DISTANCE USER'S GUIDE

Version 2.2

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INTRODUCTION

DISTANCE provides an analysis of distance sampling data to estimate density and abundance of a population. We assume the reader is familiar with the concepts of distance sampling. For details about data collection and analysis methods, refer to the following book:

Buckland, S.T., Anderson, D.R., Burnham, K.P., and Laake, J.L. (1993). Distance sampling: estimating abundance of biological populations. Chapman & Hall, London.,

which replaces the older monograph:

Burnham, K.P., Anderson, D.R., and Laake, J.L. (1980). Estimation of density from line transect sampling of biological populations. Wildlife Monograph No. 72.

Throughout this Guide, the notation, (pg:xxx-xxx), refers to relevant page numbers in Buckland *et al.* (1993) which contain details on the notation, concepts and analysis methods.

DISTANCE evolved from program TRANSECT (Burnham *et al.* 1980). However, DISTANCE is quite different from its predecessor as a result of changes in analysis methods and expanded capabilities. The name DISTANCE was chosen because it can analyze several forms of distance sampling data (pg:4-7): line transect, point transect (variable circular plot) and cue-count. By contrast, TRANSECT was designed only for line transect data. In addition, the following features have been added:

1. A wider choice of estimation models developed around a key/adjustment function (pg:46-48) approach is included. Monotonicity constraints can be imposed on the models (pg:73). The "best" model is selected from the chosen set of models (pg:73-77).

2. Several methods of adjustment term selection (pg:112,399-400) are available including sequential, forward selection and fitting all possible combinations. In addition, specific adjustment terms can be selected.

3. Clustered populations (*i.e.*, animals observed in groups) (pg:12-13) are fully supported with size-bias analysis (pg:79-80) of expected cluster size and estimation of cluster density and density/abundance of animals.

4. Stratified estimates of density and abundance can be constructed (pg:99-102).

5. Both left truncation (pg:15,273-277,377-379) and right truncation (pg:15,50,106-109) of the data are supported .

6. Bootstrap re-sampling can be requested for robust estimates of variance (pg:94-96,119-120,155-158).

DISTANCE understands and interprets a relatively simple command language. You "tell" DISTANCE what you want to do by entering commands and data. The command approach was chosen over a menu or question-answer interface because it easily allows the program to be used in either interactive or batch mode (commands and data stored in files). This Guide describes the commands and the way you will use them to analyze a set of data. In addition, we give several examples showing the commands and data used as input and an explanation of the output.

Installation Instructions

A single floppy disk accompanies this manual. It contains the following files that must be installed before use:

DIST.ARC	- contains the executable program and help files
README	- installation instructions and other notes as needed
INSTALL.BAT	- batch file for program installation
EXAMPLES.ARC	- contains example input files
PKUNZIP.EXE	- program to unpack the .ARC files

We assume that you will be installing the software onto your hard disk which is designated by C: and the installation floppy disk is in drive A:. If either disk is designated by another letter, use that letter wherever we use C: or A:. Create a separate directory for the DISTANCE program and associated files, by entering the following commands:

```
C:
CD\
MD YourDirectory
```

and replace *YourDirectory* with the name you want to give the directory (*e.g.*, *DISTANCE*). After creating a directory, install DISTANCE by entering the following:

```
A:INSTALL  A:  YourDirectory
```

For example,

```
A:INSTALL A: C:\DISTANCE
```

will install the software from drive A: into the directory *DISTANCE* on drive C:. Various files will be installed:

1) *DIST.EXE*, the default executable file,
2) *DISTL.EXE*, an alternate executable file,
3) *DIST.HLP*, a text document containing help accessed by the program,
4) *BROWSE.COM*, a file listing utility,
5) *README*, a text file containing any corrections or new material not in this Guide, if needed, and
6) numerous template and example input files described in the EXAMPLES section.

Program Requirements and Limitations

DISTANCE will only run on an IBM-PC or compatible microcomputer. A numeric co-processor is not required but will improve the speed substantially (note: a co-processor is built into an 80486DX processor or above). Approximately 1 MB of disk space plus additional space for input and output files is required. Also, your computer's configuration file (CONFIG.SYS) should specify FILES=20 or greater.

Available conventional memory should be sufficient on a machine with at least 640K of memory unless numerous TSR (Terminate-Stay-Resident) programs or large device drivers (*e.g.*, network drivers) are used. A problem exists, if either of the following error messages is given upon running DISTANCE:

Not enough memory

or

Heap space limit exceeded.

Check the amount of free (available) memory for your computer with either of the DOS commands, CHKDSK or MEM. Several solutions are given below for insufficient memory:

1) Load device drivers or TSR's into high memory, if you have DOS 5.0 or higher,
2) Use the alternate executable file (described below) which requires less memory but runs slower,
3) Reduce the memory setting for the overlay area (described below), or
4) Do not load optional TSR's or device drivers while running DISTANCE.

It is possible to change the memory requirements within certain limits. If you increase the memory, the speed may increase and vice versa. The program memory is changed by setting the environment variable BLINKER with the set command, before running DISTANCE. The format of this command is *SET BLINKER=/OOxx*, where OO represents Overlay Opsize and xx is the amount of memory in kilobytes (KB). The default value is 40 and it can be set to as low as 28 and as high as 128. If you increase the memory requirements beyond the amount of free conventional memory, a fatal error will be given when you attempt to run the program. An example setting is, SET BLINKER=/OO28, which will decrease the memory requirements by 12K.

Two executable files are included to provide some flexibility in memory, speed and limits on the amount of data that can be analyzed. The requirements and limits of each are as follows:

DIST.EXE - requires approximately 480K of conventional memory and has the following limits: 1000 observations, 700 samples, 100 strata.

DISTL.EXE - requires approximately 470K of conventional memory and has the following limits: 5000 observations, 2000 samples, 400 strata.

DISTL requires less memory and has larger limits only because the program is heavily overlaid and as a result will run more slowly. Hopefully, the limits of *DIST.EXE* will be sufficient for most applications. If so, you can save disk space by deleting *DISTL.EXE* after it is installed. If you choose to use *DISTL.EXE*, do either of the following:

1. use the command *DISTL* in place of *DIST* to execute the program, or
2. rename *DIST.EXE* to another filename and rename *DISTL.EXE* to *DIST.EXE*.

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How to Start DISTANCE

If you want to start DISTANCE from any disk drive and directory, place *YourDirectory* in the computer's PATH statement (*e.g.* SET PATH=C:\ ;C:\ DOS;C:\ *YourDirectory*). Then simply enter:

DIST

to start the program. If *YourDirectory* is not included in your PATH, start DISTANCE by entering:

YourDirectory\DIST

where *YourDirectory* is the directory in which you installed *DIST.EXE* or change to *YourDirectory* (CD *YourDirectory*) prior to issuing the DIST command. Either of the above commands runs DISTANCE interactively. DISTANCE displays a title screen and the *DISTANCE>* prompt on the screen. DISTANCE is ready for you to enter commands and data from the keyboard. Alternatively, DISTANCE can read commands and data entered into text files with an editor (*e.g.*, EDIT) or saved from within DISTANCE (see the *ASSIGN* and *STORE* commands described later). The latter approach, which eliminates redundant entry of commands and data, is described under Batch Operation and the ASSIGN command. Until you become familiar with DISTANCE, we recommend entering commands and data interactively.

A Simple Example

DISTANCE needs three types of information to perform an analysis:

1) OPTIONS - defines the type of sampling and data, measurement units, and various other settings which affect data entry and analysis,

2) DATA - defines the sampling structure (strata & samples), sampling effort (*e.g.*, line length), and appropriate observation data (*i.e.*, distance and cluster size), and

3) ESTIMATE - defines the parameters to be estimated, how the data are to be treated in the analysis, which estimators are to be used, and how variances are to be estimated.

This information is entered via commands that define option values, structure data input, and initiate and control estimation. Reasonable default values have been chosen for many of the options.

Figure 1 on the next page gives an example of command and data input, which are organized into sections (procedures) corresponding to the type of information. For this example, the *Options* section defines:

1) line transect sampling was used,
2) line length is measured in miles,
3) density is to be expressed in numbers per hectare, and
4) distance (perpendicular) is measured in intervals of 1 foot to a maximum distance (width) of 4 feet.

The *Data* section defines:

1) 4 lines were sampled with lengths of 11.2, 14.3, 5.6 and 111.2 miles, and
2) the number of animals sighted in each of the 4 1-foot intervals for each line (sample) (*e.g.*, for line 2: 4 were seen at distances between 0 and 1 foot, 3 were seen at distances greater than 1 foot but within 2 feet, likewise none were seen between 2 and 3 feet, and 2 were seen between 3 and 4 feet).

Two analyses are requested (one for each Estimate procedure). In each analysis, 3 estimators are defined from which DISTANCE chooses the "best" model (pg:73-77). In the second analysis, the observations beyond 3 feet are truncated (pg:15). Between the first and second analysis, the output is displayed (List) to the screen for review. Notice that the options and data are retained for the second analysis but estimate commands are not retained (*i.e.*, each *ESTIMATOR* command was repeated in the second analysis).

```
Options;
 Type=Line;
 Length/Units='Miles';
 Area/Units='Hectares';
 Distance/Intervals=0,1,2,3,4
        /Units='Feet';
End;
Data;
 Sample/Effort=11.2;
    5,6,2,1;
 Sample/Effort=14.3;
    4,3,0,2;
 Sample/Effort=5.6;
    2,0,1,0;
 Sample/Effort=111.2;
    15,6,7,0;
End;
Estimate;
 Estimator/Key=Hazard;
 Estimator/Key=Hnormal;
 Estimator/Key=Uniform;
End;
List Output;
Estimate;
 Estimator/Key=Hazard;
 Estimator/Key=Hnormal;
 Estimator/Key=Uniform;
 Distance /Width=3;
End;
```

Figure 1. Example input file.

Not all input to DISTANCE will look exactly like Figure 1. However, it does illustrate the basic structure of input to DISTANCE and the interactive nature of the analysis. Not all of the possible options need to be specified if the default values are acceptable. For example, the command *TYPE=LINE;* could be deleted for this example, because it is the default value. The format for data entry will vary depending on the type of sampling and data defined by the options. In this example, the *Distance* command within *Options*, defines grouped (interval) distance data (pg:14) will be entered (*i.e.*, the number of observations within each distance interval is entered rather than the distance for each observation). We have created numerous template files like Figure 1 that are installed into *YourDirectory*. The template files, which are described in the EXAMPLES section, provide generic sets of commands and illustrate the data format for various sampling situations. They can be modified with any text editor to include your data and other commands or options for your specific analysis.

Entering Commands

The three primary commands issued at the *DISTANCE>* prompt are: 1) *OPTIONS;*, 2) *DATA;*, and 3) *ESTIMATE;*. These commands initiate a procedure to begin entering a section of input and change the prompt to *OPTIONS>*, *DATA>*, and *ESTIMATE>*, respectively. A section of input is completed by entering the command *END;*. After completing the *OPTIONS>* and *DATA>* input sections, the *DISTANCE>* prompt will reappear. However, after completing the *ESTIMATE>* section, the analysis is performed before the *DISTANCE>* prompt reappears.

You can issue the *OPTIONS*, *DATA*, and *ESTIMATE* commands repeatedly and in any order; however, the order is important in most circumstances. For example, data must be entered before estimation is initiated and options which define the type of data, must be entered before entering the data, unless the default values are acceptable. However, after entering data or performing an analysis, options which do not change the basic data format can be changed. If you change options,

it is only necessary to set those options you want to change. All unchanged values remain as they were last set. Unlike *OPTIONS>*, if you re-enter *DATA>,* previously entered data are cleared from memory. The *ESTIMATE>* procedure can be re-entered any number of times without regard to previous analyses.

Be aware of the command prompt because different commands are accepted at each prompt. Some commands have the same name but perform different functions at different prompts. For example, the *DISTANCE* command at the *OPTIONS>* prompt defines how the distance data will be input, but at the *ESTIMATE>* prompt, the *DISTANCE* command defines how distances will be analyzed. The **header** at the top of each page in this Guide identifies the appropriate prompt for the command.

Except for the distance (or frequencies) and cluster size measurements, all information is entered via commands. The format for entering data varies depending on the type of data and is described in detail in the DATA> section.

The information contained in each command varies but the general syntax for a command is the same for all commands. The general command syntax is:

command_base /switch1 /switch2 ... /switchn;

The command_base can be one of the following forms:

command_name
or
command_name=list

where *list* is one or more elements separated by **commas**. A switch can also be one of the following forms:

switch_name
or
switch_name=list

where *list* is one or more elements separated by **commas**. Use commas to separate list elements, **not** spaces. If the elements are separated by spaces, unpredictable results will occur. The switches are not required but the base portion of the command is required. The base portion is either just the command name or a command name followed by = and a list of one or more elements. For example, for the *ASSIGN OUTPUT* command,

ASSIGN OUTPUT=FILENAME

is the base portion of the command.

Each command must end with a semi-colon (;). A command can exceed more than one line but cannot exceed 255 characters. Commands can only be split across lines between switches and between list elements. Blank space is allowed within commands except embedded spaces are not allowed within command and switch names and list values. All characters beyond the semi-colon are ignored and can be used as comments. The following are some examples which demonstrate valid and invalid ways of entering commands:

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Valid command syntax	Invalid command syntax
`ASSIGN INPUT = FILE.TST/NOECHO;`	`ASSIGN I NPUT=FILE.TST/NOECHO;`
or	*or*
`ASSIGN INPUT=FILE.TST /NOECHO ;`	`ASSIGN INPUT= FILE.TST;`

When commands are entered interactively and the [Enter] key is pressed before completing the command, DISTANCE will respond with

```
[waiting for input]
```

This mode continues until you exceed 255 characters or a semi-colon is entered to complete the command.

Commands can be entered in any combination of upper and lower case letters because all characters are changed to upper case. For Titles and Labels, put characters within single quotes to maintain lower case or to use special characters (*e.g.*, / or ;). For example, `Title='Analysis of survey 1/14';` will be a valid command which will set the title to `Analysis of survey 1/14` with the upper and lower case maintained in the output. If you wish to include a single quote in the label or title, use two contiguous single quotes to specify a single quote in the label. For example, `/LABEL='Fred''s sample'` will become `Fred's sample` in the output.

Command, switch and value names can be abbreviated to the fewest number of characters that avoids ambiguity (*e.g.*, entering D when DISTANCE and DENSITY are potential commands would be ambiguous, but DI or DE would not be ambiguous). If the value is ambiguous or unrecognized an error is issued which lists the potential values. However, if you enter extraneous characters that do not match a name, the name will not be recognized. For example, DIX will not be interpreted as DISTANCE and will generate an error. The best strategy is to use as few characters as needed to make the command simple to type but readable.

Descriptions of the commands are given below. The commands are organized alphabetically within input prompt (*DISTANCE>*, *OPTION>*, *DATA>*, and *ESTIMATE>*). For each command, the format and description of the command are given. Examples are often given to illustrate the command, and where appropriate, synonyms for command and switch names are listed. Similar command descriptions can be obtained interactively within DISTANCE via the *HELP* command. Obtain help with a particular command by entering at the appropriate command prompt:

```
HELP command_name;
```

For example at the *DISTANCE>* prompt, entering `HELP ASSIGN;` will display information about the *ASSIGN* command. One or more screens of information will be displayed which are similar to the format of the command descriptions given in this documentation. The lines ('| |') around a list of items indicates that one item from the list should be chosen.

Program Files

DISTANCE reads commands and data from input files and creates several output files as illustrated below:

```
 Input Files      >--DISTANCE-->     Output Files
INPUT  (keyboard)                   OUTPUT  (SCREEN & DIST.OUT)
DATA   (keyboard)                   RECORD  (SCRATCH)
                                    LOG     (SCREEN)
                                    PLOT    (SAS.PLT)
                                    BOOT    (BOOT.OUT)
                                    STATS   (SCRATCH)
```

The default names for the input and output files are given in parentheses. (Note: *SCRATCH* is a temporary file which disappears at the end of the program unless saved.) Each file can be given a different name. The contents of each file and the ways in which they can be manipulated are described below. The file manipulation commands are described under *DISTANCE>*. If DISTANCE terminates abnormally, scratch files (*e.g.*, beginning with XX or ZZ) that are normally deleted may remain in your directory. You can delete these files, if they exist.

Input

INPUT and *DATA* are the 2 sources of input. *INPUT* is the primary source of commands and data. *DATA* can be assigned to a separate file with the *INFILE* command. By default, command and data entry are interactive (*INPUT* and *DATA* are assigned to the keyboard). Enter commands and data interactively until you become familiar with DISTANCE. However, both input sources can be independently assigned to disk files which contain the commands and data. For example, *INPUT* can be assigned to a file *DIST.INP* with the *ASSIGN* command:

```
ASSIGN INPUT=DIST.INP;
```

which instructs DISTANCE to take all further commands and data from the file *DIST.INP* until it encounters: 1) an *EXIT;*, 2) the end of the file, 3) a new *ASSIGN* command, or 4) an *INFILE* command.

The *DATA* file contains the data to be entered at the *DATA>* prompt. By default, *DATA* is taken from the *INPUT* file. Thus, if the *INPUT* file is assigned to a disk file, the *DATA* file is also assigned to this same file by default. The *DATA* file can be assigned to its own separate file by using the *INFILE* command (described under DATA> section). This can be done independently of assigning the *INPUT* file. Figure 2 gives an example to illustrate this relationship.

INPUT file assigned to DIST.INP:

```
Enter:
   ASSIGN INPUT=DIST.INP;

File: DIST.INP

   OPT;
     DIST/INT=0,1,2,3;
   END;
   DATA;
     SAMPLE /EFFORT=12.5;
       10,8,6;
   END;
   ESTIMATE;
     ESTIMATE/KEY=UNIF;
   END;
```

INPUT file assigned to DIST.INP DATA assigned to DIST.DAT

```
Enter:
    ASSIGN INPUT=DIST.INP;


File: DIST.INP

    OPT;
      DIST/INT=0,1,2,3;
    END;
    DATA;
      INFILE=DIST.DAT;
    END;
    ESTIMATE;
      ESTIMATE/KEY=UNIF;
    END;

File: DIST.DAT

    SAMPLE /EFFORT=12.5;
      10,8,6;
```

Figure 2. Example of *INPUT* and *DATA* file contents. The *ASSIGN* statement is entered interactively to DISTANCE or the file is used as a batch input file (*I=DIST.INP*).

Output

The output files are:

OUTPUT	- analysis output
LOG	- error file
RECORD	- record of all keyboard entry
PLOT	- SAS or S+ command/data file for plots
BOOTSTRAP	- output of estimates from bootstrap runs
STATS	- estimation statistics file

All output files can be *ASSIGNed* and *CLEARed*. The first 3 can be *LISTed* and *STORED* with the appropriate commands (see *DISTANCE>* section).

LOG is used to record all errors and warning messages. Initially, *LOG* is the screen. **If *INPUT* and *DATA* are assigned to files, it is important to assign *LOG* to a permanent file so that error messages are not missed amidst the stream of output. List this file to make sure that all commands and data were entered properly.** Error messages sent to the assigned log file are no longer sent to the screen. If *INPUT* and *DATA* are assigned to files, their contents are echoed to the log file, so an error message is associated with the incorrect entry. Set *NOECHO* on the *INPUT* and *DATA* file assignment and the entries will not be echoed to the *LOG* file. The *NOECHO* is most useful for lengthy *DATA* files after all errors have been eliminated.

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RECORD is a complete recording of all keyboard entry. *RECORD* is initially a *SCRATCH* file which is temporary and it is deleted upon exiting from DISTANCE. The *RECORD* file can be *STORE*d or *ASSIGN*ed to save its contents to repeat an analysis at a later time. Saving the *RECORD* is a useful way to learn how to set up data files by entering commands and data interactively and having the results stored in *RECORD*. All lines entered from the keyboard are sent to the *RECORD* including incorrect commands. Edit the file to remove errors or unneeded commands before using as an *ASSIGN*ed *INPUT* file. *RECORD* can be *LIST*ed to observe its contents and it can be *CLEAR*ed to purge its contents.

OUTPUT contains the results of the data analysis. *OUTPUT* is sent to the screen and it is appended to the default file named *DIST.OUT*. Suppress the file copy of the *OUTPUT* and only get the screen copy by entering:

```
ASSIGN OUTPUT=SCREEN;
```

Suppress the screen copy and keep the file copy with the name "filename" by entering:

```
ASSIGN OUTPUT=filename/NOECHO;
```

OUTPUT can also be *STORE*d after it has been displayed on the screen. The *STORE* command copies the output from the default file (*DIST.OUT*) to a file of your choice. When you *STORE* the *OUTPUT* file, the default file (*DIST.OUT*) is *CLEAR*ed. New output is appended to the previous contents of *DIST.OUT* by default. Use an *ASSIGN, CLEAR or STORE* command to avoid appending to unwanted output. (Note: Do not use the DOS commands in this program to rename or delete a file which is being used by DISTANCE) If you want to overwrite the default output file each time you start DISTANCE, put the command *ASSIGN OUTPUT=DIST.OUT/REPLACE;* into the startup file which is described below.

