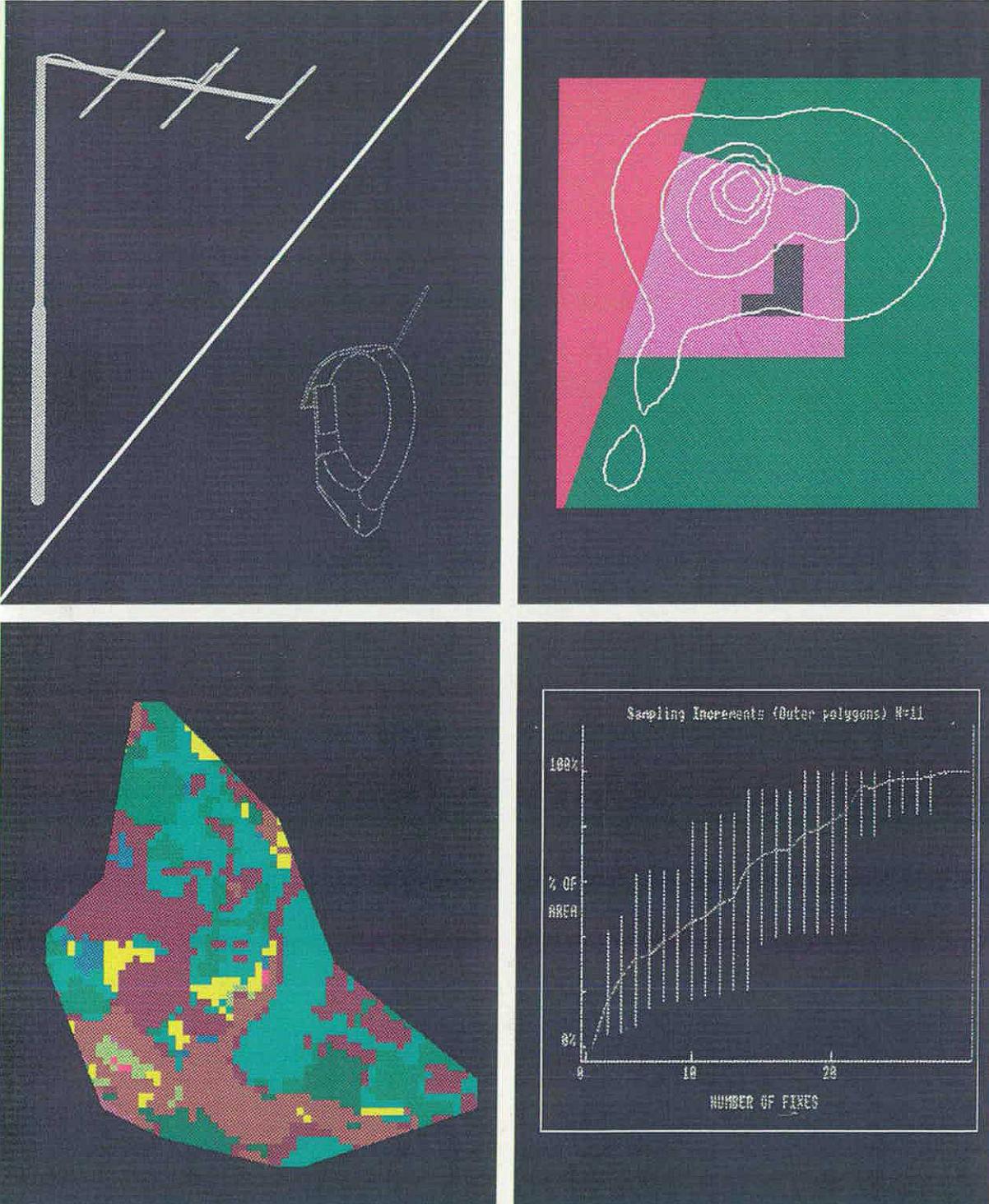


# RANGES V

## An analysis system for biological location data



*Sponsored by:*  
Norwegian Institute for Nature Research  
United States National Biological Service



INSTITUTE OF TERRESTRIAL ECOLOGY  
LIBRARY SERVICE

EDINBURGH LABORATORIES  
BUSH ESTATE, PENICUIK  
MIDLOTHIAN E26 0QB

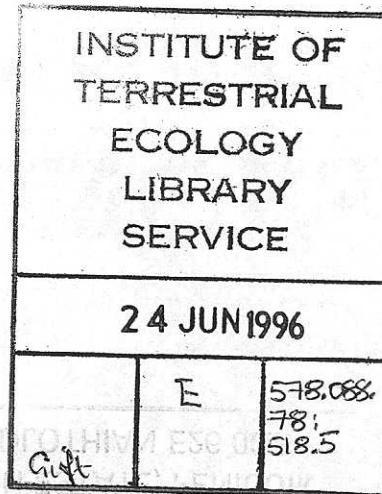
# RANGES V

An analysis system for biological location data

**R E Kenward and K H Hodder**

Institute of Terrestrial Ecology  
Furzebrook Research Station  
Wareham, Dorset  
BH20 5AS, UK

*Sponsored by:* Norwegian Institute for Nature Research  
United States National Biological Service



