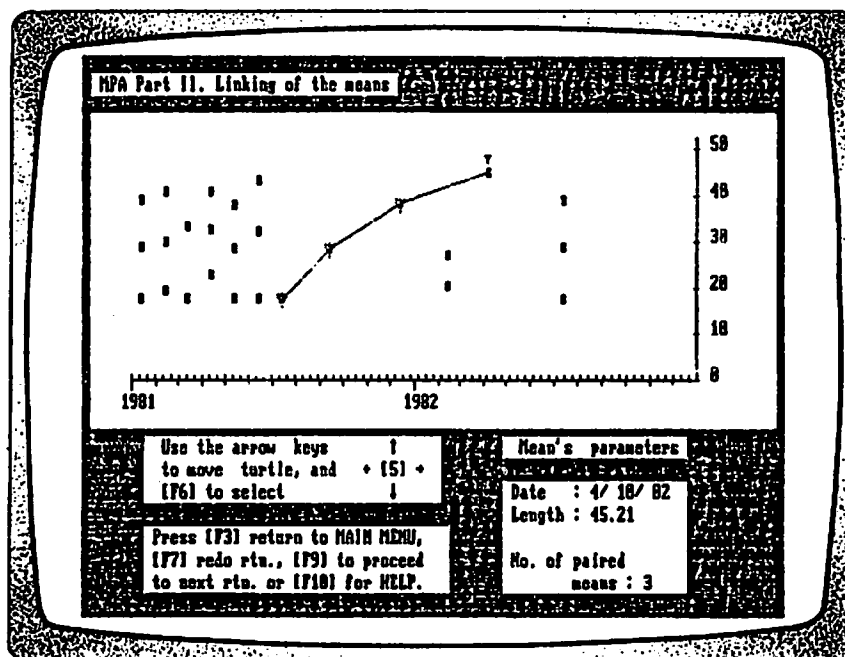

Fig. 47

C.V. vs growth rate

In this newly developed routine, a plot of the $\Delta L/\Delta t$ values vs the mean C.V. of the linked means is generated (see Fig. 48). This plot may be used to identify the most likely of two alternative hypotheses concerning the distribution of lengths about age :

(i) constant C.V.; or
(ii) C.V. declining with $\Delta L/\Delta t$ and hence with length.

In case the first alternative applies, an overall mean C.V. is computed from the individual C.V. estimates. For the second alternative to be likely, the correlation coefficient between the growth increments and the means of the paired C.V. values must be significant and positive; also the intercept of the (GM) regression (i.e. the C.V. of Loo) must be positive.
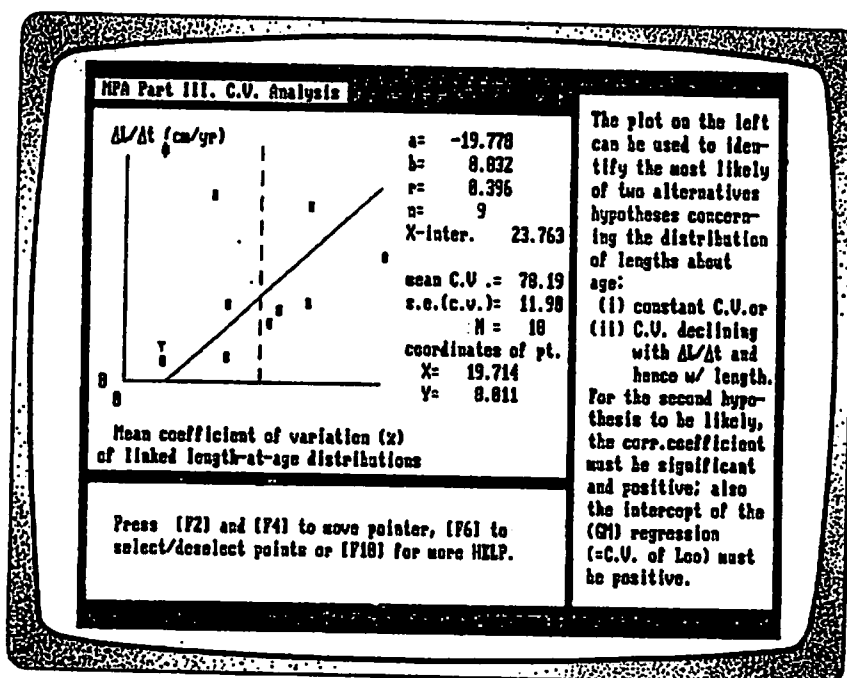

Fig. 48

Estimates of the C.V. of Loo may be used, when available, as an input to Sainsbury's (1980) method of computing population growth parameters from growth increments derived from fish with individually variable growth parameters. The linked points (i.e. growth increments) may be saved on disk as an increment data file by pressing [F9].

A re-linking of the means may be done by pressing [F7] if the above plot gives an unsatisfactory result.

ACKNOWLEDGEMENTS

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The ICLARM Software Project

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