PLOT is created if the */SAS* or */SPLUS* switch is used with the goodness-of-fit (*GOF*) command in the *ESTIMATE>* procedure. *PLOT* contains data and commands to create a high quality graphics plot specifically with SAS/GRAPH or SPLUS. If you do not Assign a filename for *PLOT*, the results are appended to the contents of the file *SAS.PLT*. *PLOT* can be used as input to other graphics packages as well, if the SAS or S+ specific commands are removed. The data format is:

```
X (distance)      Histogram(x)      g(x) (or f(x))
```

Any graphics package which can produce 2 plots on the same graph can be used to plot the function fitted to the data $g(x)$ (or $f(x)$) overlaying a histogram representation of the data by connecting a line to each point as a function of x. The values of Histogram(x) will plot horizontal bars and the values of the function will produce a smooth curve. Note: for point transects, 2 figures are produced. The first is the detection function, $g(r)$, and the second is the probability density function of observed radial distances, $f(r)$.

STATS contains estimates and other statistics which are used internally by the program for summarization and are not saved at program termination unless it is *ASSIGN*ed to a disk file. For each analysis (*ESTIMATE*), a set of records is output to *STATS*. The first record is the title of the analysis. A blank record is output if you do not specify a title. The remaining records all have the same format but some field meanings change depending on the record type, which is determined by the value of Module and Statistic. The record structure is as follows:

Stratum	- stratum number (or 0 if the estimate is for a sample or all data).
Sample	- sample number (or 0 if the estimate is for a stratum or all data).
Estimator	- number of the estimator (in the order given in the Estimate procedure)
Module	- number of the parameter module (Figure 3)
Statistic	- number of the statistic within the parameter module (Figure 3)
Value	- estimate value
Cv	- coefficient of variation of estimate or 0.0
Lcl	- lower confidence limit or 0.0
Ucl	- upper confidence limit or 0.0
Df	- degrees of freedom for interval or 0

The modules and statistics within each module are listed in Figure 3 in the order in which they are summarized in the output. The FORTRAN format for each record is:

(2(1x,i3),3(1x,i1),1x,g12.5,1x,f7.4,1x,2(g12.4,1x),i4).

Each field is separated by a space, so the records can be read into a spreadsheet or other program as space delimited or as fixed-width format. The record for a module/statistic type is only output, if it is relevant and it was computed in the analysis.

Module	Statistic/Parameter Estimate
1 - encounter rate	
	1 - number of observations (n)
	2 - number of samples (k)
	3 - effort (L or K or T)
	4 - encounter rate (n/L or n/K or n/T) *
2 - detection probability	
	1 - total number of parameters (m)
	2 - AIC value
	3 - chi-square test probability (chi-p)
	4 - $f(0)$ or $h(0)$ *
	5 - probability of detection (P_w) *
	6 - effective strip width (ESW) or effective detection radius (EDR) *
3 - cluster size	
	1 - average cluster size *
	2 - size-bias regression correlation (r)
	3 - p-value for correlation significance (r-p)
	4 - estimate of expected cluster size corrected for size-bias*
4 - density/abundance	
	1 - density of clusters (or animal density if non-clustered) *
	2 - density of animals if clustered *
	3 - number of animals if survey area specified *

(*) - implies a value for CV, LCL, UCL and DF are included, otherwise they are set to zero.

Figure 3. Definitions of module and statistic codes in *STATS* file.

An example of the *STATS* file is given in Figure 4 for the example input file given in Figure 1. The first 4 records are the statistic records for the encounter rate module (the module field, the fourth field from the left equals 1). For this module the estimator number is always 1 because these statistics are independent of the estimator. The remaining records are all dependent on the estimator and the estimator field is always 2 because the half-normal/cosine estimator was chosen as the best estimator and it was listed second in the estimate procedure (Figure 1). Six records are listed for each of the statistics in the detection probability module (field 4 = 2) and 1 record for the density module (field 4 = 4). Records for cluster size are not listed because the input was for unclustered data and the abundance statistic is not given because there was no area size specified.

Example input in Figure 1

0	0 1 1 1	54.000	.0000	.00000	.00000	0
0	0 1 1 2	4.0000	.0000	.00000	.00000	0
0	0 1 1 3	142.30	.0000	.00000	.00000	0
0	0 1 1 4	.37948	.4293	.10253	1.4046	3
0	0 2 2 1	1.0000	.0000	.00000	.00000	0
0	0 2 2 2	130.11	.0000	.00000	.00000	0
0	0 2 2 3	.74194	.0000	.00000	.00000	0
0	0 2 2 4	.48112	.1137	.38332	.60388	53
0	0 2 2 5	.51962	.1137	.41399	.65219	53
0	0 2 2 6	2.0785	.1137	1.6560	2.6088	53
0	0 2 4 1	1.8610	.4441	.48243	7.1791	3

Figure 4. Example *STATS* file for first estimate prcoedure of input file given in Figure 1

In addition, Figure 5 gives the resulting *STATS* file for the second estimate procedure in Figure 1 modified to show the results for each estimator (PICK=NONE). Records for the detection probability and density modules are output in the STATS file for each estimator.

The *BOOTSTRAP* file contains a set of *STAT* records for each bootstrap. By default, a new *BOOTSTRAP* file (*BOOT.OUT*) is created for each bootstrap analysis. If you want to append to the results of other bootstrap results from the same analysis, *ASSIGN* the file with the */APPEND* switch. When the results of the bootstrap are summarized, all of the bootstrap estimates are included. This enables you to run a large bootstrap analysis in batches (*e.g.*, 5 batches of 200 to get 1000 bootstraps). If the bootstraps are appended, make sure you use the default *SEED=0* which assigns a random seed from the computer clock or change the *SEED* between batches; otherwise, the same set of estimates will be repeated in each batch. The format of the records are as described under *STATS* with the exception that a title record is not included.

Example input in Figure 1

0	0 1 1 1	51.000	.0000	.00000	.00000	0
0	0 1 1 2	4.0000	.0000	.00000	.00000	0
0	0 1 1 3	142.30	.0000	.00000	.00000	0
0	0 1 1 4	.35840	.4028	.10437	1.2307	3
0	0 1 2 1	2.0000	.0000	.00000	.00000	0
0	0 1 2 2	108.33	.0000	.00000	.00000	0
0	0 1 2 4	.59869	.6316	.18694	1.9173	49
0	0 1 2 5	.55677	.6316	.17385	1.0000	49
0	0 1 2 6	1.6703	.6316	.52156	5.3493	49
0	0 2 2 1	1.0000	.0000	.00000	.00000	0
0	0 2 2 2	106.91	.0000	.00000	.00000	0
0	0 2 2 3	.45113	.0000	.00000	.00000	0
0	0 2 2 4	.50318	.1354	.38386	.65959	50
0	0 2 2 5	.66245	.1354	.50536	.86837	50
0	0 2 2 6	1.9874	.1354	1.5161	2.6051	50
0	0 3 2 1	1.0000	.0000	.00000	.00000	0
0	0 3 2 2	106.69	.0000	.00000	.00000	0
0	0 3 2 3	.55245	.0000	.00000	.00000	0
0	0 3 2 4	.51245	.1208	.40241	.65258	50
0	0 3 2 5	.65047	.1208	.51079	.82834	50
0	0 3 2 6	1.9514	.1208	1.5324	2.4850	50
0	0 1 4 1	2.1871	.7491	.55459	8.6252	26
0	0 2 4 1	1.8382	.4249	.59323	5.6960	4
0	0 3 4 1	1.8721	.4205	.61075	5.7383	4

Figure 5. Example *STATS* file for second estimate prcoedure of input file given in Figure 1 modified to output results from each estimator.

Startup File

An ASCII file named *STARTUP.DST* can be created which contains commands that are executed each time DISTANCE starts. This is particularly useful to change default values for options. As an example, assume that all of your sampling is from point transects (*TYPE=POINT;*) and you want to squeeze all of the output (*SQUEEZE=ON;*), by default. Also, you would like the default output file to be named *DISTANCE.LST* and you want it replaced each time. This is accomplished by creating a file named *STARTUP.DST* with the following contents:

```
ASSIGN OUTPUT=DISTANCE.LST/REPLACE;
OPTIONS;
  TYPE=POINT;
  SQUEEZE=ON;
END;
```

Any valid command can be used in this file. DISTANCE will look for *STARTUP.DST* in the current directory and in the directory which contains *DIST.EXE.* After processing any commands in *STARTUP*, DISTANCE prompts for more commands (if in interactive mode) or reads commands from the *INPUT* file (if in batch mode).

The name of the *STARTUP* file can be changed when starting DISTANCE from the DOS prompt, by including an optional argument:

```
DIST S=startfile
```

The optional argument will work when running the program interactively or in batch mode as described below. DISTANCE will look for the file named *startfile* in the current directory. If the file is not found, DISTANCE will look for *STARTUP.DST*.

Batch Operation

Batch operation (mode) is simply an efficient method of running numerous analyses by reducing the amount of typing. All command and data entry is identical in batch and interactive mode. Batch mode is equivalent to running the program interactively and using *ASSIGN* statements to specify the input, output and log files, except that DISTANCE is terminated upon completion of processing the input file.

DISTANCE is run in batch mode by specifying filenames when DISTANCE is initiated. The full specification is:

```
DIST I=infile O=outfile L=logfile S=startfile
```

The outfile, logfile, and startfile specifications are optional because each has a default value. If left unspecified, the output will be appended to *DIST.OUT*, the log output will come to the screen and the startfile is assumed to be named *STARTUP.DST*. We strongly recommend specifying a log file and examining its contents to make sure all commands and data were entered correctly. All of the switches for the *ASSIGN* command can be used with the file specifications (except with S=). For example,

```
DIST I=DIST.INP O=DUCKS.OUT/REPLACE/NOECHO
```

will use *DIST.INP* as the input file and *DUCKS.OUT* as the output file. It will replace any file currently named *DUCKS.OUT.* If the */REPLACE* switch is not used and the specified file already exists, DISTANCE displays an error message and appends the output to the default file, *DIST.OUT*. By default, output is also displayed on the screen as the data are read and analyzed. Using */NOECHO* after the output file suppresses the screen output. Spaces are **not** allowed anywhere within a file specification nor between it and its associated switches; however, there should be one or more spaces between the file specifications. The following would be an invalid way to run the program in batch mode because the space indicated by the ^ will create an error:

```
DIST I= DIST.INP  O =DIST.OUT/NOECHO
       ^          ^
```

One way to reduce typing is to specify the *ASSIGN* statements for the *OUTPUT* and *LOG* file in the *INPUT* file. For example, entering:

```
DIST I=DIST.INP
```

where *DIST.INP* has as its first 2 lines

```
ASSIGN OUTPUT=DIST.OUT/REPLACE;
ASSIGN LOG=DIST.LOG/REPLACE;
```

is the same as entering:

```
DIST I=DIST.INP O=DIST.OUT/REPLACE L=DIST.LOG/REPLACE
```

However, if the input file contains *ASSIGN* commands the *O=* and *L=* assignments will not override those values.

If you wish, explore running the program in batch mode, by using one of the example input files which have been included on the installation disk. The example files are installed into *YourDirectory* during the installation process (see Installation Instructions). These files have been constructed from the examples in Burnham et al. (1980) and Buckland et al. (1993). All of the example input files have a *.inp* file extension. Some of the example filenames are *Pgxx.inp* where *xx* refers to the page number in Burnham et al. (1980). Other filenames are *EXn.inp* where *n* refers to one of the numbers of the Illustrative Examples in Burnham et al. (1980) or *CHxx.inp* which refers to the chapter and example number in Buckland et al. (1993).

DISTANCE>

DISTANCE> is the initial command prompt. When the commands, *DATA;*, *ESTIMATE;*, and *OPTIONS;*, are issued at the *DISTANCE>* prompt, the prompt is changed to *DATA>, ESTIMATE>* and *OPTIONS>*, respectively. The valid commands for each of the prompts are defined in individual sections of this Guide. Each section is identified by the outlined title on the top of the page.

Also, at the *DISTANCE>* prompt, file manipulation commands can be issued to assign, clear, list, print and store files. DOS commands from within DISTANCE can be issued from this prompt. The following are valid commands at the *DISTANCE>* prompt:

Procedure Initiation

DATA	- enter distance sampling data
ESTIMATE	- estimation of density
OPTIONS	- sets various program options

File Manipulation

ASSIGN	- assign filenames
CLEAR	- clear file contents
LIST	- list file contents to screen
PRINT	- print options/data
STORE	- store file contents

Miscellaneous

DOS	- execute a DOS command
EXIT	- exit program
HELP	- display help files
PAUSE	- pause execution

The commands are described below in alphabetical order.

DISTANCE>

ASSIGN

Syntax:

```
                |LOG        |             |/APPEND |
        ASSIGN  |PLOT       | = filename  |        |   ;
                |RECORD     |             |/REPLACE|
                |BOOTSTRAP  |
                |STATS      |

    or

                                        |/APPEND |   |/ECHO   |
        ASSIGN   OUTPUT  = filename     |        |   |        |   ;
                                        |/REPLACE|   |/NOECHO|
    or

        ASSIGN   INPUT   = filename  /NOECHO     ;

    or

        ASSIGN   HELP    = filename ;
```

Description:

Assigns filenames to the *INPUT*, *LOG*, *RECORD*, *OUTPUT*, *PLOT*, *BOOTSTRAP*, *STATS* and *HELP* files. The filename must be a valid DOS filename or one of the following special names: *LOG* can be *SCRATCH* or *SCREEN*, *OUTPUT* can be *SCREEN*, *RECORD* can be *SCRATCH*, and *STATS* can be set to *NULL* to terminate output of statistics. If you use *SCRATCH*, the file is maintained (and can be *LISTed* and *CLEARed*) but is deleted upon exiting DISTANCE unless it is explicitly stored with a *STORE* command. Assigning *HELP* is only necessary if you change the name of the *HELP* file or store it in a directory other than the one containing *DIST.EXE*. The default values for each file are:

LOG	- *SCREEN*	*STATS*	- *NULL*
PLOT	- *SAS.PLT*	*OUTPUT*	- *DIST.OUT*
RECORD	- *SCRATCH*	*INPUT*	- *KEYBOARD*
BOOTSTRAP	- *BOOT.OUT*	*HELP*	- *DIST.HLP*

For output files, if you *ASSIGN* a file that already exists and do not specify either */APPEND* or */REPLACE*, an error is issued and output is sent to the default file. For *INPUT* filenames, if the file does not exist, an error message is issued. By default, the contents of *INPUT* files are echoed in the *LOG*. Use the */NOECHO* switch to override this default. If you use */ECHO* (the default) for the *ASSIGN OUTPUT* command, output is sent to the *SCREEN* as well as the file. If you use */NOECHO*, *SCREEN* output is suppressed. If sufficient memory is available, assigning the *STATS* or *BOOTSTRAP* file to a RAMDRIVE, can reduce execution time.

Examples:

```
ASSIGN INPUT=TEST.INP;
ASSIGN OUTPUT=TEST.OUT/REPLACE;
ASSIGN PLOT=SPLUS.OUT/APPEND;
```

DISTANCE>

CLEAR

Syntax:

```
              |LOG    |
        CLEAR |OUTPUT|   ;
              |RECORD|
```

Description:

CLEAR empties the contents of the *LOG*, *OUTPUT* or *RECORD* files. It has no effect on the *LOG* file if the *LOG* file is the *SCREEN*.

Example:

```
CLEAR OUTPUT;
```

DATA

Syntax:

```
DATA ;
```

Description:

DATA initiates a separate command processor for entering distance data. The prompt will change to *DATA>* . See the section on the *DATA>* prompt for further information.

DOS

Syntax:

```
DOS command_name  ;
```

Description:

Executes the DOS command given by command_name and then returns back to the *DISTANCE>* prompt. This will work for DOS commands and small programs. It is limited by the amount of free memory available on your computer.

If a command_name is not given, the DOS prompt will appear. DISTANCE remains in the background and you can issue several DOS commands. This is termed "shelling out". It is necessary to type EXIT at the DOS prompt to return to DISTANCE. **Do not** issue the command to start DISTANCE again because this will run DISTANCE within itself. Unexpected and possibly unpleasant results will occur.

Examples:

```
DOS EDIT filename;
DOS DIR C:*.*;
```

DISTANCE>

ESTIMATE

Syntax:

```
ESTIMATE ;
```

Description:

ESTIMATE initiates a separate command processor for estimation of density. The prompt will change to *ESTIMATE>*. Various commands that can be given to control estimation are described in the *ESTIMATE>* prompt section.

EXIT

Syntax:

```
EXIT  ;
```

Synonyms: *STOP*, *QUIT*, *END*, or *BYE*

Description:

Stops DISTANCE and returns control to DOS.

HELP

Syntax:

```
HELP;
or
HELP command_name;
```

Description:

If you type *HELP;* several pages of introductory information are displayed. If you type *HELP command_name;* a description of the specific command is given. Use PgUp and PgDn or the up and down arrow keys to scan the help information. Press the Esc key to leave help. *HELP* should only be used when running program DISTANCE interactively.

Example:

To obtain a description of the *SELECTION* command at the OPTIONS> prompt, enter:

HELP SELECTION;

To obtain a description of the *INFILE* command at the DATA> prompt, enter:

HELP INFILE;

DISTANCE>

LIST

Syntax:

```
              |LOG     |
        LIST  |OUTPUT  |   ;
              |RECORD  |
              |DATA    |
              |OPTIONS |
```

Description:

LIST allows you to browse the contents of the *LOG*, *OUTPUT* or *RECORD* files. It will also display the current data (*LIST DATA*) or the current values of the program options (*LIST OPTIONS*). The command *LIST* is not intended for use in batch files. *LIST* sends output to the screen with Browse and it will wait until an ESC key is pressed before continuing. If you want to output data and options to the output file, use *PRINT DATA;* or *PRINT OPTIONS*; at the *DISTANCE>* prompt.

Example:

```
LIST LOG;

LIST OPTIONS;
```

OPTIONS

Syntax:

```
OPTIONS ;
```

Description:

OPTIONS initiates a separate command processor for setting various options which affect program operation and output. The prompt will change to *OPTIONS>* after typing this command. Further information on setting options is given in the *OPTIONS>* prompt section.

PAUSE

Syntax:

```
PAUSE ;
```

Description:

Pauses program in between commands until the Enter key is pressed. It can be useful when running program DISTANCE in batch mode (*e.g.*, for demonstration purposes).

DISTANCE>

PRINT

Syntax:

```
                |OPTIONS|
        PRINT   |       |   ;
                |DATA   |
```

Description:

Prints either the option values or the data values to the *OUTPUT* file but not to the screen.

STORE

Syntax:

```
                |LOG    |                |/APPEND |
        STORE   |OUTPUT| = filename      |        |    ;
                |RECORD|                |/REPLACE|
```

Description:

The *STORE* command copies the contents of a program file into a named DOS file. If the file specified by the filename already exists, an error is issued. Use */APPEND* to append to an existing file. Use */REPLACE* to replace an existing file. If you specify a file which is currently being used by the program, an error will be issued. The following example creates an error because *ASSIGN* opens *TEST.OUT* and then *STORE* attempts to write to *TEST.OUT* which is already open:

```
ASSIGN OUTPUT=TEST.OUT;
STORE LOG=TEST.OUT;
```

Examples:

Store *LOG* into the file *TEST.LOG* and append to the current contents of the file.

```
STORE LOG=TEST.LOG/APPEND;
```

Store *OUTPUT* into the file *TEST.OUT* and replace its contents if it already exists.

```
STORE OUTPUT=TEST.OUT/REPLACE;
```

OPTIONS>

Various options can be set to control program operation. Once an option value has been set, it retains its value until you change it or exit the program. The data options define the characteristics of the data collected and how they are to be entered. The model fitting options define values to be used in fitting a probability density function to the distance data, some of which can be overridden in the estimation procedure. Print options control the amount and format of program output and bootstrap options control the number of bootstrap samples and the random number seed used to generate a bootstrap sequence.

Below are the valid commands at the *OPTIONS>* prompt by category.

Miscellaneous

DEFAULT	- options reset to default
END	- ends options command
HELP	- help with options
LIST	- lists option values

Output

PRINT	- controls amount of output
SQUEEZE	- controls output pagination
TITLE	- value of output title

Data Options

AREA	- set area quantities
CUERATE	- set cue rate
DISTANCE	- set distance quantities
LENGTH	- set length quantities
OBJECT	- *SINGLE* or *CLUSTER*
SF	- sampling fraction
TYPE	- *POINT*, *LINE* or *CUE*

Model Fitting

EPSILON	- tolerance for fitting
ITERATIONS	- max # of iterations
LOOKAHEAD	- max for sequential fit
MAXTERMS	- max no. of adjustments
PVALUE	- significance level (α-level)
SELECTION	- term selection mode

Bootstrap

BOOTSTRAPS	- no. of bootstrap samples
SEED	- random number seed

Each option and its possible values are individually described below in alphabetical order.

OPTIONS>

AREA

Syntax:

```
AREA    /CONVERT=value  /UNITS='label' ;
```

Description:

This command defines the area unit for expressing density (D) (pg:1). The switches are:

/UNITS='label' - a label for the unit of area of the density estimate. The single quotes are only required to retain lowercase. Only the first 15 characters are used.

/CONVERT=value -value specifies a conversion factor which is used as a multiplier to convert the estimated density to new units for area. It is needed for atypical units.