© NERC Copyright 1996

RANGES V Manual

ISBN: 1 870393 35 X

# CONTENTS

---

<b>1. Introduction</b>	1	C. Merging and splitting files and ranges	24
<b>2. Acknowledgements</b>	1	D. Viewing files	25
<b>3. Getting started</b>			
A. To get started	2	<b>6. Data analyses</b>	26
B. Understanding menu organisation in the programme	2	A. Range analyses	26
C. Understanding file and directory organisation in the programme	4	A.1 Introduction	26
D. Using the data handling and analyses routines	4	A.2 Range analyses menus	27
E. Practising with example files	4	A.3 Interfix measurements	29
<b>4. Installation and general information</b>	6	A.4 Convex polygons	31
A. Installing RANGES on the hard disc	6	A.5 Concave polygons	33
B. Loading and exiting, RANGES and selecting directories	6	A.6 Ellipses	35
C. Limitations to file size	6	A.7 Cluster analyses	35
D. MICROSOFT WINDOWS compatibility	6	A.8 Harmonic mean analyses	36
E. Conversion of RANGES IV files	7	A.9 Kernel analyses	40
F. Structure of RANGES V files	7	B. Utilisation and increment plots	41
G. Printing	7	C. Overlap analyses	44
<b>5. Data input, import and export</b>	9	C.1 To display plot overlap outlines	44
A. Data entry and editing	9	C.2 To make an overlap matrix	45
A.1 General points on the data entry and editing menu	9	C.3 To examine an overlap matrix	46
A.2 Starting new fix files	9	D. Interaction analyses	47
A.3 Editing fix files	14	D.1 Autocorrelations	47
A.4 Transforming fixfiles	14	D.2 Dynamic interactions	48
A.5 Inputting and editing outline maps	15	D.3 Fix-site distances	50
A.6 Inputting and editing habitat shapes	17	D.4 Range-centre spacing	51
A.7 Inputting and editing habitat points	19	E. Habitat analyses	52
A.8 Editing raster maps	19		
A.9 Viewing files	19	<b>7. Bibliography</b>	57
B. Import/export of files	19		
B.1 Importing ASCII text	20	<b>Appendix 1. Data file structure in RANGES V</b>	59
B.2 Exporting fix, map, habitat and range outline (edge) files as columns	22	<b>Appendix 2. Example files</b>	63
B.3 Import/export of DXF files (graphics)	22	<b>Appendix 3. Terms and conventions</b>	65
B.4 Import and export of raster maps	23		

---



## **1. INTRODUCTION**

---

RANGES IV was released in 1990, following development of RANGES I-III during the 1980s. In 1992, an agreement was reached with the Norwegian Institute for Nature Research (NINA) and with researchers from the US Fish and Wildlife Service (now National Biological Service) and Greenfalk consultancy, to cooperate in the development of an analysis system with many more facilities and greater ease of use. The result is RANGES V, which has become a user-friendly Geographic Information System for analysing biological location data. Although named for its origin in animal radio-tracking, its ability to quantify location and habitat layers has already been used to study plant biology.

Your purchase has helped to ensure the future of the RANGES suite, which must now pay for its own development. There are plans for upgrade features, and registered users will be notified as these become available. We have tried to get errors out of the routines, which have spent more than a year being tested. Unfortunately, it is impossible to predict behaviour of such a complex analysis system with all your data sets. If you find a bug, please let us know. We will if possible correct it, and provide a new version for you to test before it is generally distributed. Contact us by e-mail on REKE@wpo.nerc.ac.uk or KHH@wpo.nerc.ac.uk, or by fax on +44 1929 551087.

## **2. ACKNOWLEDGEMENTS**

---

Very many people have contributed to the development of RANGES V. In particular, support from Mark Fuller of the United States National Biological Service, and Torgeir Nygård of the Norwegian Institute for Nature Research was crucial for obtaining resources to continue development beyond RANGES IV, as was the support of John Goss-Custard, Ian Newton and Mike Roberts of the UK Institute of Terrestrial Ecology (ITE). Over the years, especially valuable suggestions for improvements have come from Nicholas Aebischer, Frank Ball, Rolf Brittas, Pete Brown, Miguel Capelo, John Cary, Brian Cresswell, Frank Doyle, Kevin Dunham, Kai Eliassen, Patricia Hall, Jonathon Hardcastle, Samuli Heikkinen, Manual Hinge, Ian Hill, Jessica Holm, Brett Hoover, Rolf Imms, Brian Kimsey, Herwig Leirs, John Linnell, John Marzluff, Mike McGrady, Grant Norbury, Murray Potter, Stephen Pugh, Pete Robertson, Sean Walls, Craig Weatherby, Thomas Weiss and Tomas Willebrand with essential advice on statistics from Ralph Clarke and on implementing kernel analyses from Bruce Worton. The raster map example files, a small part of ITE's UK landcover map prepared from Landsat data, was kindly made available by Robin Fuller and Sue Wallis; the squirrel data were collected by Brian Cresswell, the buzzard data by Sean Walls and the blackbird locations by Ben Kenward. Penny Ward and Karen Goodsite at ITE Merlewood prepared the manual for publication and set up the RANGES V demo on the ITE web site. Grateful thanks to all these contributors, and to many others who have helped by purchasing RANGES IV.

### 3. GETTING STARTED

There are so many facilities in RANGES V that it will take any user a long time to discover them all. We have therefore provided a routine for getting started (below) and two features to help you get acquainted with the programme. For explanations of terms and conventions used in the manual, see Appendix 3.

The first feature is a demonstration which shows RANGES V in action. Go to the [RANGESV] directory and either double-click on DEMO.EXE or type DEMO at the DOS prompt. The second feature is a Quickstart guide to using example files, on page 5.

#### A. TO GET STARTED

- ☛ Select the drive containing your RANGES V disc and go to the [RANGESV] directory.
- ☛ Double-click on R5.BAT or type R5 from the DOS prompt.
- ☛ Press a key (or wait 10 seconds) for the Main Menu (Figure 1) to replace the start-up page.

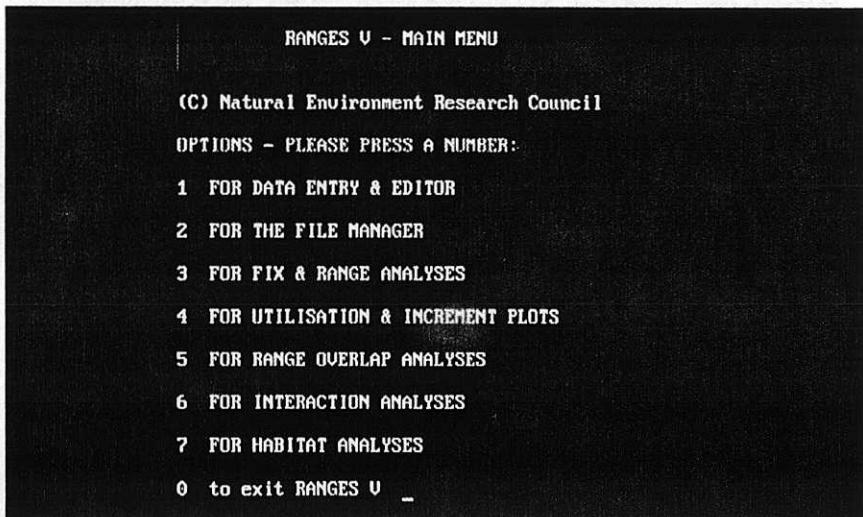


Figure 1. RANGES V Main Menu

- ☛ Choose suitable example files for each Main Menu option from the Quickstart table.

NB. If you need to change directory to find a file, you need to:  
1. press \ and then (the RETURN key),  
2. enter the full pathname for the directory, e.g.

**A:\RANGESV\BUZZARD**

The programme will run faster from your hard drive, so you may like to install first:

- ☛ type A:\INSTALL C \ to install to the root directory of drive C.

#### B. UNDERSTANDING MENU ORGANISATION IN THE PROGRAMME

RANGES V options are accessed by menus. A summary of the options is given in Figure 2, p. 3. The system is non-linear: it is possible to loop back to earlier stages in the routine to choose different options (e.g. analysis or print options, or a selection of ranges). Do this either by pressing the appropriate function key at the end of a run, or pressing ESCAPE and then a function key.

- In addition to the menus in which you choose a routine, most of the routines include a Run Specifications menu. When you complete a run, a function key command allows you to return to choose other run specifications for the same routine and file(s) selection. The options available in the RS menu depend on the routine, but will be similar to the example below:

P TO PRINT  
F TO FILE  
N NON-STOP RUN  
A ANALYSIS OPTIONS

Further details on the use of RS menus in RANGE ANALYSES are given on p. 27–28.

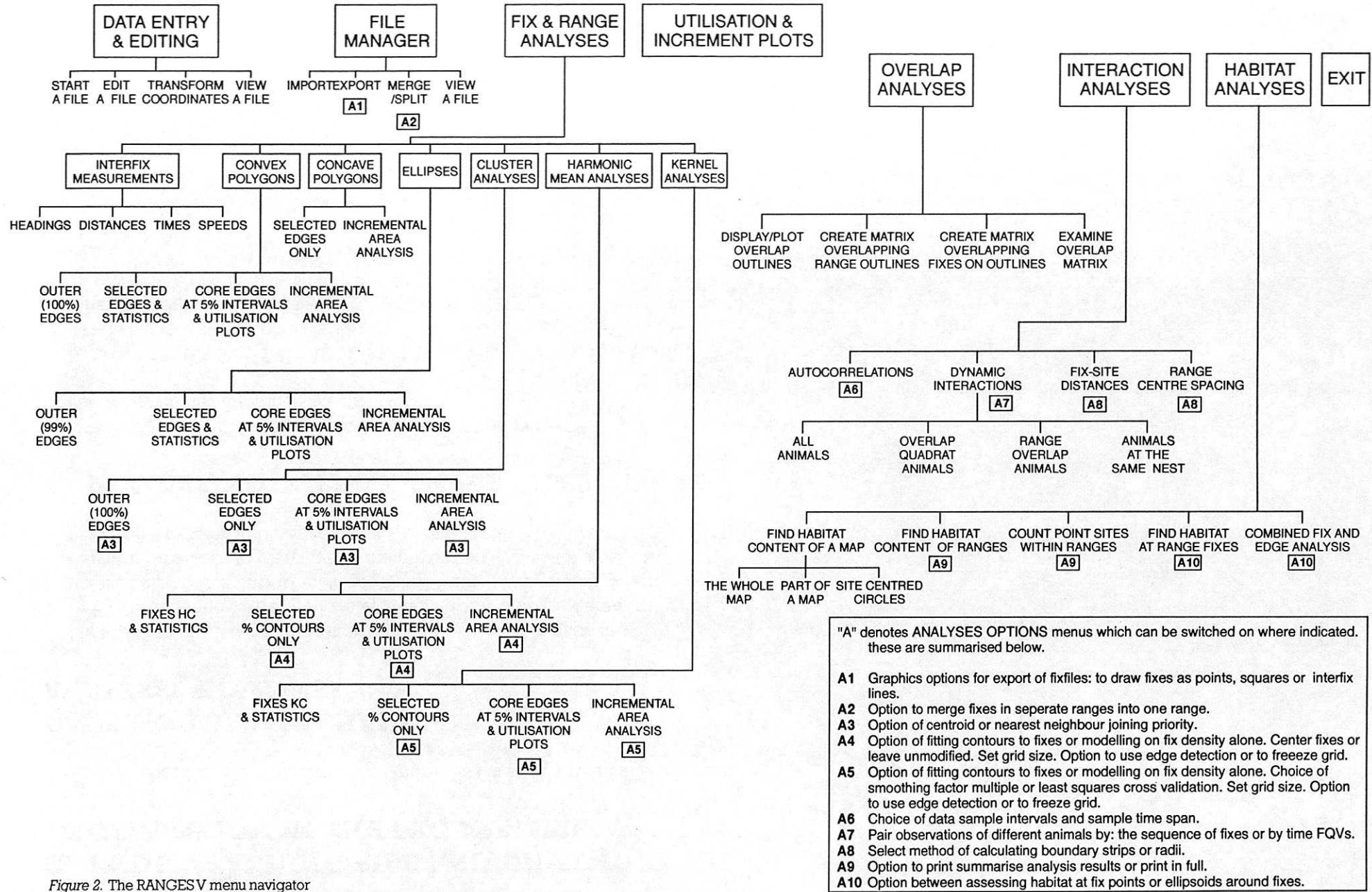


Figure 2. The RANGES V menu navigator

## **C. UNDERSTANDING FILE AND DIRECTORY ORGANISATION IN THE PROGRAMME**

Read sections C, E & F in Part 6. For more details see Appendix I.

## **D. USING THE DATA HANDLING AND ANALYSES ROUTINES**

First read through the information in the appropriate section in part 7 or 8 of the manual. The sections include step by step procedures where helpful. It is important to read the "Explanatory notes" where they are provided, to plan and interpret your analyses. It may be necessary to refer to other sections where directed.