If DISTANCE recognizes the measurement unit for *DISTANCE* (and *LENGTH* for line transects) and if it recognizes the Area *UNITS* label, it will calculate the appropriate conversion factor. However, if one or more of the *UNITS* is not recognized, you will need to specify the conversion value with the *CONVERT* switch. The Area units recognized by the program are those listed under the *DISTANCE* command and *HECTARES (HEC)* and *ACRES (ACR)*. For example, the unit can be entered as *Squared Meters* or *Metres Squared* because DISTANCE recognizes the unit based on the character string *MET.* See the *DISTANCE* command below for a definition of recognized units

Default: *AREA /UNITS=HECTARES;*

Examples:

Distances are measured in feet but analyzed in meters, length is measured in miles and density is estimated as numbers per square kilometer. DISTANCE will do necessary unit conversions because all unit labels are recognized.

```
DISTANCE/MEASURE=FEET/UNITS='Meters';
LENGTH/UNITS='Miles';
AREA /UNITS='Sq. kilometers';
```

BOOTSTRAPS

Syntax:

```
BOOTSTRAPS=value ;
```

Description:

'Value' is the number of bootstrap samples (pg:94-96, 119-120, 155-158) which should be generated. For a reasonable variance estimate, this number should be at least 100. We recommend setting *BOOTSTRAPS=1000;* to construct a bootstrap confidence interval.

Default: *BOOTSTRAPS=1000;*

OPTIONS>

CUERATE

Syntax:

```
CUERATE = value1 /SE=value2 ;
```

Description:

For cue counting (pg:8-9, 270-275), 'value1' is the average rate at which animals issue visual or auditory detection cues. The rate should be given in the same units of time as the values given for sampling effort in the data. For example, if effort is measured in hours then the cue rate should be number of cues per hour. The cue rate must be a positive number (>0). Optionally a standard error for the cue rate can be given with 'value2'. This standard error is accounted for in the estimated standard error of the density and abundance estimates. This option is only used if *TYPE=CUE* is specified.

Default: *CUERATE=1/SE=0;*

Example:

An estimate of the cue rate is 12 per hour with a standard error of 2 per hour. The sample effort for this cue counting example be specified in hours sampled.

```
CUERATE=12 /SE=2 ;
```

DEFAULT

Syntax:

```
DEFAULT ;
```

Description:

This command resets all of the options to their default values. Remember that an option remains in effect until it is changed or DISTANCE is terminated. The default values for each of the options are:

PVALUE=0.15	PRINT=SELECT	TYPE=LINE
SELECT=SEQUENTIAL	SQUEEZE=OFF	OBJECT=SINGLE
MAXTERMS=5	BOOTSTRAPS=1000	DISTANCE=PERP/EXACT/UNITS=METERS
ITERATIONS=100	SEED=0	LENGTH/UNITS=KILOMETERS
LOOKAHEAD=1	SF=1	AREA/UNITS=HECTARES
EPSILON=1.0E-7	CUERATE=1/SE=0	

OPTIONS>

DISTANCE

Syntax:

```
                                /WIDTH=width      /NCLASS=nclass
                  |PERP   |
        DISTANCE = |       |   /CONVERT=value    /UNITS='label'          ;
                  |RADIAL|
                                /MEASURE='label'  /RTRUNCATE=t

                                /LEFT=left      | /INTERVALS=c0,c1,...,cu  |
                                                | /EXACT                   |
```

Synonyms: *RIGHT=WIDTH*

Description:

This command describes numerous features about the distance data and defines the default values for estimation. The format of the data entry within *DATA>* is determined by the values set with this command. Whereas, the *DISTANCE* command at the *ESTIMATE>* prompt only determines how the distance data are analyzed. In the EXAMPLES section the difference and use of the 2 commands are illustrated.

For line transect data (*TYPE=LINE*), this command defines whether the data will be entered as either perpendicular distances or as radial distance and angle measurements (pg:4-6).

PERP - perpendicular distance was measured for a line transect
RADIAL - radial distance and angle were measured in line transects

For *TYPE=POINT* (which includes trapping webs) or *CUE* (pg:6-8), *DISTANCE=RADIAL* is assumed and only radial distances are expected.

Distances can be entered as ungrouped or grouped (pg:13-14). Ungrouped implies an exact distance is entered for each observation in the data. Grouped means a set of distance intervals is given and the frequency of observations in each interval is entered. Ungrouped distances are indicated by the switch */EXACT* and grouped data is indicated by the */INTERVALS* switch which also specifies the distance intervals (c_0-c_1,c_1-c_2,c_2-c_3,...). The value c_0 specifies the left-most distance and c_u the right-most distance for grouped data. Typically, c_0=0 and c_u=w. Intervals can also be specified by using the */NCLASS* and */WIDTH* and optionally the */LEFT* switch. These switches will create 'nclass' equal width distance intervals between the values of 'left' and 'width' (i.e., each interval is of length (width-left)/nclass). For ungrouped data, it is also possible to specify left and right truncation with the */LEFT* and */WIDTH* switches (pg:15). Any values outside of these bounds are excluded from the analysis. Right truncation as a percentage of the observations can also be specified for both grouped and ungrouped data with */RTRUNCATE* switch. The value of *t* must be between 0 and 1. In the analysis, no more than *t**100% of the data is truncated from the right. For ungrouped data, the width is set at the distance which represents the (1-*t*)*100% quantile. For grouped data, intervals are truncated from the right as long as no more than *t**100% of the data is truncated. If *t*=0 and the data are ungrouped data, the width is set to the largest distance measurement and if the data are grouped, the width is set to the endpoint for the right-most interval

with a non-zero frequency. For ungrouped data, if both the */WIDTH* and */RTRUNCATE* switch are specified, the *RTRUNCATE* value specifies the value of width.

The *DISTANCE* command is also used to define the measurement unit for distances:

/MEASURE='label' - a label for the units in which distance was measured. Single quotes are only required to retain lowercase. Only the first 15 characters are used

/UNITS='label' - a label for the units for distance after conversion, if any. Single quotes are only required to retain lowercase. Only the first 15 characters are used.

/CONVERT=value - value specifies a conversion factor which is used as a multiplier to convert the input distances for atypical units.

MEASURE and *UNITS* switches are used to convert from the unit in which the data are recorded and entered (*MEASURE*) to the unit for analysis (*UNITS*). It is not necessary to convert distances to different units for analysis as long as it is a unit that is recognized by DISTANCE (see list below). It is only provided as a convenience and it is probably easier to leave measurements in their original units. If you do convert units, take note that values such as $f(0)$, $h(0)$, effective strip width (ESW) (pg:23,56) and effective detection radius (EDR) (pg:154,175) are expressed in the converted units. Thus, the point estimate and standard errors will change by the conversion factor from the measured to analysis units. If you are not converting distance units, you can specify the units with either switch (*/MEASURE* or */UNITS*). The most common measurement units are recognized by DISTANCE and there is no need to enter a conversion value (*/CONVERT*= value). The following are the recognized measurement unit labels:

CENTIMETERS	*METERS*	*KILOMETERS*	*MILES*
INCHES	*FEET*	*YARDS*	*NAUTICAL MILES*

Each label is recognized by its first 3 characters which allows variations in spelling. For example, if you enter METRES, it will use METRES as the label and will recognize it based on MET. Values are given in uppercase but can be entered in upper or lowercase. If DISTANCE recognizes the /UNITS and /MEASURE labels and you specify the */CONVERT*= switch it will display a warning message that you are overriding the conversion value. Values for /WIDTH, /LEFT, and /INTERVALS should be given in original measurement units and **not** in converted units.

Default:

```
DIST=PERP/UNITS='Meters'/MEASURE='Meters'/EXACT/LEFT=0/RTRUNCATE=0;
```

Examples:

Perpendicular distance measured in intervals of 2 feet to a distance of 10 feet and converted to metres (meters) for analysis. The grouped data are entered as the frequency of observations in each of the 5 distance intervals (see *DATA>*). Notice that WIDTH is specified in the original measurement units of feet and not in meters.

```
DIST=PERP /MEASURE='Feet' /UNITS='Metres' /WIDTH=10 /NCLASS=5 ;
```

OPTIONS>

Radial distance measured and analyzed in the specified intervals of feet. The label will be displayed in uppercase because it is not in quotes. If this is line transect data the program will generate an error because grouped data entry is not allowed for distance/angle data (see *SMEAR* as an option for the *DISTANCE* command in the *ESTIMATE* procedure).

```
DIST=RADIAL /MEASURE=Feet /INTERVALS=0,2,5,8,12,25;
```

Perpendicular distance measured in rods and converted to feet with a user specified conversion factor because the program will not recognize the Rods unit. 10% of the observations will be right truncated in the analysis.

```
DIST=PERP /MEASURE='Rods' /UNITS='Feet' /CONVERT=16.5 /RTRUNCATE=0.10;
```

END

Syntax:

```
END ;
```

Description:

END completes entry of options and returns to the *Distance>* prompt.

EPSILON

Syntax:

```
EPSILON=value ;
```

Description:

'Value' is a relative measure of closeness of parameter estimates obtained between iterations in assessing the maximum of the likelihood function (pg:65-66). The default value is 1.0E-7 which means roughly 6 digits of accuracy is achieved. *EPSILON* can be set to any value between 0.1 and 1.0E-8. Typically, it is not necessary to change its value unless error messages are given indicating difficulty with fitting the model.

Default: *EPSILON=1.0E-7;*

OPTIONS>

HELP

Syntax:

```
HELP;
or
HELP command_name;
```

Description:

If you type *HELP;* several pages of introductory information will be displayed. If you type *HELP command_name;* a description of the specific command will be given. Use PgUp and PgDn or the up and down arrow keys to scan the help information. Press the 'Esc' (Escape) key to leave help. *HELP* should only be used interactively. It will work in batch mode, but it will interrupt processing until you press the 'Esc' key.

ITERATIONS

Syntax:

```
ITERATIONS=value ;
```

Description:

'Value' is the maximum number of iterations that the algorithm will perform to determine the parameters that maximize the likelihood function (pg:65-66).

Default: *ITERATIONS=100;*

LENGTH

Syntax:

```
LENGTH /CONVERT=value /UNITS='label' /MEASURE='label' ;
```

Description:

This command sets the measurement unit for line length (pg:4-6) and any desired conversion to different units for analysis. It is not necessary to convert line length, but may be desirable depending on the original units.

/MEASURE='label' - a label for the units in which line length was measured. Single quotes are only required to retain lowercase. Only the first 15 characters are used.

/UNITS='label' - a label for the units for length after conversion, if any. Single quotes are only required to retain lowercase. Only the first 15 characters are used.

/CONVERT=value - value specifies a conversion factor which is used as a multiplier to convert length measured in atypical units.

OPTIONS>

See further explanation under *DISTANCE* for the */MEASURE, /UNITS* and */CONVERT* switches. The *LENGTH* command is used for line transects only.

Default:

LENGTH /UNITS=KILOMETERS /MEASURE=KILOMETERS;

Example:

Length is entered in miles but converted to kilometers for display and analysis.

```
LENGTH /UNITS='Kilometers' /MEASURE='Miles'  ;
```

LIST

Syntax:

```
LIST;
```

Description:

Lists current values of the program options and the program limits to the screen.

LOOKAHEAD

Syntax:

```
LOOKAHEAD=value ;
```

Description:

For term selection modes *SEQUENTIAL* and *FORWARD* (see *SELECTION),* 'value' specifies the number of adjustment terms which should be added to improve the fit, before the added terms are considered to be non-significant (pg:399-400). For example, if *LOOKAHEAD*=2 and a model with 2 adjustment terms does not significantly improve the fit over a model with 1 term, a model with 3 adjustment terms is fitted. If the 3-term model is an improvement over a 1-term model, the algorithm will continue with the 3-term model as the new base model. If it is not an improvement, the 1-term model would be chosen. If *LOOKAHEAD*=1 (the default), in the above example, the 3-term model would not have been examined because upon finding the 2-term model was not an improvement, the 1-term model would have been used.

Default: *LOOKAHEAD=1;*

OPTIONS>

MAXTERMS

Syntax:

```
MAXTERMS=value ;
```

Description:

'Value' is the maximum number of model parameters (pg:62-68). The maximum number of adjustment terms (defined as m, pg:65) that may be added is MAXTERMS minus the number of parameters in the chosen key function (defined as k, pg:65). MAXTERMS must be less than or equal to 5. This option is only useful to limit the number of model combinations with the term selection mode that considers also possible combinations of adjustment terms (*SELECTION=ALL*). Use the *NAP* switch on the *Estimator* command to specify an exact number of adjustment terms to be used. The maximum number of adjustment terms is also limited by the number of observations for ungrouped data or number of distance intervals for grouped data.

Default: *MAXTERMS=5;*

OBJECT

Syntax:

```
                |SINGLE  |
        OBJECT=|        | ;
                |CLUSTER |
```

Description:

This option defines whether objects are detected individually (*SINGLE*) or as clusters (*CLUSTER*) (pg:11-13).

SINGLE - Object always detected as a single animal or other entity (*e.g.*, duck nest)

CLUSTER - Object detected as a cluster (*e.g.*, herd, flock,pod of whales)

Default: *OBJECT=SINGLE;*

OPTIONS>

PRINT

Syntax:

```
          |SELECTION|
    PRINT=|RESULTS  | ;
          |ALL      |
          |SUMMARY  |
```

Description:

This option sets the default level of printing in the output. The various settings are hierarchical and more control over the amount of results can be obtained with the *PRINT* command in the *ESTIMATE>* procedure.

ALL	- print fitting iterations, model selection results and estimation results
SELECTION	- print model selection results and estimation results
RESULTS	- print estimation results only
SUMMARY (*NONE*)	- only summary tables are printed

Note: if you choose *RESULTS* or *SUMMARY*, warnings are not given about the algorithm having difficulties fitting a particular model or constraining the fit to achieve monotonicity.

Default: *PRINT=SELECTION;*

PVALUE

Syntax:

```
PVALUE=α ;
```

Description:

α is the significance level of likelihood ratio tests (pg:74-75) to determine significance of adding adjustment terms and is the default value for the significance test for size-bias regression of cluster sizes (pg:79-80)

Default: *PVALUE=0.15;*

OPTIONS>

SEED

Syntax:

```
SEED=value ;
```

Description:

SEED specifies the random number seed for generating a sequence of random numbers for bootstrap samples (pg:155-158). 'Value' should be a large odd number preferably greater than 2,000,000. If you use the same seed, the same sequence of random numbers will be generated. You can use SEED=0; (the default) which will use a value from the computer's clock to generate a seed.

Default: *SEED=0;*

SELECTION

Syntax:

```
                |SEQUENTIAL|
SELECTION=      |FORWARD   | ;
                |ALL       |
                |SPECIFY   |
```

Description:

This command specifies the default mode for adjustment term selection in the *ESTIMATE* procedure for fitting the detection function. The */SELECT* switch of the *ESTIMATOR* command overrides the default value. See the *ESTIMATE>* section for a description of adjustment term and model selection.

SEQUENTIAL - add adjustments sequentially (e.g., for simple polynomial, in increasing order of the exponent).

FORWARD - equivalent to forward selection in regression; select the adjustment term which produces the largest increase in the maximum of the likelihood function

ALL - fit all combinations of adjustment terms with the key function and use the model with smallest Akaike Information Criterion (AIC) value.

SPECIFY - user-specified number of adjustment terms and possibly order of the adjustments.

Default: *SELECTION=SEQUENTIAL;*

OPTIONS>

SF

Syntax:

```
SF=c ;
```

Description:

SF defines the value of the sampling fraction which is typically 1 (pg:53). However, if only one side of a transect line is observed *c*=0.5, or if some fraction of the circle surrounding a point transect is searched, *c* is the fraction searched (e.g., *c*=0.5 if a semi-circle is observed). For cue counting, *c* is the proportion of a full circle that is covered by the observation sector. For a sector of 90° (45° either side of the line) with cue counting, *c* = 0.25

Default: *SF=1;*

SQUEEZE

Syntax:

```
          |ON |
SQUEEZE = |   |    ;
          |OFF|
```

Synonyms: *ON=YES=TRUE, OFF=NO=FALSE*

Description:

If this option is set 'off' a formfeed and title line is printed at the top of each page. If it is set 'on' , a formfeed is not included which has the effect of squeezing the output.

Default: *SQUEEZE=OFF;*

TITLE

Syntax:

```
TITLE='yourtitle' ;
```

Description:

This command sets a value for the title which is printed at the top of each page. *Yourtitle* should contain no more than 50 characters. Excess characters are not used. There is only 1 title line. Re-specifying the title will replace the previous value.

OPTIONS>

TYPE

Syntax:

```
            |POINT|
    TYPE =  |LINE |   ;
            |CUE  |
```

Description:

This option defines the type of sampling (pg:3-8) which determines what types of data can be entered and how data are analyzed.

POINT - point transect data (pg:6-7)
LINE - line transect data (pg:4-6)
CUE - cue counting data (pg:8-9)

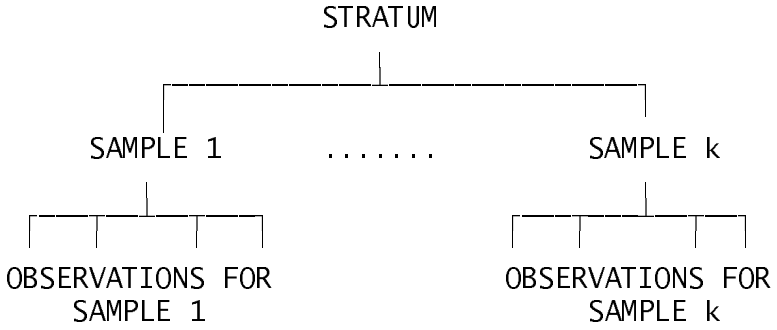
Trapping webs (pg:7-8) should be treated as point transects.

Default: *TYPE=LINE;*

DATA>

Distance data are entered at the *DATA>* prompt. There are two ways of entering data: 1) from the *INPUT* file (either the keyboard or an *ASSIGN INPUT* file), or 2) from a separate file specified with the *INFILE* command.

Data are structured and entered in a hierarchical manner. The levels of the hierarchy can be viewed as follows:



The structure is specified by the order in which the commands and data are entered. A *STRATUM* command is entered to begin a stratum and a *SAMPLE* command is entered to define and begin a sample. All observation data (e.g., distances, cluster sizes) for a sample (i.e., line or point) follow the *SAMPLE* command. For example, if the data are from two strata each with two samples, conceptually the data are entered as follows:

```
STRATUM 1
  SAMPLE 1
      OBSERVATIONS FOR SAMPLE 1
  SAMPLE 2
      OBSERVATIONS FOR SAMPLE 2
STRATUM 2
  SAMPLE 3
      OBSERVATIONS FOR SAMPLE 3
  SAMPLE 4
      OBSERVATIONS FOR SAMPLE 4
```

It is not necessary to stratify the data. An equally valid layout for the above example would be:

```
SAMPLE 1
  OBSERVATIONS FOR SAMPLE 1
SAMPLE 2
  OBSERVATIONS FOR SAMPLE 2
SAMPLE 3
  OBSERVATIONS FOR SAMPLE 3
SAMPLE 4
  OBSERVATIONS FOR SAMPLE 4
```

Incomplete assignment of the data to strata is not allowed. The following example would not be a

DATA>

valid layout for the data because it is incompletely stratified:

```
SAMPLE 1
   OBSERVATIONS FOR SAMPLE 1
STRATUM 1
   SAMPLE 2
      OBSERVATIONS FOR SAMPLE 2
```

At the very minimum one *SAMPLE* and its observation data must be defined. Observation data must always be preceded by a *SAMPLE* command and are entered in a variety of formats (described below).

The *STRATUM* command which begins a stratum, also may specify a label and an area size. The most obvious use for a stratum is to represent different areas which were sampled or the same area at different times. Estimates of density can be obtained separately by stratum and then combined over strata. Use the *DENSITY* command at the *ESTIMATE>* prompt to define how stratum estimates are combined. Another use for strata is to represent a second level of replicate sampling within the same area. For example, several observers or several different platforms of observation. Or strata can be used to stratify the data based on some characteristic of the population (e.g., sex, or cluster size (pg:77-78)).

Point transects or cue counts (*TYPE=POINT* or *=CUE*):		
1.	Grouped radial distances	$n_1, n_2, n_3, \ldots, n_u$;
	Ungrouped cluster sizes	$s_1, s_2, s_3, \ldots, s_n$;
2.	Ungrouped radial distances and cluster sizes	$r_1, s_1, r_2, s_2, \ldots, r_n, s_n$;
Line Transects (*TYPE=LINE*):		
Radial distance & angle (*DISTANCE=RADIAL*)		
3.	Ungrouped radial distances, angles, and cluster sizes	$r_1, \theta_1, s_1, \ldots, r_n, \theta_n, s_n$;
Perpendicular Distance (*DISTANCE=PERP*)		
4.	Grouped perpendicular distances	$n_1, n_2, n_3, \ldots, n_u$;
	Ungrouped cluster sizes	$s_1, s_2, s_3, \ldots, s_n$;
5.	Ungrouped perpendicular distances and cluster sizes	$x_1, s_1, x_2, s_2, \ldots, x_n, s_n$;

Legend:
For i=1,...,n (number of observations):
- r_i - i^{th} radial distance measurement
- x_i - i^{th} perpendicular distance measurement
- θ_i - i^{th} angle measurement in degrees
- s_i - i^{th} cluster size

For j=1,...,u (number of intervals):
- n_j - number of observations in j^{th} distance interval

Table 1. Data entry formats assuming objects are clusters. If objects are single animals, cluster size is always 1 and is not entered.

The *SAMPLE* command defines the basic sampling unit. It represents a line for line transects, a point for point transects, a web for trapping webs, and a search period for cue counting. Each *SAMPLE* is treated as an independent replicate for variance estimation (pg:90-98). For each *SAMPLE*, a measure of the sampling intensity or effort (*e.g.,* line length for line transects) must be specified and optionally a label can be given.

Observation data are the distances and cluster sizes for the set of detected objects. The type of data and their format (the way they are entered) (Table 1) depend on the values of the following *OPTIONS:* 1) *TYPE*, 2) *OBJECT*, and 3) *DISTANCE*. *TYPE* defines the type of sampling and determines the appropriate distance measurement (*i.e.,* perpendicular distance (x) for line transects and radial distance (r) for point transects or cue counting (pg:4-8)). *OBJECT* specifies whether the population is clustered

or not (pg:12-13). If the population is clustered, the size (s) of each observed cluster must be entered. *DISTANCE* defines whether the distance data are entered as grouped (pg:14-15) or ungrouped (pg:13-14) and whether distance for line transects is entered as perpendicular distance (x) or as a radial distance (r) and angle (θ) measurement from which perpendicular distance is calculated (*i.e.*, $x = r \sin(\theta)$) (pg:4-6). For ungrouped distances, a measurement (*e.g.*,x_i) is entered for each observed object i. For grouped distances, the frequency of observations (n_1, n_2, n_3,...,n_u) in each of u intervals are entered (pg:14-15). The corresponding intervals of distance are defined by the set of cutpoints (c_1, c_2, c_3,...,c_u) specified by the *INTERVALS* switch of the *DISTANCE* command.

Very few restrictions are applied to the data values. Distances (x or r) must be non-negative (≥ 0). The distance units are defined by the *DISTANCE* command at the *OPTIONS>* prompt. Cluster sizes (s) must be positive and the units are assumed to be integral values of animals, but the input value is not restricted to be an integer. Angle (θ) measurements (pg:5) should be entered in degrees between 0-360° assuming the standard full circle representation. This representation for the angle is provided as a convenience and it is not required. The orientation of the object is not included in the analysis. Angle measurements are used only to calculate the perpendicular distance. At present, angle measurements cannot be entered or used with point transects to indicate the orientation of the object relative to the observer. Angle values can be limited to the half-circle interval (0-180°), or to the quadrant (0-90°) by entering the acute angle formed by the line and the ray from the observer to the object. At present, the angle and radial distance measurements cannot be entered as interval (grouped) values. However, if the angle-distance data are collected in intervals, the analysis can be modified with the *SMEAR* switch of the *DISTANCE* command at the *ESTIMATE>* prompt.

Frequencies (n_i) for the grouped distance data must be non-negative. They are typically integral values but are not restricted to integers. For grouped distance data with a clustered population, DISTANCE checks to make sure that the sum of the frequencies of the grouped distances matches the number of entered clustered sizes (*i.e.*, $n_1+n_2+\cdots+n_u = n$) An error message is issued and the data are discarded, if they do not match. When the data are entered as frequencies, it is <u>not</u> necessary to enter all of the frequencies in the tail, if they are zero. For example, if there were 7 distance intervals, the following could be entered: 5,2,0,1; and the remaining 3 frequencies for intervals in the tail would be assumed to be zero.

The format for data entry depends on the data being entered. Table 1 displays the possible formats assuming *OBJECT=CLUSTER*. If you enter the data from the keyboard, DISTANCE will display the appropriate order and format. The same format should be used for data stored in a file (*INFILE*). If there is any confusion as to the appropriate format, enter part or all of your data from the keyboard to see how they should be formatted. Your keyboard entry can be stored in a file using *STORE RECORD* from which a more complete input file can be constructed with an editor. Examples of each of the data entry formats are given in template files described in the EXAMPLES section.

It is **important** that the data match the *OPTIONS* used to define the data. With very few restrictions placed on the input data, it is possible to create situations in which data are input without error but the data are incorrectly interpreted. Consider what would happen if the population is treated as unclustered (*OBJECT=SINGLE*) but cluster sizes are entered with the distances (format 2 or 5 in Table 1). DISTANCE would incorrectly treat each of the cluster sizes as a distance and the result would be to double the sample size. Depending on the distance measurement units, a plausible but incorrect detection curve may result. A similar situation could occur if distance for line transects was defined as perpendicular (*DISTANCE=PERP*) but radial distances and angles were entered.

DATA>

In each of the data formats, the data can be put on as many lines as needed but each line must not exceed 80 characters. Values on a line must be separated with commas **or** one or more spaces. Notice that a semi-colon separates different types of input data when both grouped and ungrouped data formats are used for clustered populations and specifies the end of data input for the sample. Unlike commands, information entered beyond the semi-colon will create an error. The following example for format 1 would not be valid because distances are grouped and cluster sizes ungrouped:

$n_1,n_2,n_3;\ s_1,s_2,s_3,\ldots,s_n;$

Instead, the grouped data (frequencies) and ungrouped data (cluster sizes) must start on a separate line as shown in Table 1.

If there are no observations for a *SAMPLE*, data values are not given, but the semicolons must still be entered to indicate a sample of size 0. For formats 1 and 4, two semicolons must be given on separate lines and for formats 2, 3 and 5, only one semi-colon is required.

If the observed objects are clusters, we recommend that you do not use format 1 and 4 in Table 1. Instead, we recommend that the measurements (distance and cluster size) be entered ungrouped (*EXACT*) (formats 2 or 5), even if they were recorded in intervals (grouped). Use the interval midpoint as the distance measurement for each observation in an interval. This enables a more detailed analysis because the distance and cluster size measurements are paired for each object. For instance, if a *WIDTH* is chosen which truncates some of the distance observations, it is not possible to discard the appropriate cluster sizes unless the measurements are paired as they are in ungrouped data entry. Likewise, if you wish to use cluster sizes which were observed within a pre-specified distance or perform a size-bias regression, this can only be done if distances and cluster size measurements are entered in pairs. Proper estimation with the true interval nature of the distance data is obtained by specifying *INTERVALS* with the *DISTANCE* command at the *ESTIMATE* prompt (pg:110-111,149-150). This also allows one or more intervals to be combined into larger intervals in the analysis. A simple example with "unrealistically" small numbers of observations and intervals is given below to show how interval distance data are entered as exact using the midpoint and then analyzed using the intervals in which they were collected:

```
OPTIONS;
  DIST=PERP;        <-- exact is assumed
  OBJECT=CLUSTER;
END;
DATA;
  SAMPLE/EFFORT=14.5;
    .5 2  .5 4  .5 1  1.5 6  1.5 2   2.5 7;
  SAMPLE/EFFORT=4.5;
    .5 1  1.5 4  2.5 2  2.5 6;
END;
ESTIMATE;
   DIST/INTERVALS=0,1,2,3;  <-- data originally collected in these intervals
    ESTIMATE/KEY=HN /ADJUST=POLY;
END;
```

The commands, which are valid at the *DATA>* prompt, are described below in alphabetical order.

DATA>

END

Syntax:

```
END ;
```

Description:

Finishes data entry and returns to the *Distance>* prompt.

HELP

Syntax:

```
HELP;
  or
HELP command_name;
```

Description:

If you type *HELP;* several pages of introductory information will be displayed. If you type *HELP command_name;* a description of the specific command will be given. Use PgUp and PgDn or the up and down arrow keys to scan the help information. Press the Esc key to leave help. *HELP* should only be used interactively.

INFILE

Syntax:

```
                    |/ECHO   |
INFILE=filename     |         |  ;
                    |/NOECHO|
```

Description:

This command redirects data entry to the file given by "filename" (if it is found). After all data are entered from "filename" further input is obtained from the *INPUT* file (either the keyboard or *ASSIGNed INPUT* file). The only exception is if the specified data file contains another *INFILE* command. It will then "chain" (jump) to the next file specified by the *INFILE* command. Upon completion of the second file (assuming it does not have any *INFILE* statements), DISTANCE will return to the *INPUT* file and not the data file. Thus the files cannot be truly "nested" because any data after the first *INFILE* command will be ignored. Multiple *INFILE* commands can be given throughout the *INPUT* file to enable several data files to be merged together. For this reason it is suggested that you do not include the *END;* statement in the file containing the data because it will halt data entry.

The *ECHO* and *NOECHO* switches control whether the data are *ECHOed* to the *LOG* file. By default, if commands are being *ECHOed* to the *LOG* file, the data will be *ECHOed*; likewise, if the commands are not echoed (*NOECHO*), the data will not be *ECHOed* by default (see the */ECHO* switch on the *ASSIGN* command). These default values can be changed by adding either the */ECHO* or */NOECHO* switch. The */ECHO* is most useful in tracking down errors in the data because errors are printed in the *LOG* directly after the incorrect data line. If the data are not *ECHOed*, it may be

difficult to determine which line of data contains the error. Once you are certain that the data are free of errors, using */NOECHO* will reduce the amount of output to the *LOG* file.

The *INFILE* contents must contain the *SAMPLE* command and the corresponding data associated with the *SAMPLE*. The file may also contain *STRATUM* commands. However, the file cannot contain the data without the *SAMPLE* commands. The following is an invalid use of the *INFILE* command because the observation data for the first sample are either missing or they are included in *TEST.DAT*, which is not valid:

```
DATA;
  SAMPLE/EFFORT=1;
  INFILE=TEST.DAT;
```

However, if *FILE1.DAT* and *FILE2.DAT* contain *SAMPLE* commands and data, the following is valid:

```
DATA;
  STRATUM /LABEL=STRATUM 1;
    INFILE=FILE1.DAT;
  STRATUM /LABEL=STRATUM 2;
    INFILE=FILE2.DAT;
```

Example:

```
DATA;
  INFILE=FILE1.DAT;
  INFILE=FILE2.DAT /NOECHO;
END;
```

LIST

Syntax:

```
LIST;
```

Description:

Lists values of the entered data.

SAMPLE

Syntax:

```
SAMPLE  /EFFORT=value   /LABEL='label name'  ;
```

Description:

The SAMPLE command defines the sample effort and initiates entry of the observation data for a sample. The sample-observation pairing is necessary for empirical and bootstrap variance estimation (pg: 90-91, 94-96) of the encounter rate (numbers observed per unit effort) (pg: 186-198). The encounter rate for the ith sample is computed as the number of observations (n_i) detected divided by the sample effort (*e.g.*, l_i, length of a line transect). The number of observations (n_i) is determined after left or right truncation of the data (note: the notation for number of observations per sample is the same as that used for frequency of observations in a distance interval but they represent

different values). Sample 'effort' was chosen as a generic term to represent very different measures of sampling intensity which determine the amount of area searched for the various types of distance sampling.

For **point transects**, the basic unit of sample effort is 1 for each time a complete point or web is sampled. If some constant fraction, *c*, of the complete circle is searched for all of the points, it is easiest to set effort=1 and use the command *SF=*c at the *OPTION>* prompt, where *c* is the proportion of the circle searched. However, if only some of the point transects are searched partially, set the effort for those samples to the fraction of the circle searched. **Do not** set both the effort to *c* and *SF=c*. As an example, if for 1 point transect only 1/2 the circle was searched once and the remaining points were completely searched once, let *SF* remain at its default value of 1 and enter the effort for each sample as follows:

```
DATA;
  SAMPLE/EFFORT=0.5;
      ...
  SAMPLE/EFFORT=1;
      ...
  SAMPLE/EFFORT=1;
      ...
  {etc}
```

If a series of point transects are surveyed along a line and the distance between the points is small relative to the size of the area, it is more reasonable to consider the line of points as a replicate rather than the point. In this case, each line would be represented as a sample and the effort would be the number of point transects along the line (if *c*=1 for each point) or the sum of the fraction of the circle observed at each point (if $c < 1$ for one or more points).

For **line transect** sampling, effort is the length of a line (l_i) for each time it is sampled. As with point transects, if only 1 side of the line transect is searched, sampling effort can be adjusted for a few lines by halving the line length or it can be adjusted for all lines by setting the value of *SF=0.5;* at the *OPTIONS>* prompt to adjust all of the lines. A partial example is illustrated below, with the first 3 lines each sampled a single time and the lengths are 10.5,12.1 and 1.5 miles respectively.

```
OPTIONS:
  LENGTH/UNITS='Miles';
END:
DATA;
  SAMPLE/EFFORT=10.5;
      ...
  SAMPLE/EFFORT=12.1;
      ...
  SAMPLE/EFFORT=1.5;
      ...
  {etc}
```

For **cue counting**, the sampling effort is the time spent searching. The discussion above also applies to cue counting.

DATA>

In some studies, to increase the number of observations (of animals), lines or points are sampled more than once in a short period of time (pg:91). These should not be treated as independent spatial replicates. Instead, define a *SAMPLE* for each point or line but set effort to be *t*e*, where *t* is the number of times a sample is searched and *e* is the effort for a single visit (*e.g.*, *e* is the length of the line or is 1 for a point transect (if c=1)). For example, if a point transect is observed twice in a short time period, the sample is specified as:

```
SAMPLE /EFFORT=2;
```

All of the observations from both visits to the point would follow the *SAMPLE* command. Re-sampling the same line or point for immobile objects is inappropriate for obvious reasons.

The */LABEL* can be used to give a label for the sample which is used to label the output if the density is estimated for each sample. The quote marks are only necessary to maintain lowercase letters and to include the special characters "/" and ";". Only the first 50 characters of the label are used.

Note: An early test version of DISTANCE used the syntax: *SAMPLE=effort*. That form is still accepted, but the current syntax is preferred.

Examples:

```
SAMPLE  /EFFORT=1 /LABEL=SAMPLE A;
SAMPLE  /EFFORT=14.2;
```

STRATUM

Syntax:

```
STRATUM   /LABEL='label name'  /AREA=asize ;
```

Description:

The *STRATUM* command starts entry of the data associated with a stratum. The */LABEL* switch can be used to give a label that identifies the stratum in the output if density is estimated separately for each stratum. The quote marks are only necessary to maintain lowercase letters. Only the first 50 characters of the label are used. The */AREA* switch specifies gives the size of the stratum, if appropriate. The area size must be in the units specified by *AREA/UNITS*. For example, if *AREA/UNITS='Sq. Kilometers';* is given in *OPTIONS>*, *STRATUM/AREA=1500*; specifies an area of 1500 square kilometers.

Examples:

```
STRATUM /LABEL=STRATUM A;
STRATUM;
STRATUM /AREA=1500 /LABEL='Plains area';
```

ESTIMATE>

The following are valid commands at the *ESTIMATE>* prompt:

BOOTSTRAP	- bootstrap variance/confidence intervals
CLUSTER	- estimation of expected cluster size
DENSITY	- resolution of density estimation
DETECTION	- resolution of detection probability estimation
DISTANCE	- analysis treatment of distances
ENCOUNTER	- resolution of encounter rate estimation
END	- initiates estimation
ESTIMATOR	- model for *g(x)*
GO	- estimate of *g(0)* and its standard error
GOF	- intervals for goodness-of-fit test/display
HELP	- help information
MONOTONE	- monotonicity constraints on *g(x)*
PICK	- method of model choice
PRINT	- detailed control of output
SIZE	- resolution of expected cluster size estimation
VARF	- variance estimation of *f(0)*
VARN	- variance estimation of *n*

The commands are described below in alphabetical order. You will use these commands to define:

1) which quantities you want to estimate and at what level of resolution (*DENSITY, DETECTION, ENCOUNTER, SIZE*),

2) how distance and cluster size are treated in the analysis and which models are used for estimation (*DISTANCE*, *CLUSTERS*, *ESTIMATOR*, *MONOTONE*, *PICK*, *GOF*, *GO)*,

3) how variances are estimated (*VARN*, *VARF*, *BOOTSTRAP)*, and

4) how much output should be generated (*PRINT*).

Density and abundance estimates are comprised of the following components: 1) detection probability, 2) encounter rate, and 3) expected cluster size (if the detected objects are clusters). It is possible to restrict estimation to one or more of these components without estimating density; however, all components must be estimated to obtain an estimate of density. You will use the commands *DENSITY, DETECTION, ENCOUNTER*, and *SIZE* to define which components will be estimated. If you do not use any of these commands, each component and density is estimated, by default. Likewise, if you use the *DENSITY* command, density and all of its components are estimated. If you use any or all of the *DETECTION, ENCOUNTER*, and *SIZE* commands and not the *DENSITY* command, only the specified components are estimated. For example,

```
ESTIMATE;
  ENCOUNTER ALL;
END;
```

will only estimate encounter rate.

ESTIMATE>

Estimates of density and its components can be made at different levels of the sampling hierarchy (Sample < Stratum < All). The *DENSITY*, *DETECTION*, *ENCOUNTER*, and *SIZE* commands are used to specify the level at which each quantity is estimated. Different levels can be used for the various quantities; although, some combinations are incompatible. An error message is given, if the levels are incompatible. The lowest level of resolution specified for *DENSITY* is the default level for each of its components, if they are unspecified. For example,

```
ESTIMATE;
    ESTIMATOR/KEY=UNIFORM;
    DENSITY BY STRATUM;
END;
```

will estimate density and each of its components for each stratum defined in the data. The lowest level for density must coincide with a level assigned to encounter rate. The level of any component cannot be lower then the lowest level specified for density. For example, the following is not valid:

```
ESTIMATE;
   ESTIMATOR/KEY=UNIFORM;
   DENSITY BY STRATUM;
   DETECTION BY SAMPLE;
END;
```

If a size-bias regression estimate of expected cluster size is computed, the level for *SIZE* must be no greater than the level for *DETECTION.* This feature is most useful for estimating density by stratum when too few observations exist in each stratum to estimate $f(0)$ (or $h(0)$). A solution is to assume $f(0)$ is the same for all strata, which is illustrated in the following example:

```
ESTIMATE;
    ESTIMATOR/KEY=UNIFORM;
    DENSITY BY STRATUM;
    DETECTION ALL;
END;
```

All of the observations are pooled to estimate a common value for $f(0)$, which is used in each stratum density estimate.

Possibly the most confusing aspect of estimation with DISTANCE will be the specification of models for detection probability and model selection. A model is specified with the *ESTIMATOR* command which defines a type of key function and adjustment function. The adjustment function is actually a series of terms which are added to the key function to adjust the fitted function to the data (pg: 62-65). Model selection (pg: 73-77) includes 1) selecting how many and which adjustment terms are included in the model (term selection) and 2) selecting a "best" model (estimator) from the specified set of competing models.

The default method of selecting terms (term selection mode) is defined by the *SELECTION* command under *OPTIONS>*. Its value can be overridden with the */SELECT* switch of the *ESTIMATOR* command. Related options include *LOOKAHEAD* and *MAXTERMS*. There are 4 types of term selection modes described below: 1) *SEQUENTIAL*, 2) *FORWARD*, 3) *ALL*, and 4) *SPECIFY.* The maximum number of adjustment terms that can be included in the model is limited by the value of (*MAXTERMS* - number of parameters in the key function) and less frequently by either the number of observations,

for ungrouped data, or the number of distance intervals for grouped distance data. DISTANCE will issue a warning message if the number of parameters is being limited by the amount of data.

Term selection mode *SPECIFY* implies the user will specify which adjustment terms are included in the model. Typically, this is used to specify that a key function without adjustment terms is to be fitted to the data, as in the following example:

```
ESTIMATE;
    ESTIMATOR/KEY=HNOR/NAP=0/SELECT=SPECIFY;
END;
```

It is not necessary to include the */SELECT* switch, but it will prevent DISTANCE from issuing a warning message that you are specifying the model. It is also possible to specify any combination of terms and give starting values for their coefficients. DISTANCE does not select the terms to include in the model but does estimate the parameters to fit the model to the data. For example,

```
ESTIMATE;
    ESTIMATOR/KEY=UNIFORM/NAP=2/SELECT=SPECIFY/ORDER=1,3;
END;
```

specifies the model as the following 2-term cosine series for which the parameters a_1 and a_2 are estimated:

$$f(x) = \frac{1}{w}\left(1 + a_1\cos\left(\frac{\pi x}{w}\right) + a_2\cos\left(\frac{3\pi x}{w}\right)\right) \quad .$$

ALL, as its name implies, examines all possible combinations of a limited number of adjustment terms. If z is the maximum number of parameters (*MAXTERMS=z*) and k is the number of parameters in the key function, then there are 2^{z-k} combinations of the adjustment terms. Each model is fitted to the data and the model with the smallest value of the Akaike's Information Criterion (AIC) is selected.

SEQUENTIAL and *FORWARD* both consider a subset of models with different combinations of adjustment terms. For each of these term selection modes, a sequence of models is considered. An adjustment term is added at each step of the sequence. The sequence of models can be represented as:

M_1 - key function with no adjustment terms
M_2 - key function with 1 adjustment term
M_3 - key function with 2 adjustment terms
.
.
M_v - key function with v-1 adjustment terms

A stopping rule (*CRITERION*) is either based on a likelihood ratio test or minimizing AIC. Model M_t is chosen if there is no model in the sequence $M_{t+1},\ldots,M_{t+l}$ which provides a significantly better fit as determined by the specified *CRITERION*. The *LOOKAHEAD* option determines the length (l) of the sequence of models that is examined before choosing model M_t. *SEQUENTIAL* and *FORWARD* only

differ in their choice of which adjustment term is included at each step in the sequence. *SEQUENTIAL* term selection adds the terms sequentially based on the order of the term. For polynomial adjustment functions, the order of the adjustment term is the exponent of the polynomial. Terms are added in the following sequence: (x^t, x^{t+2},...). For cosine adjustments, cosine terms are added in the following sequence: (cos(tπx/w),cos((t+1)πx/w),...). The beginning value, *t*, is determined by the shape of the key function. *FORWARD* selection adds 1 term at a time but not necessarily in sequential order. For each model in the sequence, each term not already in the model is added and the adjustment term which increases the likelihood the most is chosen as the term to add. For example, to find model M_2, *z-k* models are fitted to the data, each with a single adjustment term of a different order (e.g., x^2, x^4, x^6, x^8,or x^{10}). The term which maximizes the likelihood is selected for model M_2. Model M_3 would then consider adding another term not included in M_2. With *FORWARD* selection it is possible to select models that cannot be selected with the *SEQUENTIAL* mode. For example, the following model might be chosen with *FORWARD* selection:

$$f(x) = \frac{1}{w}\left(1 + a_1\cos\left(\frac{\pi x}{w}\right) + a_2\cos\left(\frac{3\pi x}{w}\right)\right) \quad .$$

However, with *SEQUENTIAL* selection, the adjustment term cos(3πx/w), could not be added without first adding the adjustment term cos(2πx/w) .