## **E. PRACTISING WITH EXAMPLE FILES**

Use the Quickstart Guide (Table 1) on the next page to get a summary of files and analysis options.

Lists of example files and more detailed suggestions on analyses and interpretations are given in Appendix 2. The files include location data, map data and analysis output.

Table 1. Quickstart guide to example files

This guide gives a summary of the way in which the example files can be used. The necessary filenames and key presses are shown. The examples are linked with the main text, so that the output screens are given on the page numbers in the table. Note that you can use several different example files for each of the suggestions in the table below. For instance, for INTERFIX MEASUREMENTS you could use any of the fix files (BUZZARDS, BLA90FIX, B90FIX). A complete list of examples and further suggestions for their use are given in Appendix 2.

ANALYSIS NAME	MAIN MENU AND 2ND MENU CHOICE	EXAMPLE DIRECTORIES & FILE(S)	OTHER MENU CHOICES & KEY PRESSES	PP IN MANUAL
Interfix measurements - Distances	3 (0)	SQUIRREL\FIXFILE	1 Distances, 3 (number of fix-fix values), O to overlay plots ↴ ↴	
Convex polygons - Selected edges	3 (1)	SQUIRREL\FIXFILE	1 Selected edges and statistics, E to enlarge plots ↴, 25 ↴, 50 ↴, 75 ↴, 100 ↴ ↴, 1 Hc, ↴	
Concave polygons - Selected edges	3 (2)	SQUIRREL\FIXFILE	1 Selected edges and statistics, E to enlarge plots ↴ ↴ to set edge length	
Cluster analysis - Selected edges	3 (4)	SQUIRREL\FIXFILE	1 Selected edges and statistics, E to enlarge plots ↴, 25 ↴, 50 ↴, 75 ↴, 100 ↴ ↴	
Harmonic mean analysis - Selected edges	3 (5)	SQUIRREL\FIXFILE	1 Selected % contours, E to enlarge plots ↴, 25 ↴, 50 ↴, 75 ↴, 95 ↴ ↴	
Kernel Analysis - Selected edges	3 (6)	SQUIRREL\FIXFILE	0 Fixed kernels, E to enlarge plots, 25 ↴, 50 ↴, 75 ↴, 95 ↴ ↴	
Utilisation plot - Multi-range plot	4	SQUIRREL\UC	M means and limits ↴	
Incremental plot - Multi-range plot	4	BLAKBIRD\BLACKINC	M means and limits ↴	
Display overlap outlines	5 (0)	BLAKBIRD\BLA90CLU	E to enlarge plots ↴, 2 for solid line males & dotted females, ↴ ↴, then ↴ for each range	
Autocorrelation	6 (0)	BLACKFIX		
Interactions analysis - Fix site distances	6 (2)	BUZZARD\B90FIX & B90NEST	A Analysis options ↴, ↴, 500 ↴	
Interactions analysis - Range centre spacing	6 (3)	BUZZARD\B90EDGE	↳	
To find habitat content of a map	7 (0)	BUZZARD\RASTER	↳	
To find habitat content of ranges	7 (1)	BUZZARD\BUZZEDGE & RASTER	↳	
To find habitat around fixes	7 (2)	BUZZARD\BUZZARDS & RASTER	A for analysis options ↴, 1 for ellipse, ↴ for 50m ellipse, ↴ ↴	

## 4. INSTALLATION AND GENERAL INFORMATION

---

### A. INSTALLING RANGES ON THE HARD DISC

RANGESV is installed by typing `a:\INSTALL [drive][directory]`.

The programme can run in any directory. For instance, it can be installed to the root directory `C:\` or to `C:\[STATS]` by typing:

`a:\INSTALL C\` which gives the default drive `C:\` or `INSTALL C STATS`

If you type the directory name incorrectly e.g., `INSTALL D:\STATS` or `INSTALL D: STATS`, it will install in the default directory `C:\`

If the specified directory does not exist it will be created.

If you need to install from drive `B:\`, use `INSTALLB` or `INSTALLB D STATS`.

### B. LOADING AND EXITING RANGES, AND SELECTING DIRECTORIES

- When starting RANGES from the DOS prompt, you need to be in the `[RANGESV]` directory. Then type `R5`. If you have a very large dataset you can type `BIGR5` which runs a version of RANGES with extended memory (see section C). It is only advisable to use `BIGR5` if you require extended memory, as there is a processing speed reduction of 5-10%.
- The menu at the bottom of the first screen allows selection of both drive and directory. Defaults are `C:\`. So, if the RANGES V directory is not in `C:\` press `1` and give the correct location.
- If you change the data directory during a session, the new one is remembered. The settings are also retained between sessions and the current settings are indicated on the first screen.

- At the end of all runs or on pressing `ESC`, `F8` now provides an `EXIT` to the operating system for non-RANGES operations (e.g.. file renaming and copying). You can return to the routine you were using by typing `RE` at the command prompt or by double-clicking `RE.BAT` in Microsoft Windows (type `BIGRE` or double-click `BIGRE.BAT` if you need extended memory). Typing `R5` (or `BIGR5`) or double-clicking their batch files enters RANGES V via the start-up screen, as before.

### C. LIMITATIONS TO FILE SIZE

- In RANGES V the limit for fix files is now 6000 values (i.e. fixes and FQVs) for each range if you are starting a new file. This allows for 3000 fixes without FQVs or 500 fixes with 10 FQVs. You can add 1200 values to each range providing that the total does not exceed 6000. This is enough to add 100 fixes with 10 FQVs to the range with most fixes, during each editing session.

If you add more than 6000 values, an error message will direct you to save the file and start again, using `BIGR5` (see section B).

- For outline and habitat maps, the initial limit is 1000 coordinate pairs per shape; 500 more per shape can be added at a time using `BIGR5`.

### D. MICROSOFT WINDOWS COMPATABILITY

- RANGES works in a MICROSOFT window if you open a window with the MSDOS prompt, then go to the `R5` directory and type `R5`. Alternatively, you can use the Windows File Manager to click on `.BAT` files in the `RANGESV` directory (`R5`, `BIGR5`, `RE` or `BIGRE`, or `DEMO`).
- Processing stops if you iconize the window, but you can reduce it to use other packages while RANGES is running. However, processing

is faster when RANGES V is run from the DOS prompt after exit from Windows.