The additional level to model fitting is to choose between the competing models (*ESTIMATORs).* This model selection step is determined by the *PICK* command. It has 2 values: *NONE* and *AIC*. If you assign the value *NONE*, DISTANCE will not choose between the different models and will report the estimates for each model. However, if you accept the default value, *AIC* (pg:75-76) DISTANCE will only compute estimates based on the model which has the smallest AIC value.

ESTIMATE>

BOOTSTRAP

Syntax:

```
                    |/STRATUM   |
BOOTSTRAP           |            |   /SAMPLES  /OBS ;
                    |/INSTRATUM|
```

Description:

The *BOOTSTRAP* command initiates a non-parametric bootstrap (pg:94-95, 119-120, 155-158) of the density estimation procedure. The number of bootstraps performed is determined by the *BOOTSTRAP* command in *OPTIONS.* The basic re-sampling unit of the bootstrap is a *SAMPLE*; however, if strata are replicates they can also be re-sampled with the */STRATUM* switch. If both are specified, re-sampling occurs at both levels (see example below). The switch */INSTRATUM* can be set to restrict the re-sampling of samples or observations within stratum It would be used if density is estimated by stratum or sampling was stratified apriori.

The switch */OBS* can be set to re-sample distances. Using *BOOTSTRAP/OBS;* will provide a non-parametric bootstrap of $f(0)$ or $h(0)$ and, if the population is clustered, E(s). However, the variances and confidence intervals are conditional on the sample size and do not include the variance of the encounter rate. The */OBS* switch has been included for completeness but its routine use is not recommended. Reasonable confidence intervals for density could only be obtained by adding a variance component for the encounter rate. It is also possible to include the */OBS* switch with */SAMPLES*, however, this is not recommended unless the number of observations per sample is reasonable (> 15).

By default, issuing the *BOOTSTRAP* command without switches is equivalent to *BOOTSTRAP/SAMPLES/INSTRATUM;*. We recommend the default or dropping the */INSTRATUM* if sampling across strata is appropriate. The use of */STRATUM* is only appropriate if the strata represent an additional level of sampling *(e.g.*, independent observers (stratum) traversing an independent set of line transects (sample)).

The bootstrap summary is given at the end of the output. Two sets of confidence intervals are given: 1) log-based confidence intervals based on a bootstrap standard error estimate, and 2) 2.5% and 97.5% quantiles of the bootstrap estimates (i.e., percentile confidence intervals). See Program Files for a complete description of the *BOOTSTRAP* file.

Example:

Re-sample strata and samples within each stratum.

```
BOOTSTRAP /STRATUM /SAMPLES;
```

ESTIMATE>

CLUSTER

Syntax:

```
CLUSTER    /WIDTH=value   /TEST=α
                                                  ;
                  |/MEAN            |
                  |       | X     |   |
                  |/BIAS=| XLOG  |   |
                  |       | GX    |   |
                  |       | GXLOG|   |
```

Description:

The *CLUSTER* command, like the *DISTANCE* command, is used to modify the way the cluster sizes are used in the estimate of density. By default, the *WIDTH* is chosen to match the truncation value set by the *DISTANCE* command and DISTANCE computes a size-bias regression estimate (*/BIAS=GXLOG*) by regressing the $\log_e(s)$ (natural logarithm specified as log() in the output) against $\hat{g}(x)$, where x is the distance at which the cluster was observed.

The *WIDTH* switch specifies that only cluster sizes for observations within a distance less than *WIDTH* are used in the calculation of the expected cluster size. This treatment of the data can only be accomplished if the distances and cluster sizes are both entered as ungrouped.

The *MEAN* switch specifies that the expected cluster size is to be estimated as the average (mean) cluster size. Likewise, the *BIAS* switch specifies that expected cluster size is to be estimated by a size-bias regression defined by the value of the switch.

Value	Meaning
X	Regress cluster size against distance x
XLOG	Regress $\log_e(s)$ against distance x
GX	Regress cluster size (s) against $\hat{g}(x)$
GXLOG	Regress $\log_e(s)$ against $\hat{g}(x)$

The *TEST* switch specifies the value of the significance level to test whether the regression was significant. If it is non-significant, the average cluster size is used in the estimate of density. The default value for the significance level is set by *PVALUE* in *OPTIONS*. If the *TEST* switch is not specified, the size-bias regression estimate will be used regardless of the test value.

Examples:

Estimate the expected cluster size from the $\log_e(s)$ vs. $\hat{g}(x)$ regression, but use the average cluster size if the correlation is non-significant as determined by the α-level set with *PVALUE* (default=0.15).

```
CLUSTER /BIAS=GXLOG /TEST;
```

ESTIMATE>

DENSITY

Syntax:

```
                                        |NONE     |
            DENSITY by SAMPLE /DESIGN=  |         |   ;
                                        |REPLICATE|


     or
                                         |NONE     |
            DENSITY by STRATUM /DESIGN = |STRATA   |
                                         |REPLICATE|

                                         |EFFORT|
                                /WEIGHT= |      |      ;
                                         |AREA  |
                                         |      |
                                         |NONE  |
     or

            DENSITY by ALL ;
```

Description:

These commands define the levels at which density estimates are made and how these estimates are weighted. If the *DENSITY by ALL;* command is used or if none of the commands (*DENSITY, ENCOUNTER, DETECTION, SIZE*) are given, all of the data are used to make one overall estimate of density.

If the *DENSITY BY SAMPLE* command is given, density is estimated for each sample. The *DESIGN* value defines how the estimates should be treated to create a pooled estimate. If *DESIGN=REPLICATE* (default), each sample is treated as an independent replicate from the stratum or the entire area. In this case, the estimates are weighted by effort (e.g., line length) to get a stratum density estimate (if *DENSITY by STRATUM* is also specified) or a pooled overall density estimate (see eqns. 3.11-3.14 in Buckland *et al.* (1993)). If *DESIGN=NONE*, the sample estimates are not pooled.

If *DENSITY BY STRATUM* is specified, an estimate is made for each stratum. A stratum estimate is a pooled estimate of the sample estimates within the stratum, if *DENSITY by SAMPLE;* is specified, or it is an estimate based on the data within the stratum. An overall (pooled) estimate of density is made unless *DESIGN=NONE* is specified. If *DESIGN=REPLICATE*, the stratum estimates are treated as replicates to create a pooled estimate and variance weighted by effort (eqns. 3.11-3.14 in Buckland *et al.* (1993), treating stratum as a sample). If *DESIGN=STRATA*, the pooled estimate is a weighted sum of the estimates and the variance is a weighted sum of the stratum variances (Section 3.8.1 in Buckland et al. (1993)). Weighting is defined by the *WEIGHT* switch. If *WEIGHT=NONE*, the densities are summed, which is only useful if the population is stratified as by sex or age. If *WEIGHT=AREA*, the densities are weighted by area (which is the same as adding abundance estimates) and if *WEIGHT=EFFORT*, the densities are weighted by effort.

Prior to version 2.1, a combined estimate of abundance (N) was created by multiplying the

combined density estimate by the sum of the areas specified on each of the *STRATUM* commands. This produces obviously erroneous results when *DENSITY by STRATUM/DESIGN=REPLICATE*; is used and the area size is repeated on each *STRATUM*. To avoid this problem in the following two situations the combined abundance estimate uses the area from the first stratum:

1) *DENSITY by STRATUM/DESIGN=REPLICATE*;

2) *DENSITY by STRATUM/DESIGN=STRATA/WEIGHT=NONE;*

In all other cases, the area is totalled from all of the strata.

Default:
For *DENSITY by SAMPLE*: */DESIGN=REPLICATE*

For *DENSITY by STRATUM: /DESIGN=STRATA*
/WEIGHT=AREA

Examples:
An estimate is needed for each stratum and it will be weighted by stratum area:

```
DENSITY BY STRATUM;
```

An estimate is needed for each stratum and there are enough observations in each sample to get an estimate from each. The strata represent different platforms surveying the same area so the strata are treated as replicates.

```
DENSITY BY SAMPLE;
DENSITY BY STRATUM /DESIGN=REPLICATE;
```

DETECTION

Syntax:

```
                              |SAMPLE |
                DETECTION by  |STRATUM|     ;
                              |ALL    |
```

Description:
This command explicitly specifies that detection probability (and its functionals $f(0)$, $h(0)$) should be estimated and the resolution at which the estimate(s) should be made (by *SAMPLE*, by *STRATUM*, or *ALL* data).

Example:
Density is estimated by stratum but the estimates are based on an estimate of $f(0)$ for all the data.

ESTIMATE>

```
DENSITY by STRATUM;
DETECTION ALL;
```

Estimate detection by stratum choosing between 2 models but do not estimate any other parameters. Different models may be selected for each stratum.

```
ESTIMATE;
  DETECTION BY STRATUM;
  ESTIMATOR/KEY=HAZ;
  ESTIMATOR/KEY=UNIF;
END;
```

DISTANCE

Syntax:

DISTANCE /WIDTH=value /INTERVALS=$c_0, c_1, c_2, c_3, \ldots, c_u$

/LEFT=l /RTRUNCATE=t /NCLASS=nclass ;

/SMEAR=angle,pdist

Description:

The *DISTANCE* command is used to specify the way the distances should be treated in the analysis. It can be used to specify left and right truncation of the distance, to group the distances into intervals prior to analysis, and to "smear" radial distance / angle measurements into perpendicular distance intervals.

Right truncation (pg: 15, 50, 106-109) is specified with either the *WIDTH* or *RTRUNCATE* switch. If *WIDTH=w*, only distances less than or equal to *w*, are used in the analysis. If *RTRUNCATE=t*, the right truncation distance is set to use (1-*t*)*100% of the data. If the data are ungrouped the (1-*t*)*100 percentile is used as the truncation distance. If the distances are grouped or being analyzed as such, the truncation distance is set to the uth interval end point where *u* is the smallest value such that no more than *t*100% of the distances are truncated. The value of *t*=0 trims the intervals to the right most interval with a non-zero frequency. If both the *WIDTH* and *RTRUNCATE* are specified, the value of *RTRUNCATE* defines the truncation unless the *WIDTH* is used with *NCLASS* (see below).

Left truncation (pg: 15, 273-277) is accomplished with the *LEFT* switch which works in an analogous fashion to *WIDTH*. If *LEFT=l*, only distances greater than or equal to *l* are used in the analysis. If *LEFT* is not specified, it is assumed to be 0.

ESTIMATE>

The *INTERVALS* command is used to specify u distance intervals for analyzing data in a grouped manner when the data were entered ungrouped. The value c_0 is the left most value and so it can be used for left truncation. If there is no left truncation, specify c_0=0. The values $c_1, c_2, ..., c_u$ are the right end points for the u intervals. The value c_u is the right-most point and is used as the *WIDTH* which defines the right truncation point. If all of the distances are less than or equal to c_u, DISTANCE will not truncate data on the right unless *RTRUNCATE* is set. Perpendicular distance intervals can also be created for analysis with the *NCLASS* and *WIDTH* commands. *NCLASS* intervals of equal length are created between 'Left' and 'Width', if both *NCLASS* and *WIDTH* are given.

The *SMEAR* switch is used only if *TYPE=LINE* and radial distance/angle measurements were entered (*DISTANCE=RADIAL*). "Angle" defines the angle sector around the angle measurement and "Pdist" defines the proportional sector of distance to use as the basis for the smearing (pg: 319-322). If an observation is measured at angle "a" and radial distance "r", it is smeared uniformly in the sector defined by the angle range (a-angle,a+angle) and distance range (r*(1-pdist),r*(1+pdist)). The *NCLASS* and *WIDTH* switches must also be given to define a set of equal perpendicular distance intervals. The proportion of the sector contained in each perpendicular distance interval is summed as an observation frequency and these non-integer frequencies ("grouped data") are analyzed to estimate detection probability.

Note: Distances specified by *WIDTH*, *LEFT*, and *INTERVALS* should be in the same units used for the entered data, even if the distance units are converted in the analysis.

Examples:

Truncate the distances at 100 feet, hence only use those less than or equal to 100 feet in the analysis. This value would be used even if the distances were converted to meters for analysis. The conversion is applied to the input width of 100 feet.

```
DIST /WIDTH=100;
```

The distance data were entered ungrouped but they were actually collected in these intervals; alternatively, to mediate the effects of heaping, these intervals were chosen to analyze the data.

```
DIST /INT=0,10,20,30,40,50,60,70,80,90,100;
```

The above example could also be entered as:

```
DIST/NCLASS=10/WIDTH=100;
```

ESTIMATE>

ENCOUNTER

Syntax:

```
                                |SAMPLE |
                ENCOUNTER by    |STRATUM|      ;
                                |ALL    |
```

Description:

This command explicitly specifies that encounter rate should be estimated and the resolution at which the estimate(s) should be made (by *SAMPLE*, by *STRATUM*, or *ALL* data). This command is only necessary if density is not being estimated.

Examples:

A user wishes to explore the variability in encounter rate by listing the encounter rate for each sample. The variance of the encounter rate for each sample is assumed to be Poisson because the sample is a single entity.

```
ESTIMATE;
  ENCOUNTER by SAMPLE;
END;
```

A user wishes to explore the variability in encounter rate by listing the encounter rate for each stratum. The variance of the encounter rate for each stratum is computed empirically for each stratum with more than one sample; otherwise, it is assumed to be Poisson.

```
ESTIMATE;
  ENCOUNTER by STRATUM;
END;
```

A user wishes to only see the average encounter rate and an estimate of its variance. The variance of the encounter rate is computed empirically if there is more than one sample; otherwise, it is assumed to be Poisson.

```
ESTIMATE;
  ENCOUNTER ALL;
END;
```

END

Syntax:

```
                END ;
```

Description:

END Finishes definition of the estimation procedure and initiates estimation. After the analysis is completed the *Distance>* prompt reappears.

ESTIMATE>

ESTIMATOR

Syntax:

```
                        |UNIFORM|
                        |HNORMAL|              |COSINE |
      ESTIMATOR  /KEY=  |NEXPON |   /ADJUST=   |POLY   |
                        |HAZARD |              |HERMITE|

                          |SPECIFY   |
                /SELECT=  |SEQUENTIAL|   /ORDER=O(1),O(2),...,O(nap)
                          |FORWARD   |
                          |ALL       |

               /NAP=nap            /START=a(1),a(2)...a(nkp+nap)

                           |AIC|
               /CRITERION= |   |          ;
                           |LR |
```

Description:

The *ESTIMATOR* command specifies the type of model for detection probability ($g(x)$) (pg: 46-49) to estimate $f(0)$ or $h(0)$. The *KEY* switch specifies the key function to be used and the *ADJUST* switch specifies the type of adjustment function. The *SELECT* switch specifies the type of adjustment term selection which overrides the default value specified by the *SELECTION* command in the *OPTIONS* procedure (see the discussion on adjustment term selection above).

If *SELECT=SPECIFY* is chosen, you can specify the number of adjustment parameters, the order of the adjustment term and starting values for the parameters. The number of adjustment parameters is set with the *NAP* (*N*umber of *A*djustment *P*arameters). *NAP* must be less than or equal to *MAXTERMS* - 'nkp' (number of key parameters). The orders of the adjustment term(s) are specified with the */ORDER* switch. Starting values (*/START*) for the key and adjustment parameters can be given if the optimization algorithm suggests there are problems in finding the maximum of the likelihood function. The first 'nkp' starting values in the list should be the values for the key parameters and the remaining are for the 'nap' adjustment parameters. One reason for using the *SELECT* and *NAP* switches is to specify that only the key function should be fitted to the data. An example is given below.

CRITERION specifies the manner in which the number of adjustment terms is chosen for *SELECT=FORWARD* and *SEQUENTIAL*. *LR* specifies that a likelihood ratio test (pg: 74-75) be performed using the *PVALUE* specified in *OPTIONS*. *AIC* specifies using the Akaike's Information Criterion (pg: 75-76) for adjustment term selection.

Multiple *ESTIMATOR*s can be specified within an *ESTIMATE* procedure and the "best" model is selected or estimates are given for each model (see *PICK*).

ESTIMATE>

The only portion of the command required is the command name *ESTIMATOR* because all of the switches have default values.

Default Values:

KEY = *HNORMAL*
ADJUST = *COSINE*
SELECT = *SEQUENTIAL* (or value set in *OPTIONS*)
CRITERION = *LR* (except if *SELECT=ALL*)

Examples:

Use the following to fit a model with a half-normal key function (by default) and Hermite polynomials for adjustment functions. DISTANCE fits all possible combinations of adjustment terms and uses AIC to choose the best set of adjustment terms:

```
ESTIMATOR /ADJ=HERM /SEL=ALL;
```

Use the following to fit a model that uses the uniform key function with simple polynomial adjustment functions:

```
ESTIMATOR /KEY=UNIFORM /ADJ=POLY;
```

Use the following to fit a model that uses the hazard key without adjustments:

```
ESTIMATOR /KEY=HAZARD /SELECT=SPECIFY /NAP=0;
```

Use the following to fit a 2-term cosine series with terms of order 1 and 3 and specify the parameter starting values (note: nkp=0 for a uniform key):

```
ESTIMATOR /KEY=UNIF /SELECT=SPECIFY /NAP=2 /ORDER=1,3
          /START=0.3,0.05;
```

G0

Syntax:

```
G0=value /SE=value ;
```

Description:

This command assigns a value to $g(0)$ which is assumed to be 1 unless a value is assigned with this command. The SE switch is used to specify a standard error for the estimate so that estimation uncertainty of $g(0)$ can be incorporated into the analytical variance of density.

Default:

G0=1.0/SE=0.0;

Example:

G0=0.85/SE=0.12;

ESTIMATE>

GOF

Syntax:

```
GOF /INTERVALS=c0,c1,c2,... ,cu    |/SAS   |    ;
                                   |/SPLUS|
```

or

```
GOF |/SAS   |    /NCLASS=nclass    ;
    |/SPLUS|
```

or

```
GOF |/SAS   |                      ;
    |/SPLUS|
```

Description:

This command has two purposes. The first purpose is to specify the distance intervals for plotting a scaled version of the histogram of distances against the function *g(x)* (and *f(x)*) and for the chi-square goodness of fit test (pg:76-77). The second purpose is to specify that the PLOT file should be created for SAS/GRAPH or SPLUS. See Program Files for a complete description of this file. It is an ASCII file and can be modified with a text editor.

If the data are entered and analyzed ungrouped (*/EXACT*), the first 2 forms can be used to define the intervals which are used for plotting the data and for the chi-square goodness of fit test. The first form specifies the intervals exactly and the second form provides a shortcut approach of specifying 'nclass' equal intervals (Note: the syntax from previous versions of GOF=c_0,c_1...; will also work). You can enter up to 3 of these commands to specify different sets of intervals. If you do not specify this command and the data are analyzed as ungrouped, 3 sets of intervals are constructed with equally spaced cutpoints and the number of intervals being the $n^{0.5}$ and 2/3 $n^{0.5}$ and 3/2 $n^{0.5}$. You can optionally specify */SAS* or */SPLUS* after the intervals to create a PLOT file. If you want to use the default intervals and create the PLOT file, use the second form of the command.

If the data are entered grouped or entered ungrouped and analyzed as grouped (*DISTANCE/INTERVALS=* used in *ESTIMATE*) then only the third form can be used to specify that the PLOT file should be constructed. It is not possible to specify goodness of fit intervals other than those used to analyze the data.

Examples:

Data are ungrouped and 2 different sets of intervals are specified.

```
GOF  /NCLASS=5;
GOF=0,5,10,20,30,40,50;
```

Data are grouped but the SAS plot file is desired.

```
GOF /SAS;
```

ESTIMATE>

HELP

Syntax:

```
        HELP;
   or
        HELP command_name;
```

Description:

If you type *HELP;* several pages of introductory information will be displayed. If you type *HELP command_name;* a description of the specific command will be given. Use PgUp and PgDn or the up and down arrow keys to scan the help information. Press the Esc key to leave help.

MONOTONE

Syntax:

```
                    |WEAK   |
          MONOTONE=|STRICT|  ;
                    |NONE   |
```

Description:

The estimators are constrained by default to be strictly monotonically non-increasing (i.e., *MONOTONE=STRICT;* the detection curve is either flat or decreasing as distance increases from 0 to *w*) (pg:73). In some instances, depending on the tail of the distribution this can cause a poor fit at the origin(x=0). Two options exist: 1) truncate the observations in the tail, or 2) use the command *MONOTONE=WEAK;* or *MONOTONE=NONE*;. *MONTONE=WEAK*; will only enforce a weak monotonicity constraint (i.e., $f(0) >= f(x)$ for all distances x). This will allow the curve to go up and down as it fits the data but it will not let the curve dip down at the origin. In some instances this will allow the estimator to achieve a better fit at the origin which is the point of interest. Setting *MONTONE=NONE;* will allow the curve to take any possible form except that it must remain non-negative.