## E. CONVERSION OF RANGES IV FILES

Files from RANGES IV are converted automatically when imported to all RANGES V routines. If fixes have Fix Qualifying Variables (see p. 10), you are asked to name these. If they are time variables they need to have labels **DD**, **MO**, **YY**, **HH**, **MI** or combinations of these (e.g. **HHMI**, **DDMO** or **DDMOYY**) if they are to be read in further analyses. The time labels must be capital letters.

After conversion, the original file is renamed with the .BAK extension. Conversion will fail if a .BAK extension already exists for this file.

## F. STRUCTURE OF RANGES V FILES

Files are stored as text. They can therefore, be pulled directly into text editors if required.

The information required by RANGES V to run files is stored as an appendix. This includes details of the file type and labels (e.g. FQVs, habitat types, grid edge coordinates, scale, number of ranges and locations, etc.).

The value of variable 9 (the number of ranges or shapes in a file) in the appendix must always be *correct*. So, if the number of ranges or shapes are altered while using a text editor the value in the appendix *must* be changed to give the new value.

The value of variable 12 (the maximum number of coordinates in a range or shape) in the appendix must always be *equal to or greater than* the actual value in the file. So, if the number of coordinates are *increased* while using a text editor the value in the appendix *must* be increased.

- More details on file structure are provided in Appendix 1 on File Structure.

## G. PRINTING

You can print text from RANGES V by selecting **P TO PRINT** in the RS menu (see p. 2), or text and graphics by screen-dumping with the **SHIFT-PRINT SCREEN** key combination. Text and graphics (.DXF files) can also be exported to other packages (see section 5B); when hard copies of maps or diagrams are required for presentation, this is the best option.

Print operations selected from the RS Menu direct a stream of text (ASCII characters) to the printer, which must be configured correctly in order to print.

- All print operations are set by default for Epson-compatible dot-matrix printers (if you use another dot-matrix printer, make sure its DIP-switches are set correctly).
- The default screendump driver is set as **\DOS\GRAPHICS**, on the assumption that the root directory of the drive you are using for RANGES V has a DOS directory containing GRAPHICS.EXE or GRAPHICS.COM.
- For screen dumping from laser and bubble-jet printers, you need to use the **printer\_type** option with the **graphics** command:

e.g., **C:\DOS\GRAPHICS LASERJETII**

A start-up screen, which is given before the MAIN MENU if you press **1** (to alter setup), allows you to enter a suitable command for screen-dumping to your printer. This is then filed for future use. If you are using DOS 6 you can access a list of printer types supported by graphics.com by using MS-DOS HELP. (Type help at the DOS prompt

and then click on "graphics". Printer types supported by DOS 5 are given in table 2.

Plotter output is not supported in RANGES V. It is much easier and more versatile to export edge and map graphics as DXF files into graphics packages for enhancement and labelling for presentation.

Table 2. Printer types supported by GRAPHICS.COM in DOS 5

Printer type	Description
GRAPHICSWIDE	IBM Personal Graphics Printer, with an 11 inch wide carriage
HPDEFAULT	Any Hewlett-Packard PCC printer
DESKJET	Any Hewlett-Packard DeskJet printer
LASERJETII	Hewlett-Packard LaserJet series II printer
PAINTJET	Hewlett-Packard PaintJet printer
QUIETJET	Hewlett-Packard QuietJet printer
QUIETJET PLUS	Hewlett-Packard QuietJet Plus printer
RUGGEDWRITER	Hewlett-Packard RuggedWriter printer
RUGGEDWRITERWIDE	Hewlett-Packard RuggedWriter Wide printer
THINKJET	Hewlett-Packard ThinkJet printer

(Table adapted from Jamsa, 1991)

## 5. DATA INPUT, IMPORT AND EXPORT

---

### A. DATA ENTRY AND EDITING

Use Main Menu option 1

#### A.1 GENERAL POINTS ABOUT DATA ENTRY AND EDITING

The input and edit functions of RANGES V allow mistakes to be found easily and rectified. You can scroll up and down the rows of fixes using the cursor, HOME and END keys, and move between pages using the page keys. When you terminate data entry, for instance to correct an error, and press E to EDIT, the programme re-starts on the last fix entered. The programme remembers your current directory during and between sessions, and is also able to recognise file types (i.e. fix, map or habitat).

When you select Main Menu option 1 the following menu (fig. 3) will be displayed.

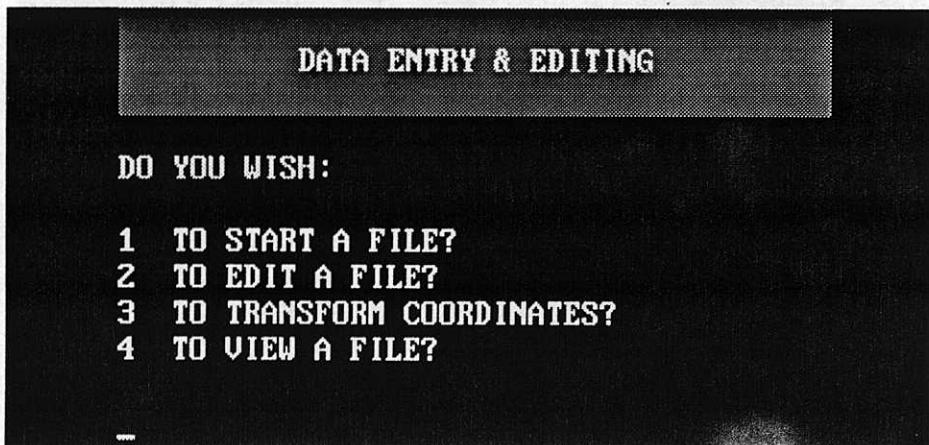


Figure 3. The DATA ENTRY AND EDITING MENU

A sub-menu offering a choice between file types (fixes, map, habitat shapes or habitat points) only appears if you select 1 TO START A NEW FILE.