Monotonicity is achieved by constraining the function at a fixed set of points. In some circumstances it is possible that the curve can be non-monotone between the fixed points. Typically, this results from trying to over-fit the data with too many adjustments with a long-tailed distribution. Truncate the data rather than attempting to over-fit.

Default: *MONOTONE=STRICT;*

ESTIMATE>

PICK

Syntax:

```
                |NONE|
          PICK=|    |   ;
                |AIC |
```

Description:

If more than one *ESTIMATOR* command is given a choice must be made as to which model will be used for the final estimate (pg:50-51,73-76). The command *PICK=AIC;* instructs the program to choose the model that minimizes Akaike's Information Criterion. The command *PICK=NONE*; instructs the program not to choose a model and to present the results of each. If no command is given *PICK=AIC;* is assumed. (Note: prior to Version 1.20 this command was not available and the results of all estimators were displayed (i.e., *PICK=NONE* assumed).

If the *BOOTSTRAP;* command is given and *PICK=NONE* is specified a bootstrap procedure is performed for each estimator. Whereas, if *PICK=AIC,* the bootstrap is performed and the estimator is chosen for each analysis. Thus, even though a single estimator is chosen for the point estimate, different estimators can be chosen for each bootstrap and the standard errors and interval estimates incorporate the uncertainty of the model selection process.

Default: *PICK=AIC;*

PRINT

Syntax:

```
        PRINT /YES=option list /NO=option list ;
```

Description:

This command can further expand or limit the output from the estimate procedure beyond what is defined by the *PRINT* command in *OPTIONS.* The *PRINT* command in *OPTIONS* allows hierarchical control of the output and defines the default values for this print command and thus retains its functionality. However, this command can be used to define whether each component is printed to the *OUTPUT* file by specifying it either in the */YES* or */NO* list. The following are the values of the option list:

Option List:

All	- Used in place of listing all options	Fxplot	- Function/histogram plots
Estimate	- Density estimate table	Fxtest	- Chi-square goodness of fit test
Explain	- Explanation of estimation options	Sbarest	- Estimates of E(S)
Fxest	- Function parameter estimates	Sbarplot	- Size-bias regression plot
Fxfit	- Function fitting/model selection		
Fxiterations	- Iterations of MLE		

ESTIMATE>

Below are listed the default values of the print options as defined by the value set by *PRINT=* in *OPTIONS*. (Y=Yes and N=No)

OPTIONS PRINT= command value	ESTIMATE	FXEST	FXPLOT	FXTEST	SBAREST	SBARPLOT	FXFIT	FXIT
SUMMARY	N	N	N	N	N	N	N	N
RESULTS	Y	Y	Y	Y	Y	Y	N	N
SELECT	Y	Y	Y	Y	Y	Y	Y	N
ALL	Y	Y	Y	Y	Y	Y	Y	Y

By default, */YES=EXPLAIN* is set to provide a printed explanation of the estimation options and models chosen (Note: in Versions prior to 1.20, the default was *NO* and it was set to *YES* with the more limited *PRINT OPTIONS* command).

SIZE

Syntax:

```
                        |SAMPLE |
                SIZE by |STRATUM|     ;
                        |ALL    |
```

Description:

This command explicitly specifies that expected cluster size should be estimated and the resolution at which the estimate(s) should be made (by *SAMPLE*, by *STRATUM*, or *ALL* data). This command is only necessary if density is not being estimated or to specify a level of resolution different from density. The level of resolution for estimating cluster size must be less than or equal to the level for estimating detection probability, if a size bias regression estimate is computed.

Example:

A user wishes to examine detection probability and expected cluster size but not density at this point:

```
ESTIMATE;
  ESTIMATOR/KEY=UNIF;
  DETECTION ALL;
  SIZE ALL;
END;
```

EXAMPLES

VARF

Syntax:

```
                    |MLE       |
          VARF =    |           |        ;
                    |BOOTSTRAP  |
```

Description:

This command specifies the type of variance estimation technique for $f(0)$. *MLE* specifies that the theoretical variance estimate should be used. *BOOTSTRAP* specifies that a parametric bootstrap should be performed. This is a bootstrap variance estimate of $f(0)$ or $h(0)$ and not of density, so it should not be confused with the *BOOTSTRAP* command. If you choose a bootstrap variance estimate you can use a default value of 0 for the *SEED* which starts the random number generation with a random seed from the computer clock or you can specify a *SEED* in the *OPTIONS* section so that the same set of random numbers is generated in different runs.

NOTE: This command is of limited use and is only included for compatibility to previous versions. The *BOOTSTRAP* command should be used to get bootstrap variances and confidence intervals.

Default: *VARF=MLE;*

VARN

Syntax:

```
                    |POISSON   |
          VARN =    |'b'       |        ;
                    |EMPIRICAL |
```

Description:

This command specifies the type of variance estimation technique for encounter rate. The value *POISSON* specifies that the distribution of n (number of observations) is Poisson (pg: 50,88,109-110). *EMPIRICAL* specifies that the variance should be calculated empirically from the replicate *SAMPLE*s (pg: 90-92). If only one *SAMPLE* is defined in the data, the *POISSON* assumption is used unless a value *b* is specified. If a value *b* is specified it is used as a multiplier such that *var(n)= bn* (pg: 186-198). The Poisson assumption is equivalent to specifying *b=1*. The default for *VARN* is *EMPIRICAL* unless there is only one *SAMPLE*, in which case, the default is *POISSON*.

Default: *VARN=EMPIRICAL*

EXAMPLES

For each example, the DISTANCE input is contained in a file which is placed into *YourDirectory* during installation. The output for an example can be generated by entering:

DIST I=examplefilename O=outputfilename

and replacing *examplefilename* and *outputfilename* with appropriate filenames. The general structure of the output and a detailed description of model selection output is given with Example 1. Less detailed description is given with Example 2 .

Example 1

Description

This example of line transect sampling is described in Chapter 4 of Buckland *et al.* (1993). Twelve lines (samples) covering 48 km were "sampled" and n=105 objects were "observed" from a half-normal detection curve. True density is 79.788 groups/km^2 and 239.4 animals/km^2. Cluster size for each observation was generated from a Poisson distribution with E(s)=3. The analysis of cluster density is described in Sections 4.3-4.7 of Buckland et al. (1993) and the estimation of expected cluster size in Section 4.8.1. We have further structured this example by arbitrarily splitting the 12 samples into 2 strata, to illustrate a stratified analysis.

Input

The input file is named *EXAMPLE1.INP*. An abbreviated listing, excluding most of the data, is given in Figure 6. The input file contains commands to: 1) assign filenames for the output and log, 2) specify options, 3) structure and input the data, and 4) perform 3 analyses.

The options specify that perpendicular distance is measured in metres, length is measured in kilometres and area is specified to be km^2 for density estimates. Also, each observation is defined to be a cluster and an appropriate value for an output title is specified.

The sampled area is composed of two strata each representing an area of 50 km^2. Six lines were sampled in each stratum. The line lengths (effort) are: 5, 2, 6, 4, 3, 1, 4, 4, 5, 7, 3, and 4 kms. Perpendicular distance and cluster size measurements are entered as a list with each pair of measurements for an observation on a line. For example, the first observation from transect 1 was a single animal (cluster size=1) at 7.8595 metres from the line. (Note: the data are computer-generated and the precision is exaggerated beyond what is needed). Several measurements could be put on the same line (up to 80 characters per line) but the layout shown is more readable. Observation data for this example are entered corresponding to format 5 (Table 1, see *DATA*>). Option values are important to the structure and input of the data. For example, if *OBJECT=CLUSTER;* is removed from the option list, cluster sizes are not expected. If the cluster sizes are not removed from the data, each cluster size would be read in as a perpendicular distance measurement and it would falsely appear that twice as many observations had been made.

EXAMPLES

```
assign output=example1.out/replace;
assign log=example1.log/replace;
options;
  dist/units='metres';
  length/units='kilometres';
  area/units='sq. kilometres';
  object=cluster;
  title='Chapter 4, example 1, pgs 105-115,122-125';
end;
data;
stratum /Label='Stratum 1' /Area=50;
sample/effort=5/label='Line 1';
 7.8595      1
10.2435      4
12.4435      2
 3.7600      3
 4.7777      7
 8.4531      3
13.4136      2
 5.8039      2
 7.4507      5
11.4513      3
 0.8634      4
 9.2329      6
12.5082      4
 6.0755      8
;
sample/effort=2/label='Line 2';
 9.1468      1
 6.3828      2
21.2129      3
;
.
.
.
sample/effort=4/label='Line 12';
 0.9703      2
 6.6183      3
12.4475      2
 4.8554      2
15.4140      4
;
end;
estimate;
   dist/width=19;
   cluster/test=0.05;
   est /key=unif /adj=cosine;
   est /key=unif /adj=poly;
   est /key=hn /adj=hermite;
   est /key=hazard /adj=cosine;
   gof/nclass=5;
   pick=none;
end;
estimate;
   dist/width=19;
   est /key=hn /adj=hermite;
   size all;
   detection all;
   gof/nclass=5;
   cluster/test=0.05;
end;
estimate;
   dist/width=19;
   est /key=hn /adj=hermite;
   density by stratum;
   gof/nclass=5;
   cluster/mean;
   print/no=all/yes=explain;
   detection all;
end;
```

Figure 6. Abbreviated input listing for example 1 (EXAMPLE1.INP).

Each of the three *Estimate;...End;* command sets performs an analysis (note: indentation of the commands is for readability and is not required). The first *ESTIMATE* procedure specifies:
1) observations with a perpendicular distance exceeding 19m are excluded (w=19) and the analysis is performed on ungrouped (exact) measurements,
2) expected cluster size is to be analyzed by the default size-bias regression but if the observed probability exceeds a significance level of 0.05, the average cluster size should be used instead,
3) 4 detection models should be examined: uniform + cosine, uniform + polynomial, half-normal + Hermite, and hazard + cosine. By default, selection of adjustment terms is determined by sequential fitting (*SELECTION = SEQUENTIAL*) with *LOOKAHEAD=1* and the criterion is a likelihood ratio test (*CRITERION=LR*) with a default significance level of 0.15 (*PVALUE*),
4) results for each detection model are given because DISTANCE has been instructed not to pick the best model (*PICK=NONE*), and
5) the goodness-of-fit test and plot use 5 equal intervals over the range 0-19.

The second *ESTIMATE* procedure illustrates how to restrict estimation to certain parameters of interest. In this example, only expected cluster size (*Size All;*) and detection probability ($f(0)$) (*Detection All;*) are estimated for all of the data combined. Density is not estimated because a *Density;* command is not included. See *ESTIMATE>* for an explanation of these commands.

A stratified analysis is illustrated in the third *ESTIMATE* procedure. Density is estimated for each stratum (*Density by Stratum;*) but a common $f(0)$ is estimated across strata (*Detection all;*) An overall (pooled) density estimate is computed as an area-weighted average of the stratum estimates. The half-normal+Hermite is the only detection model considered. Expected

cluster size is estimated by the mean cluster size. Output is limited to an explanation of estimation options and summary tables by the command *Print/No=all/Yes=explain;*. The switch, */No=all,* eliminates all output other than summary tables and the switch, */Yes=explain*, reinstates the explanation of the estimation options (see *PRINT* command within *ESTIMATE>*).

Output

The type of output will vary depending on the analysis and the restrictions placed on the type of output; however, the general structure is as follows:

I. Estimation Options Listing - A short semi-narrative description of the estimation options and detection models and a glossary of terms (Figure 7).

II. Probability Function Estimation - Estimation of average detection probability p (equivalent to P_w or P_a in Buckland et al. (1993)) and related quantities ($f(0)$ & effective strip width (ESW) or $h(0)$ and effective detection radius (EDR)). It is organized in the following manner:

a) Model Fitting and Selection
b) Parameter Estimation Table
c) Detection Probability Plot(s)
d) Chi-square goodness-of-fit test

If DISTANCE chooses the best model (default of *Pick=AIC*), section a) is repeated for each detection model and b)-d) is only given for the best model. If several detection models are considered and *Pick=None;* is specified, sections a)-d) are repeated for each model.

III. Expected Cluster Size Estimation - this section is generated if *Object=Cluster;*(in *OPTIONS>*) If a size-bias regression estimator is used a plot of the data and regression equation are also given. This section is repeated for size-bias regression, if several detection models are considered and the best model is not chosen by DISTANCE.

IV. Density Estimation Results - a summary table of estimation results including density (and abundance if area size is given). This section is also repeated for each detection model if the best model is not chosen.

V. Estimation Summary - summary tables of Encounter Rate, Detection Probability, Expected Cluster Size, and Density/Abundance. These tables summarize estimates of each quantity and related values at the chosen level (Sample, Stratum, All) of estimation. Estimates are also summarized by detection model, where appropriate.

VI. Bootstrap Summary of Density/Abundance - if a bootstrap analysis for density is requested, tables summarizing bootstrap coefficient of variation (CV) and confidence interval are given.

The amount of output can be restricted at a general level with the *PRINT* command within *OPTIONS>* and in greater detail with the *PRINT* command within *ESTIMATE>*. We recommend that you accept the default level of output until you become familiar with the analysis techniques.

```
                          ************************************
                        *       Estimation Options         *
                        *           Listing                *
                        ************************************

Parameter Estimation Specification
----------------------------------
Encounter rate for all data combined
Detection probability for all data combined
Expected cluster size for all data combined
Density for all data combined

Distances:
----------
Analysis based on exact distances
Width specified as:    19.00000

Clusters:
---------
Analysis based on exact sizes
Expected value of cluster size computed by : regression of log(s(i)) on g(x(i))
   unless regression is non-significant,  with significance level =   .050

Estimators:
-----------
Estimator  1
Key: Uniform, k(y) = 1/W
Adjustments - Function                : Cosines
            - Term selection mode     : Sequential
            - Term selection criterion: Likelihood ratio test
Estimator  2
Key: Uniform, k(y) = 1/W
Adjustments - Function                : Simple polynomials
            - Term selection mode     : Sequential
            - Term selection criterion: Likelihood ratio test
Estimator  3
Key: Half-normal, k(y) = Exp(-y**2/(2*A(1)**2))
Adjustments - Function                : Hermite poynomials
            - Term selection mode     : Sequential
            - Term selection criterion: Likelihood ratio test
Estimator  4
Key: Hazard Rate, k(y) = 1 - Exp(-(y/A(1))**A(2))
Adjustments - Function                : Cosines
            - Term selection mode     : Sequential
            - Term selection criterion: Likelihood ratio test

Estimator selection: None, display all estimates
Estimation functions: constrained to be nearly monotone non-increasing

Variances:
----------
Variance of n: Empirical estimate from sample
Variance of f(0): MLE estimate

Goodness of fit:
----------------
Based on user defined cut points


Glossary of terms
-----------------
Data items:
n    - number of observed objects (single or clusters of animals)
L    - total length of transect line(s)
k    - number of samples
K    - point transect effort, typically K=k
T    - length of time searched in cue counting
ER   - encounter rate (n/L or n/K or n/T)
W    - width of line transect or radius of point transect
x(i) - distance to i-th observation
s(i) - cluster size of i-th observation
r-p  - probability for regression test
chi-p- probability for chi-square goodness-of-fit test

Parameters or functions of parameters:
m    - number of parameters in the model
A(I) - i-th parameter in the estimated probability density function(pdf)
f(0) - 1/u = value of pdf at zero for line transects
u    - W*p = ESW, effective detection area for line transects
h(0) - 2*PI/v
v    - PI*W*W*p, is the effective detection area for point transects
p    - probability of observing an object in defined area
ESW  - for line transects, effective strip width = W*p
EDR  - for point transects, effective detection radius  = W*sqrt(p)
DS   - estimate of density of clusters
E(S) - estimate of expected value of cluster size
D    - estimate of density of animals
N    - estimate of number of animals in specified area
```

Figure 7. Options listing for first *ESTIMATE* procedure of example 1.

EXAMPLES

Each of the above sections of output is labelled at the top with a sub-title which is outlined with asterisks. Most of the output is also labelled with a block of text below the sub-title which identifies the data subset being analyzed. Text in the identification block will vary depending on the level (Stratum, Sample, All) at which parameters are estimated and the analysis options. Full identification text includes:

Stratum: Stratum Label/Number
Sample: Sample Label
Effort: Amount of effort
samples: Number of replicate lines/points
Width: Right truncation value
Left: Left truncation value
observations: Number of observations

If the analysis is pooled over all of the data neither the stratum nor sample labels are given. If the analysis is by stratum, the stratum label is given and if by sample, both the stratum and sample labels are given. The effort, # of samples and # of observations are the quantities for the particular data subset being analyzed. The number of observations depends on the right (width) and left truncation values. The label for left truncation is only given if it is non-zero. The right truncation value for the expected cluster size estimation can differ from the value used throughout the remainder of the analysis with a resulting difference in the number of observations. In Figure 8, the identifier text does not contain stratum/sample labels because the analysis is for all of the data combined. The total effort (line length) is 48 for the 12 samples (lines) combined. The analysis width is set at 19m and the resulting number of observations is 99 (6 distances are greater than 19m). If the results are specific to a particular detection model (e.g., detection probability, size-bias regression), a model label, which identifies the key and adjustment functions, follows the identifier block (Figure 9). For some pages of output, in particular plots, the page is not labelled with an identifier block. The identifier from previous pages should be considered to extend until a new identifier is given.

Analysis of detection probability is the most detailed aspect of the output and deserves an in-depth description. We will use the results from the uniform+cosine model as an example. Figure 8 displays the results of fitting a sequence of models with term selection mode, *SELECTION=SEQUENTIAL*, to the data from example 1. The first model is the key function with no adjustments. Each succeeding model adds another adjustment term and compares the test criterion to the previous model. The order of the cosine term refers to the value *i* in:

$$\cos\left(\frac{i\pi x}{w}\right) \quad .$$

For polynomial adjustment functions, order represents the exponent of the polynomial. Estimated models 1-3 for the uniform+cosine in this example are:

$$f_1(x) = \frac{1}{w}$$

$$f_2(x) = \frac{1}{w}\left(1 + 0.665098\cos\left(\frac{\pi x}{w}\right)\right) \quad .$$

$$f_3(x) = \frac{1}{w}\left(1 + 0.637621\cos\left(\frac{\pi x}{w}\right) - 0.079247\cos\left(\frac{2\pi x}{w}\right)\right)$$

```
                    ***********************************
                    *  Probability Function Estimation *
                    *     Model Selection/Fitting      *
                    ***********************************


Effort        :    48.00000
# samples     :    12
Width         :    19.00000
# observations:    99


Model  1
   Uniform key, k(y) = 1/W
      Results:
      Convergence was achieved with    1 function evaluations.
      Final Ln(likelihood) value =     -291.49946
      Akaike information criterion =      582.99890
      Final parameter values:


Model  2
   Uniform key, k(y) = 1/W
   Cosine adjustments of order(s) :  1
      Results:
      Convergence was achieved with    7 function evaluations.
      Final Ln(likelihood) value =     -280.48949
      Akaike information criterion =      562.97890
      Final parameter values:      .665098

   Likelihood ratio test between models  1 and  2
      Likelihood ratio test value    =    22.0199
      Probability of a greater value =    .000003
*** Model  2 selected over model  1 based on likelihood ratio test


Model  3
   Uniform key, k(y) = 1/W
   Cosine adjustments of order(s) :  1, 2
      Results:
      Convergence was achieved with   19 function evaluations.
      Final Ln(likelihood) value =     -280.30672
      Akaike information criterion =      564.61350
      Final parameter values:      .637621    -.079247

   Likelihood ratio test between models  2 and  3
      Likelihood ratio test value    =      .3655
      Probability of a greater value =    .545446
*** Model  2 selected over model  3 based on likelihood ratio test
```

Figure 8. Model selection/fitting output from uniform + cosine model of example 1.

For each model, the results include: 1) number of "iterations" (actually likelihood function evaluations) needed to find the maximum of the likelihood function (note: each iteration can be printed), 2) the final ln-likelihood value, 3) value of Akaike's Information Criterion (AIC) = -2*ln-likelihood + 2m, where m is the number of parameters (includes key function parameters and 1 parameter for each adjustment term), 4) final parameter values A(i),i=1,...,m, with the first parameters being for the key function and the remainder for the adjustment terms, in order, 5) a likelihood ratio test between the current model and the base model, and 6) a statement describing which model is best, based on the chosen decision criterion. The criterion for model choice is either minimizing AIC or a likelihood ratio test which compares the computed probability to the specified significance level (*PVALUE* in *OPTIONS>*). In this example, using a likelihood ratio test, Model 2 is judged significantly better than Model 1 (P=0.000003), but Model 3 is not significantly better than Model 2 (P=0.545446). Thus, a 1-term cosine model is chosen as the best fit for a uniform + cosine detection model. Model 2 would also be chosen if AIC was the criterion because the AIC increased from 562.9789 for Model 2 to 564.6135 for Model 3. If the significance level for the likelihood ratio test is 0.15, the likelihood ratio and AIC criterion will almost always choose the same model for sequential model fitting. The other adjustment term selection modes (*SELECTION = FORWARD* and *=ALL*) produce similar output but consider a larger

set of models rather than just adding terms sequentially; however, only rarely does the chosen model disagree with the model chosen by sequential fitting.

Model fitting and selection output is not generated if either *PRINT = RESULTS;* is set in *OPTIONS>* or *FXFIT* is included in the *NO* list of the *PRINT* command within *ESTIMATE>*. If you are unfamiliar with the analysis techniques, do not restrict the output because it includes messages about any problems encountered fitting a particular model. In particular, a message that parameters are reaching an upper or lower bound suggests that you have requested an unreasonable fit and may need to truncate the data. Also, messages are given if parameters are being constrained for monotonicity or to maintain a non-negative function. These are less important warnings but may suggest that you are overfitting the function (adding too many adjustment terms) and need to truncate the data. However, in some situations the constraints are reasonable, given the shape of the data.

```
                    ************************************
                    *  Probability Function Estimation *
                    *      Parameter Estimates         *
                    ************************************


Effort        :    48.00000
# samples     :    12
Width         :    19.00000
# observations:    99

Model
   Uniform key, k(y) = 1/W
   Cosine adjustments of order(s) :  1


            Point        Standard    Percent Coef.        95 Percent
 Parameter  Estimate       Error      of Variation     Confidence Interval
 ---------  -----------  -----------  --------------  ----------------------
   A( 1)      .6651        .1198          18.01
   f(0)      .87637E-01   .63049E-02       7.19       .75999E-01   .10106
 ---------  -----------  -----------  --------------  ----------------------
```

Figure 9. Estimates of model coefficients and f(0) for uniform + cosine model of example 1.

Following model selection and fitting, a table of parameter estimates (Figure 9) is given which includes: 1) estimated coefficients (parameters) for the key and adjustment functions, 2) either $f(0)$ for line transects or $\hat{h}(0)$ for point transects, and 3) sampling correlation of the estimated coefficients, if $m>1$.

The next 2 pages of the output display the shape of the detection function and how well the chosen model fits the data. The plot of the detection probability function (Figure 10) displays a histogram of the distance data (***) and the function values (fff). The y-axis is the probability of detecting an object (cluster or single) at a given distance from the line or point, given it is at that distance. For this example (Figure 10), at 19m it is estimated that only 20% of the clusters are detected. A histogram is another way of representing the distribution of the data and gross deviations between the 2 shapes may indicate the model poorly fits the data or numerical problems were encountered in fitting the model. A chi-square test of the model fit is given following the plot (Figure 11). For this example, P=0.85272, which suggests the fit is adequate. If P is much less than 0.05 a closer look should be given to deviations between the histogram and estimated function. Although, test rejection does not preclude using the model, it does suggest

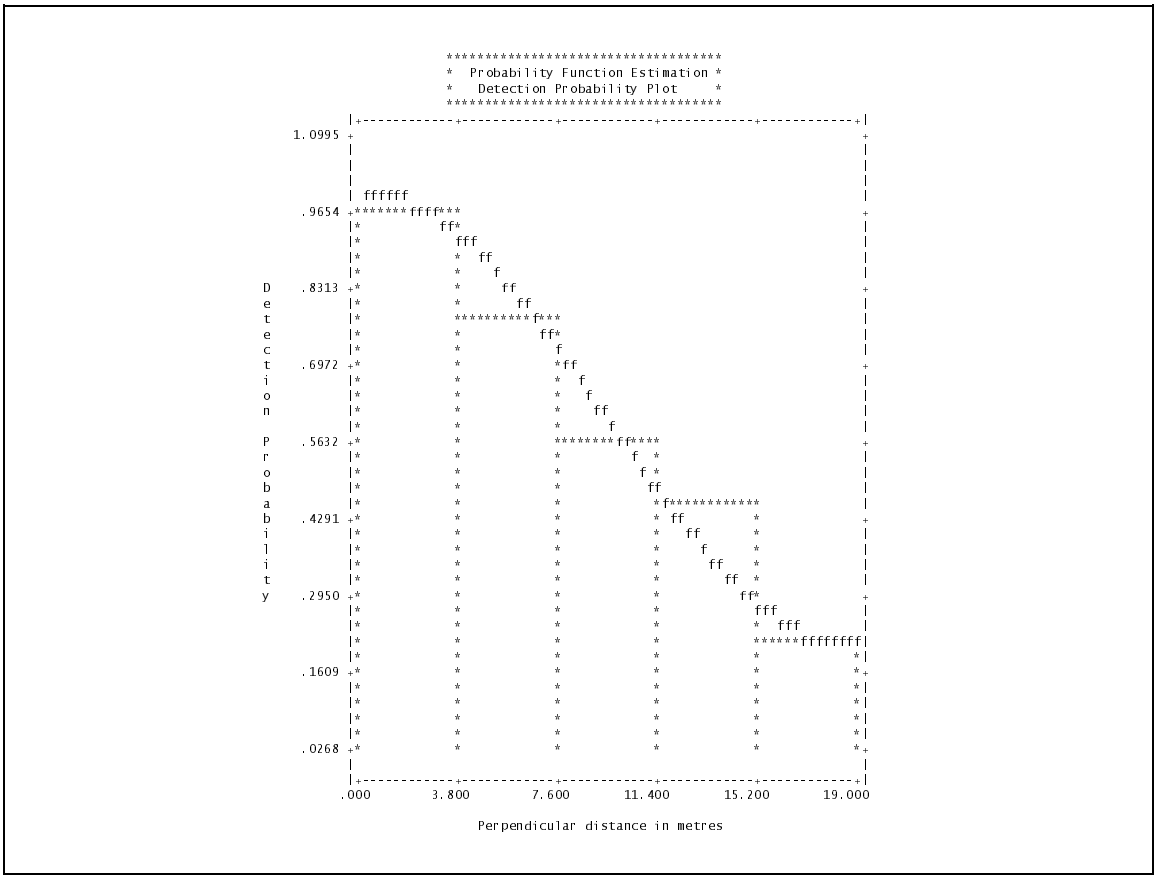


Figure 10. Detection probability plot for uniform + cosine model of example 1.

```
              ************************************
              *  Probability Function Estimation *
              * Chi-Square Goodness of Fit Test  *
              ************************************

 Cell           Cut           Observed   Expected  Chi-square
  i            Points          Values     Values     Values
-----------------------------------------------------------------
  1      .000        3.80        32.0       32.12         .000
  2      3.80        7.60        26.0       27.41         .073
  3      7.60        11.4        19.0       19.80         .032
  4      11.4        15.2        15.0       12.19         .650
  5      15.2        19.0         7.0        7.48         .031
-----------------------------------------------------------------
Total Chi-square value =      .7864  Degrees of Freedom =   3

Probability of a greater chi-square value = .85272


The program has limited capability for pooling.  The user should
judge the necessity for pooling and if necessary, do pooling by
hand.
```

Figure 11. Chi-square goodness-of-fit test for uniform + cosine model of example 1.

further models should be examined, or that problems in data collection may exist, such as heaping. The intervals used for constructing the histogram and chi-square test are determined by the GOF command which for this example was set with 5 equal intervals. If the data are ungrouped (exact) and a *GOF* command is not given, 3 default sets of intervals are used with a plot and chi-square test for each. If the distance data are grouped (intervals), the intervals used for analysis are used for the plot and test.

For the first *ESTIMATE* procedure of this example, estimation output is generated for each of the four detection models specified. If *PICK=NONE;* was not specified the model selection/fitting (Figure 8) would be repeated for each estimation followed by a description of the choice of the "best" model which minimized the AIC. Figures 9-11 would be given for the best model only. If more than one detection model is specified and a best model is not chosen, the estimation results for each are given in a summary table (Figure 12). The AIC values in Figure 12 correspond to the ungrouped, truncated (w=19m) results in Table 4.1 of Buckland et al. (1993). The half-normal + Hermite model has the smallest AIC value; although, the values for the first 3 models are all very close.

```
                          ******************************
                          *     Estimation Summary     *
                          *    Detection probability   *
                          ******************************

Pooled Estimates:
                         Estimate      %CV     df     95% Confidence Interval
                        ----------------------------------------------------------
Uniform/Cosine
                m        1.0000
                AIC      562.98
                Chi-p    .85272
                f(0)     .87637E-01    7.19    98     .75999E-01   .10106
                p        .60057        7.19    98     .52081       .69253
                ESW      11.411        7.19    98     9.8954       13.158
Uniform/Polynomial
                m        1.0000
                AIC      563.29
                Chi-p    .83365
                f(0)     .76560E-01    4.44    98     .70108E-01   .83607E-01
                p        .68745        4.44    98     .62951       .75072
                ESW      13.062        4.44    98     11.961       14.264
Half-normal/Hermite
                m        1.0000
                AIC      562.60
                Chi-p    .93093
                f(0)     .85632E-01    8.88    98     .71837E-01   .10208
                p        .61462        8.88    98     .51561       .73265
                ESW      11.678        8.88    98     9.7965       13.920
Hazard/Cosine
                m        2.0000
                AIC      565.22
                Chi-p    .60223
                f(0)     .81677E-01   11.77    97     .64724E-01   .10307
                p        .64438       11.77    97     .51063       .81318
                ESW      12.243       11.77    97     9.7019       15.450
```

Figure 12. Summary of estimation result for each model in example 1.

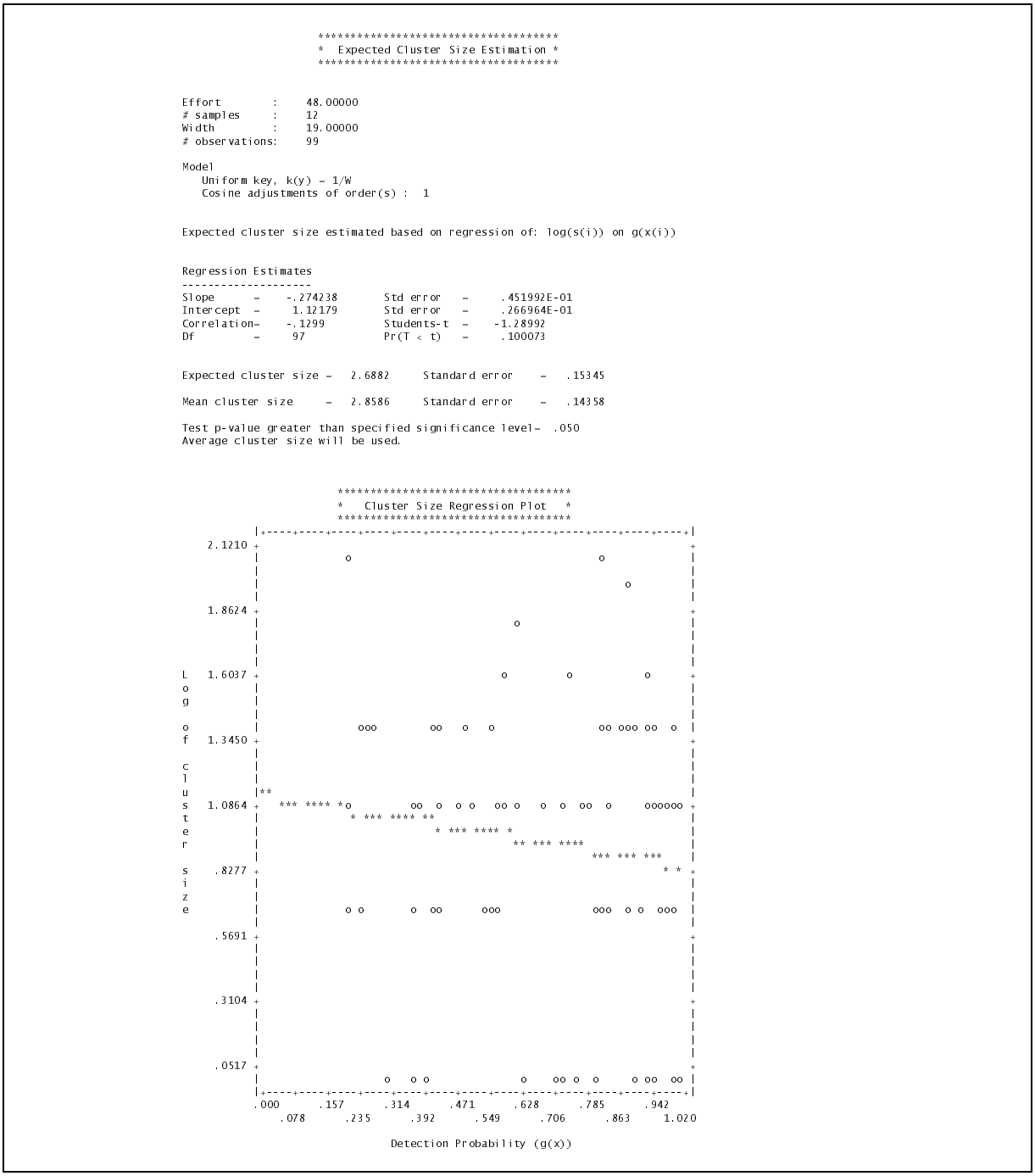


Figure 13. Expected cluster size estimation for example 1 with the uniform+cosine model.

EXAMPLES

The output for expected cluster size estimation depends on whether size-bias is considered. If the estimator is the mean cluster size, the output consists of the mean and its standard error. However, if a size-bias regression is performed, regression summary statistics and an estimate of expected cluster size and its standard error are given and followed by a plot of the regression line and observed values. If a significance test is performed the results of the test are explained. For this example (Figure 13), the slope is not significantly different from zero and the expected cluster size is estimated by the average cluster size. A one-sided t-test is performed because size-bias will typically increase the observed average cluster size at larger detection distances. If the size-bias regression uses distance as the independent variable the resulting slope will be positive, and if $\hat{g}(x)$ is used, a negative slope will result. Typically, if the test is non-significant, there is little difference between the average cluster size and size-bias estimate of expected cluster size. If there is not a significant size-bias, the average cluster size will be more precise.

Density estimation results are summarized in a table (Figure 14) which provides estimates, standard errors and confidence intervals for detection probability and related quantities ($f(0)$, P_w, ESW for line transects or $h(0)$, P_w, EDR for point transects) encounter rate (n/L for line transects, n/K for point transects, or n/T for cue counting), expected cluster size

```
                    ************************************
                    *      Density Estimation          *
                    *           Results                *
                    ************************************


Effort        :    48.00000
# samples     :    12
Width         :    19.00000
# observations:    99

Model  1
   Uniform key, k(y) = 1/W
   Cosine adjustments of order(s) : 1


             Point        Standard    Percent Coef.        95 Percent
 Parameter   Estimate       Error      of Variation     Confidence Interval
 ---------  ----------  ----------  --------------  ----------------------
   f(0)      .87637E-01   .63049E-02       7.19       .75999E-01   .10106
   p         .60057       .43207E-01       7.19       .52081       .69253
   ESW       11.411       .82093           7.19       9.8954       13.158
   n/L       2.0625       .29152          14.13       1.5134       2.8108
   DS        90.375       14.334          15.86       64.806       126.03
   E(S)      2.8586       .14358           5.02       2.5877       3.1578
   D         258.35       42.979          16.64       183.21       364.30
   N         25835.       4298.0          16.64       18321.       36430.
 ---------  ----------  ----------  --------------  ----------------------

Measurement Units
---------------------------------
Density: Numbers/sq. kilometres
    ESW: metres

Component Percentages of Var(D)
-------------------------------
 Detection probability  :  18.7
 Encounter rate         :  72.2
 Cluster size           :   9.1
```

Figure 14. Density estimation results for uniform + cosine model with data from example 1.

and density of clusters (groups), if *Object=Cluster*, density (D), and abundance (N) if area size is specified. Measurement units for the estimated quantities are given. In addition, the variance of density is partitioned into its components to illustrate the relative importance of each component of density. For example, the percentage of var(D) attributable to *f(0)* in this example is computed as:

$$100\left(\frac{(\mathrm{CV(f(0))})^2}{(\mathrm{CV(D)})^2}\right) = 100\left(\frac{(0.0719)^2}{(0.1664)^2}\right) = 18.7$$

Encounter rate variance is typically the largest contributor to variance of density. These percent variance quantities can help guide future sampling design efforts.

Summary tables of encounter rate, detection probability, expected cluster size and density estimates comprise the final section of the output. Figure 12 is an example of the summary tables for detection probability. The summary tables give estimates by level (stratum/sample) and by detection model, if results for each model are requested. Summary tables are always created, even if *PRINT=SUMMARY;* or *PRINT/NO=ALL;* is specified. The analysis and output for the second estimate procedure of this example is similar to the first analysis. However, analysis is limited to estimating detection probability and expected cluster size for all of the data with a half-normal + Hermite detection model. Restricting analysis to detection probability is useful for fitting an initial model to determine a truncation point (w), such that $g(w)=t$ Werecommend t=0.15 for line transects and t=0.10 for point transects.

The third estimate procedure illustrates a stratified analysis in which density is estimated for each stratum, but $f(0)$ is estimated by pooling all of the data. This is useful if $f(0)$ cannot be estimated reliably for each stratum but estimates of density by stratum are needed. The output is limited to the summary tables which are given in Figure 15. A summary table is given for each component (encounter rate, detection probability, expected cluster size and density). Estimates are given by stratum for each component except $f(0)$ which was estimated by combining data from both strata. The final summary table provides pooled estimates of density and abundance.

Note: If you run Example1.inp which is described in Buckland *et al.* (1993), you may notice minor differences in some of the estimates. These differences result from a change in the way DISTANCE creates the constraints for monotonicity and positivity are created. In prior versions, the constraints were maintained at a grid of equally spaced points. On some occasions this allowed monotonicity to be violated close to the origin. This was changed to a grid which puts more points near the origin and fewer with increasing distance from the origin. This both improves the monotonicity constraint and provides a better fit. Notice that the likelihood is slightly larger with the current version than the output in the book. The differences are primarily with the untruncated cases which have a long tail that create problems in fitting.

```
                        *********************************
                        *     Estimation Summary        *
                        *      Encounter rates          *
                        *********************************

                        Estimate      %CV     df     95% Confidence Interval
                        ----------------------------------------------------------
Stratum: Stratum 1
                 n      39.000
                 k      6.0000
                 L      21.000
                 n/L    1.8571       19.97     5     1.1171       3.0876
Stratum: Stratum 2
                 n      60.000
                 k      6.0000
                 L      27.000
                 n/L    2.2222       20.81     5     1.3090       3.7726



                        *********************************
                        *     Estimation Summary        *
                        *    Detection probability      *
                        *********************************

Pooled Estimates:
                        Estimate      %CV     df     95% Confidence Interval
                        ----------------------------------------------------------
Half-normal/Hermite
                 m      1.0000
                 AIC    562.60
                 Chi-p  .93093
                 f(0)   .85632E-01    8.88    98     .71837E-01   .10208
                 p      .61462        8.88    98     .51561       .73265
                 ESW    11.678        8.88    98     9.7965       13.920



                        *********************************
                        *     Estimation Summary        *
                        *    Expected cluster size      *
                        *********************************

                        Estimate      %CV     df     95% Confidence Interval
                        ----------------------------------------------------------
Stratum: Stratum 1
Average cluster size
                 E(S)   3.2821       7.59    38     2.8155       3.8260
Stratum: Stratum 2
Average cluster size
                 E(S)   2.5833       6.39    59     2.2735       2.9354



                        *********************************
                        *     Estimation Summary        *
                        *      Density/Abundance        *
                        *********************************

                        Estimate      %CV     df     95% Confidence Interval
                        ----------------------------------------------------------
Stratum: Stratum 1
Half-normal/Hermite
                 DS     79.516       21.85     7     47.713       132.52
                 D      260.97       23.13     9     155.71       437.40
                 N      13049.       23.13     9     7786.0       21870.
Stratum: Stratum 2
Half-normal/Hermite
                 DS     95.147       22.62     7     56.099       161.38
                 D      245.80       23.51     8     143.99       419.60
                 N      12290.       23.51     8     7199.0       20980.



                        *********************************
                        *     Estimation Summary        *
                        *      Density/Abundance        *
                        *********************************

Pooled Estimates:
                        Estimate      %CV     df     95% Confidence Interval
                        ----------------------------------------------------------
                 DS     87.331       17.03    19     61.308       124.40
                 D      253.39       17.64    23     176.39       363.99
                 N      25339.       17.64    23     17639.       36399.
```

Figure 15. Summary tables generated from the third estimation procedure of example 1.

Example 2

Description

This example of point transect sampling is described in chapter 5 of Buckland et al. (1993). Thirty points (k=30) were sampled from an area with true density of 79.6 animals per hectare. Observations were of single animals and 144 animals were detected. Only 131 of the animals were detected within the chosen truncation point of 20m.

Input

The input file is named *EXAMPLE2.INP*. An abbreviated listing is given in Figure 16. The input file contains commands to: 1) assign filenames for the output and log, 2) specify options, 3) structure and input the data, and 4) perform 3 analyses.

```
ASSIGN OUTPUT=EXAMPLE2.OUT/REPLACE;
ASSIGN LOG=EXAMPLE2.LOG/REPLACE;
ASSIGN BOOT=EX2BOOT.DAT/REPLACE;
OPTIONS;
   TYPE=POINT;
   DIST=RADIAL /UNITS='meters';
   AREA /UNITS='hectares';
   BOOTSTRAPS=400;
   TITLE='Chapter 5 point transect example, pgs 142-158';
END;
DATA;
   SAMPLE/EFFORT=1;
      8.40;
   SAMPLE/EFFORT=1;
      13.79,20.96;
   .
   .
   .
   SAMPLE/EFFORT=1;
      9.55,13.31,10.05,10.55,0.61,14.40,4.89,5.58,1.65;
   SAMPLE/EFFORT=1;
      19.94,18.59;
END;
ESTIMATE;
   ESTIMATOR /KEY=HN /ADJ=HERMITE;
   ESTIMATOR /KEY=UNIF /ADJ=POLY;
   ESTIMATOR /KEY=UNIF;
   ESTIMATOR /KEY=HAZARD;
   DIST /WIDTH=20.0;
   GOF/NCLASS=5;
END;
ESTIMATE;
   ESTIMATOR /KEY=HN /ADJ=HERMITE;
   ESTIMATOR /KEY=UNIF /ADJ=POLY;
   ESTIMATOR /KEY=UNIF;
   ESTIMATOR /KEY=HAZARD;
   DIST/NCLASS=5 /WIDTH=20.0;
END;
ESTIMATE;
   ESTIMATOR /KEY=HN /ADJ=HERMITE;
   DIST /WIDTH=20.0;
   GOF/NCLASS=5;
   BOOTSTRAP;
END;
```

Figure 16. Abbreviated listing of input for example 2 (EXAMPLE2.INP).