- It is possible to edit files while working in options 1 or 2 in this menu.
- Most files will be saved automatically if **ESCAPE** is pressed while entering data. However, there is still some possibility of data loss, especially in map and habitat files, so we recommend that the **ESCAPE** key is avoided if you wish to save data. If a file has been saved successfully you just need to press **E** and select **E** to continue editing.

What happens if you press **ESCAPE** while editing data in option 1 TO START A NEW FILE?

When you selected the edit option you will have been asked to choose a new file name, or confirm use of the original name. If you chose to retain the old name, RANGES V will backup your data by keeping the original file intact and storing the modified file as SAVED!.BBC.

- RANGES V will protect your data by preventing you from writing over existing files accidentally. If you attempt to start a new file with a name which has already been used, a prompt will request a name for the edited data. Then if you continue, the existing file will be presented on screen in edit mode.

#### A.2 STARTING NEW FIX FILES

Use option 1 in DATA ENTRY AND EDITING (then option 1 in the sub-menu)

The first stage in this option involves setting up the file. Here you can set up labels for the identifying variables for each range (age, sex etc.), and the variables to associate with each fix (if required). Grid edge

coordinates for the area in which data can be viewed on the screen can also be set.

Next, the location data can be entered. When you enter this data, note that the coordinates of your fixes should be located on a continuous series from west to east and south to north (e.g.. W=0, E=100, and S=0, N=100). If your study area crosses a national grid boundary, e.g.. including positions 999 and 001, you should enter these coordinates as 999 and 1001 (or 99 and 101 if your study area is small). Sometimes locations outside the expected area may cause problems when adding data to a file or you may have imported a file with discontinuous values. Section 5.A.4 on TRANSFORMING files explains how to deal with this.

After saving the file, the scale and fix resolution can be set. The following text works through each stage of this process.

#### ***SETTING UP THE FILE***

To input data in a new file, choose to start a new file in DATA ENTRY & EDITING by pressing 1.

- ☛ A list of files will appear in the directory most recently specified and you are prompted to give a data filename; you have the option of changing the directory (by pressing \ ) at this point.

If files are nested in several sub-directories, such that their complete name is more than about 30 characters

e.g., C:\JONATHON\ANALYSES\BUZZARD\BUZZARD.BBC

a "bad name" error may be generated when creating new files.

Solutions are (a) to shorten the file name within the directory if the path is not too long, or (b) to shorten the path by using fewer sub-directories.

- ☛ After naming a data file, a second file list allows you to select a BACKGROUND MAP. This is useful for checking the accuracy of data during input and edit routines. (See section 5.A.5 & 6, for entry of map data).

- ☛ Select RANGE FIXES in the submenu.

- ☛ Two screens follow which explain how the fix files are organised.

- ***Range Variables***

On the second of these screens there is an explanation of the RANGE VARIABLES which identify each range by ID, AGE, SEX, the MONTH and YEAR when recording started, and 2 COORDINATES for FOCAL SITE (e.g. nest or roost).

All 7 RANGE VARIABLES are stored as numeric values (for sorting purposes). The AGE and SEX variables can be given one letter labels to identify animals on the screen. You will specify these later as you start entering data for each range, at this stage their numerical labels can be defined. RANGES V has default RANGE VARIABLE LABELS. These are as follows:

Age: 1=J, 2=Y, 3=A

Sex: 1=M, 2=F

- ☛ You can press ↲ to use these defaults or alternatively, choose your own labels.

Although AGE and SEX variables are always displayed on screen as letters, numbers may still be used to select ranges during analyses. For instance, the format 1-3 or J-A could be used to specify ranges with the AGE labels J, Y & A.

- ***Defining Fix Qualifying Variables***

You can enter labels for up to 50 FQVs. In most studies, it is very important to include these because of their potential in analyses. For

instance, with appropriate FQVs you could exclude all locations after dark or in a certain habitat type. The FQVs are easy to use because they can be labelled. RANGES V will prompt you with a list during editing and when they are required during analyses. The format required for FQV labels is displayed on the screen as you enter them. There are standard formats for time FQVs. It is important to use these, because the programme uses them to recognise time variables in some of the analyses. The standard formats are shown below:

**FOR TIME LABELS USE 2, 4 OR 6 LETTER COMBINATIONS  
OF: YY, MO, DD, HH, MI, SS (eg. DD, YYDD, HHMI, YYMODD, DDMOYY)**

**OTHER LABELS MUST HAVE 5 LETTERS (eg. ACTIV). DEFINE  
ACCURACY ELLIPSES BY: MARAD, MIRAD, THETA OR X-VAR, Y-VAR,  
COVAR.**

When entering the FQVs, RANGES V is case sensitive: *you must enter TIME or ELLIPSE FQV labels in upper case*.

- A useful tip. If time variables are entered as "combinations" in descending order, (eg. YYMODD or HHMI), you can use these in RANGE ANALYSES to select runs of fixes which cross period boundaries. Using single labels, it is difficult to select fixes between 15 December 1994 and 1 February 1995 while excluding fixes between 1-14 December 1994 and those in January 1994. However, combination labels make it easy to select fixes between 941215 and 950201.

Customised FQVs must have 5-letter labels. Please note that although FQV labels and their range of values are listed to help make selections during analyses, you still need to record (outside of RANGES) the numerical codes of these 5-letter labels (e.g. ACTIV, 1=resting, 2=feeding, 3=preening).

A new FQV function is the opportunity to include accuracy ellipses. Variables for these may be calculated, using software such as LOCATE II, if there are more than 2 bearings for each fix. The results

can be imported into RANGES V. It is important to select the correct labels in order for the programme to recognise these.

- **Defining the GRID EDGES**

After entering the FQVs and choosing whether or not to have GRID LINES displayed on the screen, you may choose to specify the GRID EDGE (corner) coordinates within which your fixes will fall.

Alternatively you can press  to use the default which is West=0, East=100, South=0, North =100. If you are using a background map, the outer coordinates from this will be used.

### **ENTERING THE DATA**

- **Entering range variables**

You are prompted for the range variables for the first range.