The options specify that point transect sampling was used, distance is measured in meters and density is expressed in units of numbers per hectare. Also, the number of bootstrap samples is set at 400 and an appropriate title is given.

The *DATA* section of the input file has a *SAMPLE* for each of the 30 points. The effort for each point is 1. The radial distance for each observation is listed below the point from which it was detected. The data values are separated by commas but could also be separated by one or more spaces.

Three analyses are specified by the three *ESTIMATE* procedures. The first analysis specifies:
1) four different detection models from which DISTANCE will choose the best model,
2) distances are to be truncated at 20m, and
3) goodness-of-fit plots and tests are to use 5 equal intervals.
The second analysis is nearly identical, except that distances are grouped into 5 equal intervals, between 0-20m, for the analysis. The same intervals are used for the plot and goodness-of-fit test. The third analysis computes a bootstrap variance and confidence interval for density using a half-normal + Hermite detection model.

Output

As in the first example, each of the 4 models is fitted using the *SELECTION=SEQUENTIAL* term selection mode. The final model for each estimator is shown in Figure 17. DISTANCE chooses the half-normal (key function with no adjustments) as the best model, because it has the smallest AIC value. The AIC values from Figure 17 match the values in Table 5.1 of Buckland *et al.* (1993) and the half-normal + Hermite is shown to be the smallest. For the half-normal model, a parameter estimate table is given, followed by plots of the estimated detection function (*g(r)*) and the estimated probability density function (*f(r)*) for the radial distances (Figure 18). The density estimate is 70.822 animals/ha and the 95% confidence interval is (52.140, 96.199) (Figure 19). The estimated encounter rate (n/K) is 4.3667 (3.5585, 5.3583) animals per point transect. The data were generated with an expected encounter rate of 5. An estimate of abundance (N) is not given because an area size was not specified on a *STRATUM* command. The estimate of average detection probability (P_w) is 0.491.

```
                          ***********************************
                          *  Probability Function Estimation *
                          *     Model Selection/Fitting      *
                          ***********************************


 Effort       :    30.00000
 # samples    :    30
 Width        :    20.00000
 # observations:   131


    Half-normal key, k(y) = Exp(-y**2/(2*A(1)**2))
       Results:
       Convergence was achieved with   12 function evaluations.
       Final Ln(likelihood) value =     -381.15551
       Akaike information criterion =      764.31100
       Final parameter values:    11.027619
-------------------------------------------------------------------------
    Uniform key, k(y) = 1/W
    Simple polynomial adjustments of order(s) :  2
       Results:
       Convergence was achieved with   14 function evaluations.
       Final Ln(likelihood) value =     -381.23905
       Akaike information criterion =      764.47810
       Final parameter values:     -.856296
-------------------------------------------------------------------------
    Uniform key, k(y) = 1/W
    Cosine adjustments of order(s) :  1
       Results:
       Convergence was achieved with    8 function evaluations.
       Final Ln(likelihood) value =     -381.75331
       Akaike information criterion =      765.50670
       Final parameter values:      .618343
-------------------------------------------------------------------------
    Hazard Rate key, k(y) = 1 - Exp(-(y/A(1))**-A(2))
       Results:
       Convergence was achieved with   10 function evaluations.
       Final Ln(likelihood) value =     -381.60819
       Akaike information criterion =      767.21640
       Final parameter values:    11.803076    2.357346
-------------------------------------------------------------------------

 Model Selection
 ---------------
 Minimum AIC =    764.3110
 Estimator chosen based on minimum AIC:
 Model
    Half-normal key, k(y) = Exp(-y**2/(2*A(1)**2))
```

Figure 17. Excerpts from output of example 2 showing model selection for the first *ESTIMATE* procedure.

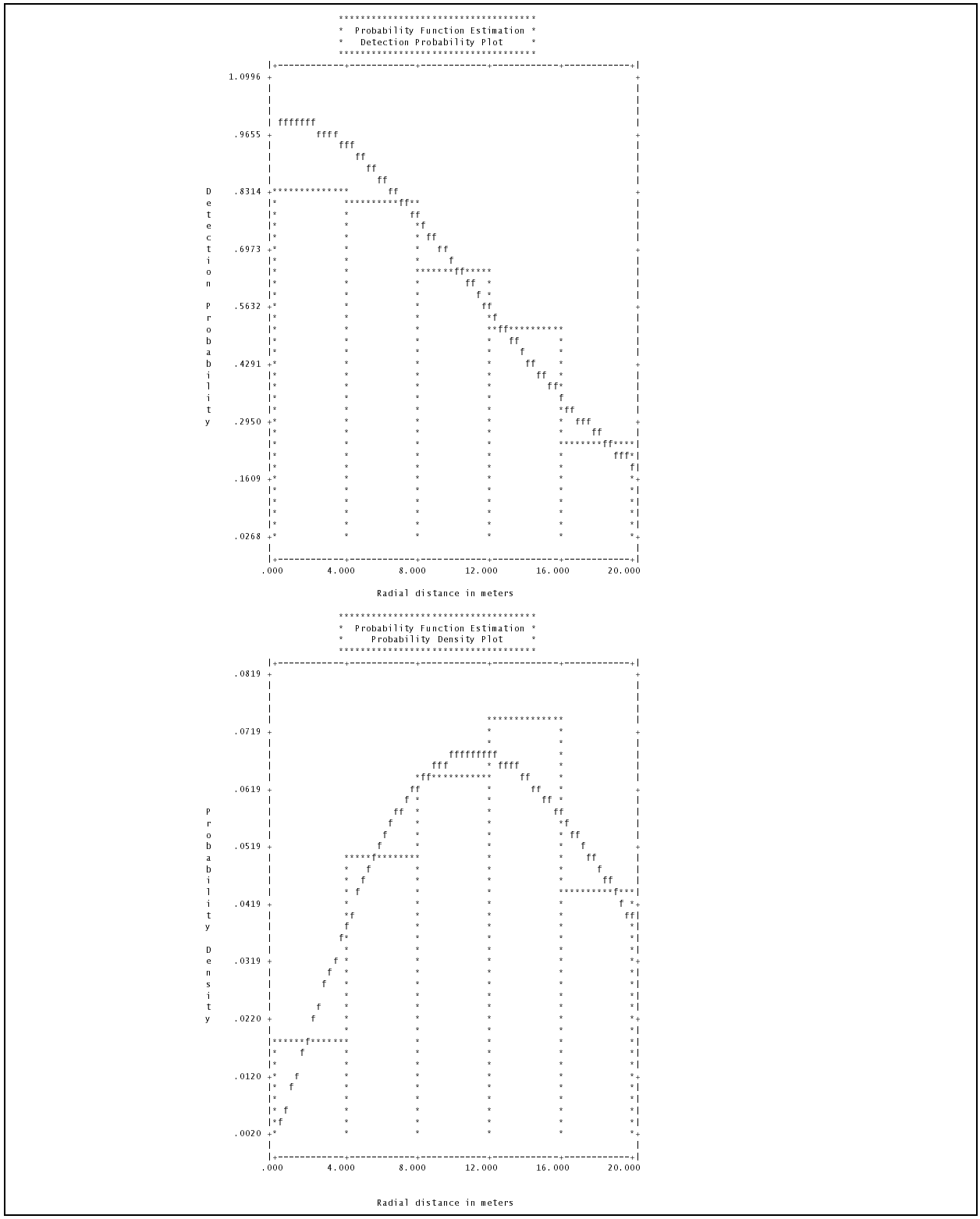


Figure 18. Plots of $\hat{g}(r)$ and $f(r)$ and matching histograms for the half-normal + Hermite model of example 2.

```
                    ************************************
                    *      Density Estimation          *
                    *           Results                *
                    ************************************


Effort        :    30.00000
# samples     :    30
Width         :    20.00000
# observations:   131

Model
   Half-normal key, k(y) = Exp(-y**2/(2*A(1)**2))


             Point        Standard    Percent Coef.        95 Percent
 Parameter   Estimate       Error     of Variation     Confidence Interval
 ---------  -----------  -----------  --------------  ----------------------
   h(0)      .10191E-01   .12334E-02      12.10       .80454E-02   .12908E-01
   p         .49065       .59385E-01      12.10       .38737       .62147
   EDR       14.009       .84780           6.05       12.444       15.772
   n/K       4.3667       .43808          10.03       3.5585       5.3583
   D         70.822       11.134          15.72       52.140       96.199
 ---------  -----------  -----------  --------------  ----------------------

Measurement Units
---------------------------------
Density: Numbers/hectares
    EDR: meters

Component Percentages of Var(D)
-------------------------------
 Detection probability  :  59.3
 Encounter rate         :  40.7
```

Figure 19. Density estimation results for ungrouped analysis with the half-normal + Hermite model of example 2.

The second analysis which groups the distances into intervals prior to analysis produces very similar results (Figure 20). The half-normal + Hermite model is also chosen and no Hermite adjustment terms are included. The model selection results from the output can be compared to Table 5.1 of Buckland *et al.* (1993). The estimate of density is slightly less at 69.059 animals/ha and the precision is comparable. In this case, grouping has no advantage and was only done as a demonstration. However, in many real situations distances are either recorded in intervals or may be heaped to convenient numbers and should often be analyzed as grouped data.

The third analysis restricts estimation to a half-normal + Hermite detection model and computes a bootstrap variance and confidence interval with 400 bootstrap samples (Figure 21). The default bootstrap re-samples with replacement from the samples (points in this example). In each bootstrap sample, the number of detections (n) and set of distances depends on the random selection of point transects. The analysis of each bootstrap sample includes selecting and fitting the model. In this case, only the half-normal + Hermite detection model was considered, but the number of Hermite adjustment terms was allowed to vary. The bootstrap model choice is not limited to the model chosen in the original analysis. If it were, the bootstrap and analytical variances would be very similar. However, it is the uncertainty in model selection which we want to capture with the bootstrap analysis. If several detection models were specified, full model selection would be performed for each bootstrap sample. The Bootstrap Summary (Figure 21) includes: 1) point estimate of density, 2) bootstrap estimate of the coefficient of variation (17.05%), which is:

$$\%CV = \left(\frac{SE_b(\hat{D})}{\hat{D}} \right) 100 ,$$

```
                    ************************************
                    *      Density Estimation          *
                    *           Results                *
                    ************************************


Effort        :    30.00000
# samples     :    30
Width         :    20.00000
# observations:   131

Model  1
   Half-normal key, k(y) = Exp(-y**2/(2*A(1)**2))


             Point        Standard    Percent Coef.        95 Percent
 Parameter   Estimate       Error      of Variation     Confidence Interval
 ---------  -----------  -----------  --------------  ----------------------
   h(0)      .99369E-02   .12351E-02       12.43       .77958E-02   .12666E-01
   p         .50317       .62540E-01       12.43       .39475       .64137
   EDR       14.187       .88165            6.21       12.561       16.023
   n/K       4.3667       .43808           10.03       3.5585       5.3583
   D         69.059       11.031           15.97       50.596       94.260
 ---------  -----------  -----------  --------------  ----------------------

Measurement Units
---------------------------------
Density: Numbers/hectares
    EDR: meters

Component Percentages of Var(D)
-------------------------------
 Detection probability  :  60.5
 Encounter rate         :  39.5
```

Figure 20. Density estimation results for grouped analysis with the half-normal + Hermite model of example 2.

where $SE_b(\hat{D})$ is the bootstrap estimate of standard error, 3) a 95% log-normal confidence interval (50.822, 98.692), which is constructed as defined in section 3.7.1 of Buckland *et al.* (1993), with the bootstrap standard error estimate,, and 4) a 95% bootstrap percentile confidence interval (49.346, 95.547), which is the lower and upper 2.5 percentiles). of the distribution of the estimates (Section 3.7.4 of Buckland et al (1993)). The first interval makes a parametric assumption about the shape of the distribution but uses a bootstrap constructed variance. A reasonable interval can be constructed with as few as 100-200 bootstrap samples. The second interval makes no assumptions about the distribution but requires many more samples (1000 is recommended) to obtain reliable estimates of the tail probabilities of the sampling distribution of $\hat{D}$. In this case, the bootstrap intervals are only slightly different than the analytical interval (52.140,96.199), which is constructed using an empirical variance for encounter rate and an analytical variance of $\hat{h}(0)$ (see Sections 3.7.1 - 3.7.2 of Buckland *et al.* (1993)).

```
                    ******************************
                    *      Bootstrap Summary     *
                    *      Density/Abundance     *
                    ******************************

Pooled Estimates:
                   Estimate      %CV      #     95% Confidence Interval
                   ------------------------------------------------------
Half-normal/Hermite
               D      70.822     17.05    400    50.822        98.692
                                                 49.346        95.547


Note: Confidence interval 1, uses bootstrap SE and log-normal with z=1.96.
      Interval 2, is the 2.5% , 97.5% quantiles of the bootstrap estimates.
```

Figure 21. Bootstrap analysis for half-normal + Hermite model of example 2.

Further Example Input Files

The following are a variety of example input files which illustrate various commands and data entry formats.

Line transect sampling with grouped perpendicular distances. The distances were measured in meters and line length was 1 kilometer, so the default units were accepted. Density will be in units of hectares. Note: text to the right of a semi-colon on a command line is treated as a comment.

```
options;
  title='Wildlife Monograph no. 72, pg 74';
  dist/int=0,1,2,3,4,5,7,9,11,15,20;
end;
; because there is only one sample
; varn=poisson assumption
data;
  sample/effort=1/label='Stake data';
    8,6,4,13,7,8,7,6,5,4;
end;
; with the first estimator the program will choose no. of terms
; with the second a 1-term cosine Fourier series  will be fit
estimate;
  est/key=unif;
  est/key=unif/nap=1/select=specify;
end;
```

The following is a line transect sampling example in which radial distance and angle were recorded instead of perpendicular distance:

```
options;
  title='Wildlife Monograph No. 72, Example page 65';
  dist=radial;
end;
; It was not necessary to line up the data like it is below but
; it does make it easier to account for all of the data.
; Each observation could have also been put on a separate line.
data;
  sample/effort=60.0 /label='Hemmingway data';
    100 46  150 10  200 17  150 38  200 55  200 25  200 55  250 39
    160 8   140 31  130 42  130 23  100 0   100 47  120 0   200 40
    200 55  170 25  250 7   230 18  180 57  120 35  180 30  190 20
    180 67  130 17  400 71  200 23   70 37  167 0   400 90  180 77
    250 7    80 26  150 35  260 7   200 90  300 65  150 10  100 50
    120 20  400 30  150 35  120 0   100 70  200 16  120 5   200 25
    120 0   300 15  130 0   150 40  370 0   100 40  200 70  250 0
    250 40  250 37  75  58  200 75  150 45  150 50  250 35  200 40
    300 55  360 20  360 20  200 50  250 35  100 20  150 40  300 60
    100 5
;
end;
estimate;
  est/key=unif;
  dist/width=400.0;
end;
```

In the following example (Burnham *et al.* 1980, Wildl. Monogr. 72), the data have been divided

in half for two strata and the density is obtained by stratum. These data were obtained from a simulated sampling plane on a 4x8 sheet of plywood so we have changed the units for area and specified the area size for each strata which is 16 sq. feet.

```
options;
  dist/measure=inches/width=24;
  length/measure=feet;
  area/units=square feet;
  title='Illustrative examples from Wildlife Monograph';
end;
data;
  stratum/label='Circle Survey D- area 1'/area=16;
    sample/effort=4/label='Line 1';
      .59 .04 .57 .84 1.48 1.48;
    sample/effort=4/label='Line 2';
      .92 .15 .98 .34 .26 .58 1.16 1.10 1.12;
    sample/effort=4/label='Line 3';
      .54 .94 1.00 .56 .26 .24 .48 1.64 .76 .54 1.41;
    sample/effort=4/label='Line 4';
      .48 .81 .14 .30 .22 1.74 1.34 1.10;
  stratum/label='Circle Survey D- area 2'/area=16;
    sample/effort=4/label='Line 5';
      .34 .4 .86 .44 .06 1.56 .3 .46 .96 1.26 .01 .42 1.42;
    sample/effort=4/label='Line 6';
      .64 .76 .42 .2 .78 1.46 1.10;
    sample/effort=4/label='Line 7';
      .06 .48 .02 .37 .18 1.32 .08 .80;
    sample/effort=4/label='Line 8';
      .36 .14 .24 .56 .26 1.32 1.42 .9 .26;
    sample/effort=4/label='Line 9';
      .4 .86 .74 .14 .36 .03;
    sample/effort=4/label='Line 10';
      .38 .48 1.36;
end;
est;
  est/key=unif;
  dist/int=0,.4,.8,1.2,1.6,2.;
  density by stratum;
end;
```

A cue-counting example in which distances were recorded in intervals:

```
options;
   type=cue;
   cuerate=34.98/se=4.74;
   selection=specify;
   dist=radial/int=0.0,0.2,0.3,0.4,0.6,0.8,1.0,1.5,2.0,3.0/units='nautical miles';
   area/units='naut. miles sq.';
end;
; Notice that the last two samples have no observations because they
; only contain a semi-colon on a separate line
data;
   sample/effort=114;
    4,4,8,29,42,72,132,111,172;
   sample/effort=50;
    ;
   sample/effort=24;
    ;
end;
; only the hazard key is fit with no adjustment terms
estimate;
```

```
   est/key=haz /nap=0;
end;
```

Line transect sampling in which the data are entered ungrouped but then grouped in the analysis. This is often useful to overcome heaping. In different estimate procedures, different intervals are used to determine its effect. If the data had been entered grouped this different grouping could only have been accomplished by re-entering the data. There are 10 different lines so the variance of n will be computed empirically, by default.

```
options;
  dist/measure=inches/units=meters/width=2;
  length/measure=feet/units=meters;
  area/units=square meters;
  title='Illustrative examples from Wildlife Monograph 72';
end;
data;
  sample/effort=4/label='Line 1';
    .59 .04 .57 .84 1.48 1.48;
  sample/effort=4/label='Line 2';
    .92 .15 .98 .34 .26 .58 1.16 1.10 1.12;
  sample/effort=4/label='Line 3';
    .54 .94 1.00 .56 .26 .24 .48 1.64 .76 .54 1.41;
  sample/effort=4/label='Line 4';
    .48 .81 .14 .30 .22 1.74 1.34 1.10;
  sample/effort=4/label='Line 5';
    .34 .4 .86 .44 .06 1.56 .3 .46 .96 1.26 .01 .42 1.42;
  sample/effort=4/label='Line 6';
    .64 .76 .42 .2 .78 1.46 1.10;
  sample/effort=4/label='Line 7';
    .06 .48 .02 .37 .18 1.32 .08 .80;
  sample/effort=4/label='Line 8';
    .36 .14 .24 .56 .26 1.32 1.42 .9 .26;
  sample/effort=4/label='Line 9';
    .4 .86 .74 .14 .36 .03;
  sample/effort=4/label='Line 10';
    .38 .48 1.36;
end;
estimate;
  est/key=unif;
  dist/int=0,.4,.8,1.2,1.6,2.;
end;
estimate;
  est/key=unif;
  dist/int=0,.2,.4,.6,.8,1.0,1.2,1.4,1.6,1.8,2.;
end;
```

EXAMPLES

Template Files

Template files with the extension *.TPL* and examples of the template files with the extension *.INP* are put into *YourDirectory* during installation. The template files contain the shell for a command and data entry input file that you can modify with an editor and then use as an input file. They illustrate the commands and data formats for line or point transects, perpendicular or radial, grouped or ungrouped, and clustered or unclustered data. The filenames have been constructed to represent the type of analysis. The first 2 characters are either *LT* or *PT* for line or point transect. The third character is either *R* or *P* for radial or perpendicular distance. The fourth character is *U* or *G*, for ungrouped (exact) or grouped (interval) distances. And the fifth character is either *U* or *C*, for unclustered or clustered. The files are:

LTPUU.TPL - line transect, perpendicular distances, Ungrouped, Unclustered
LTRUU.TPL - line transect, radial distances/angles, Ungrouped, Unclustered
LTPUC.TPL - line transect, perpendicular distances, Ungrouped, Clustered
LTRUC.TPL - line transect, radial distances/angles, Ungrouped, Clustered
LTPGU.TPL - line transect, perpendicular distances, Grouped, Unclustered
LTPGC.TPL - line transect, perpendicular distances, Grouped, Clustered

PTRUU.TPL - point transect, radial distance, Ungrouped, Unclustered
PTRUC.TPL - point transect, radial distance, Ungrouped, Clustered
PTRGU.TPL - point transect, radial distance, Grouped, Unclustered
PTRGC.TPL - point transect, radial distance, Grouped, Cluster

There is a corresponding input file for each template file which contains some dummy data entered as an illustration. Do not consider these input files as representative of the quantity or quality of the data for real situations.

The template file only illustrate a subset of the possible commands and values for switches. If you use the templates, make sure to change the measurement units, title etc. for your specific situation.