There are default variables for each range label. These are entered if you press  when prompted for the details for each range. These defaults are:

ID- sequence number, which increments by one for each consecutive range

AGE- ? (coded as 0)

SEX- ? (coded as 0)

MONTH- current

YEAR- current

FOCAL SITE COORD E. (missing, coded as -9)

FOCAL SITE COORD N. (missing, coded as -9)

- **Entering fix coordinates and FQVs**

Fix coordinates are entered at the prompt at the bottom left of the data entry screen (fig 4). First type in the EAST coordinate followed by . This value is then displayed as the beginning of the list of coordinates at the top left of the screen and the prompt for the NORTH coordinate appears. This is followed by prompts for any FQVs and the next locations. Fix coordinates and FQVs do not have to be integers.

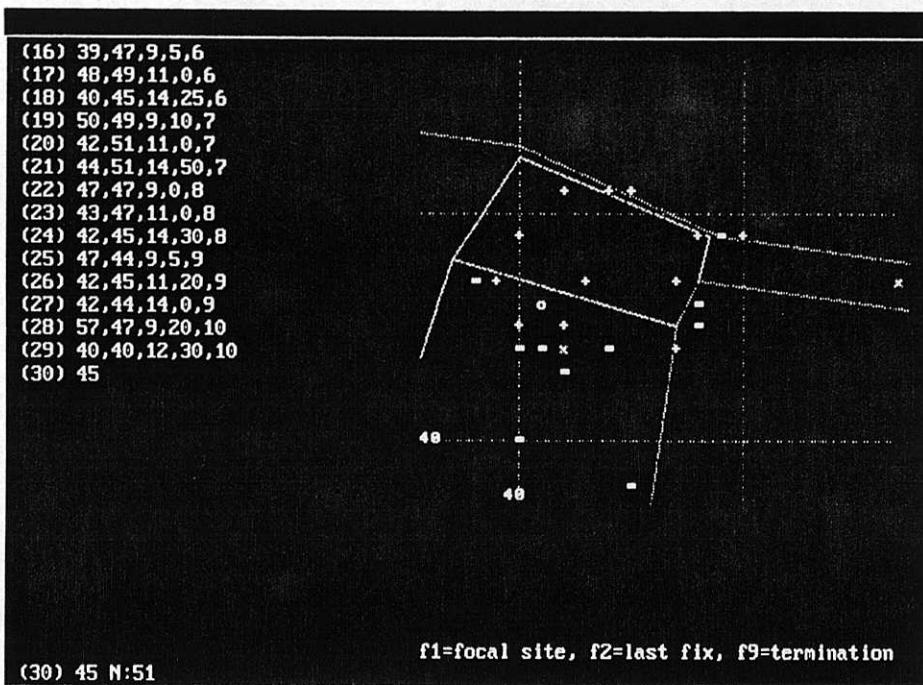


Figure 4. Data entry screen for fixes

Short cut keys are provided to speed data entry; these are listed on the data entry screen. F2 gives the previous coordinates, and is followed by F3 which gives the option of the last FQVs.

After terminating a range, details (eg. RANGE VARIABLES, FQV labels and ranges etc.) are shown at the top left of the screen. Below this there is a menu:

```
G TO TOGGLE GRID
R TO RESET LIMITS
X TO EXPAND RANGE
E TO EDIT FIXES
F TO FILE RANGE
O TO OMIT RANGE
```

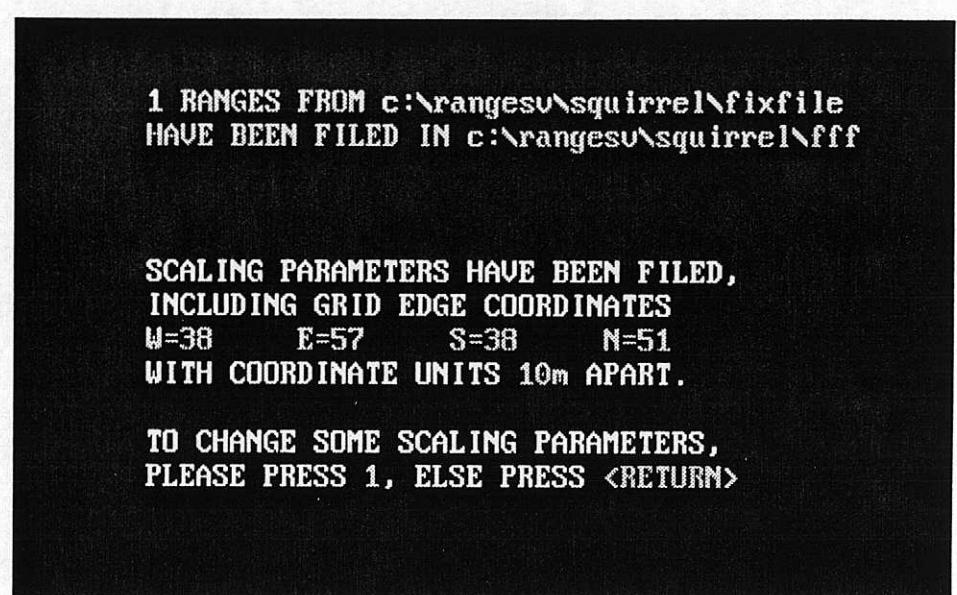


Figure 5. Summary screen displayed on completion of fix input

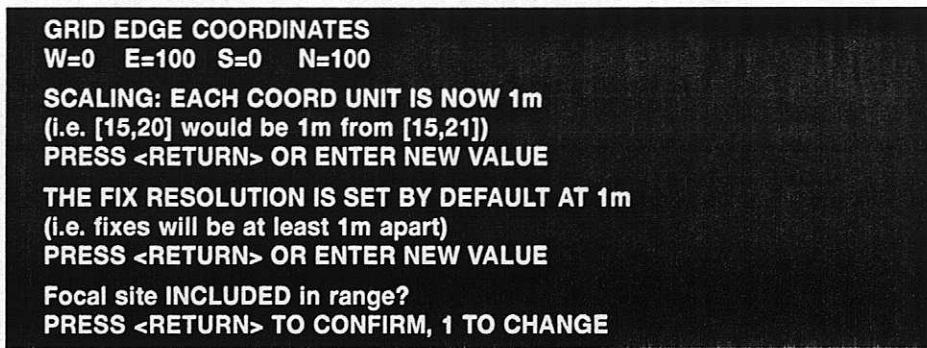
Choosing **R** allows you to alter the grid edge coordinates of your grid. **E** gives the opportunity to add more fixes or to correct mistakes. If you choose **F** the file is saved and you will be given the opportunity to edit (see below) or to add more ranges (append).

- **Summary screen**

After filing all your ranges, a summary of the file is given which shows the number of ranges, filename, grid edge coordinates and FQVs (fig.5)

Selecting a second screen gives the opportunity to change various parameters used in range analyses. This is where the *coordinate scaling* and *fix resolution* can be altered from the default 1.0 m. The grid edge coordinates can also be changed. The program won't allow you to enter impossible limits (e.g., W?0 E?0) or negative limits. You also have the option of choosing whether to include the

focal site as a fix during analyses. The default excludes the focal site. The screen looks like this:



- *Editing in option 1 of Main Menu 1 (see section F.3)*

You can edit in this option after filing a set of ranges. The following choice is given:



If you select **E**, the programme provides a file list and prompts for a new filename or **U** to overwrite the current filename. If use of the current name is confirmed, the edited version will only replace the existing file at completion of editing; if you press **ESCAPE** during editing, the new file will be listed as "SAVED!".

#### Explanatory note: fix resolution and scaling

The fix resolution will depend on the accuracy of your tracking. For instance, if you are tracking small animals from a few metres away this may be as small as 1m. However, you may record coordinates from a much greater distance such as 1km, in which case a fix resolution of 100m would usually be more appropriate.

Fix resolution is used to:

1. Set the width of the boundary strip which is included in polygon edges and areas. The boundary strip is half the value of the fix resolution e.g. 0.5m if the resolution is 1m. This means that a coordinate with a real position between 10.5 and 11.5, would be entered as 11.
2. Estimate the size of a grid cell plotted around single outlying fixes in concave polygon analyses, and multiple fixes at one site in cluster analyses. The width of the grid cell is equal to the fix resolution.
3. To define the truncation distance in one type of harmonic mean contouring. In this case, the allocation of an appropriate fix resolution can substantially affect range areas and statistics.

A coordinate scaling of 10m means that each coordinate unit (e.g. 8,8) is 10m from the next (e.g. 8,9). This scaling is often the same as fix resolution but in some circumstances is different. For example:

1. If you import data at a different scale to the accuracy of your locations
2. If you wish to suppress the boundary strip (by giving a fix resolution value of 0). This is useful if you need analysis results comparable with a system lacking boundary strip estimation.

## A.3 EDITING FIX FILES

Use option 2 of Main Menu 1

During editing in RANGES V you can move up and down the rows of fixes using the cursor keys, and move between pages using the HOME, END and page keys. On each page the selected fix is indicated on the coordinate grid by a red block, the 2 fixes before and after it by green crosses and the others in yellow.

After specifying required filenames in EDIT, the following RS menu allows you to choose whether to change anything.

```
N NO GRID LINES  
L CHANGE VARIABLE LABELS  
Q CHANGE FIX QUALIFIERS  
R SELECT RANGES  
<RETURN> TO CONTINUE
```

☛ Choose **L** to alter age and sex labels.

☛ If you select **Q** (to edit FQVs) the following screen is displayed:

```
c:\dir\myfix  
HAS 2 FIX QUALIFYING VARIABLES:  
1:DD 2:ACTIV  
  
FOR YOUR NEW FILE PRESS:  
0 TO DELETE/REPLACE THEM,  
<RETURN> TO KEEP/APPEND THEM,  
  
OR NUMBER THOSE REQUIRED IN ANY ORDER,  
WITH <RETURN> TO FINISH.
```

When you select one of these, the prompt describing the format required for FQV labels (see p. 10) is displayed. Choosing **0** deletes the current FQVs and their labels and gives the opportunity to replace them. Otherwise the labels of all current FQVs are listed and you can either change them or press ↵ to keep them. Then you can add further labels if you need to.

If you add labels to the file you are editing, the data entry screen will prompt you to enter the additional FQV values for each fix.

## A.4 TRANSFORMING FIXFILES (AND MAP AND HABITAT COORDINATES)

Use option 3 of Main Menu 1

If your coordinate scale does not form a continuous series from west to east and south to north, or if data imported to RANGES contains negative values, you should transform it using this option.

N.B. The programme will not change values -1 and -9 (which code for range termination and missing values respectively). These should be entered as slightly different values (e.g. -1.0001) or edited individually at the end of the transformation run.

- ☛ First you select a file to transform, and then name the output file.
- ☛ An RS menu then allows you to choose to change range variable labels FQVs or to select specific ranges if required.
- ☛ The next screen is an instruction screen which shows the W, E, S and N limits of the coordinates to be transformed. Here you can specify whether to transform all or some of your values (by selecting minimum and maximum values to be transformed). You then enter the required transformation.

Note that this must always start with a +, -, \* or / sign.

- ☛ Following the transformation, a summary screen is given. If you press **1** you can change the scale, fix resolution, grid corners, or inclusion of focal site. See p. 12.

### EXAMPLES

#### Problem 1

Data has been collected and stored in RANGES on a 0-99 coordinate system. Then a fix is recorded outside of the expected study area, too far west (see fig. 6). This would give a negative value which would not be accepted by analysis functions in RANGES.

### Solution 1

Enter the coordinate for this fix as 975, as if it were on a more southerly or westerly grid of 0-999.

Then use the TRANSFORM option to add 1000 to all the original values to give a new scale of 975-1099.

- *How to carry out this transformation*

The original scale was 0-99, so enter first 0, and then 99 for the minimum and maximum east coordinates to be transformed.

The program then asks you to specify the transformation for those coordinates. As the "too westerly" coordinate has been scaled 975, you need to add 1000 to all the original 0-99 values, so that your new coordinate series is 975-1099.

To do this, enter +1000.

The questions then repeat for the south-north coordinates. You don't need to transform these in this case. Press ↴ when the minimum values are requested, and then ↴ for the transformation. This causes all the coordinates, to be transformed by the default of \*1.

### Problem 2

Your study area crosses a national grid boundary, so that it includes positions 999 and 001.

### Solution 2

Enter the coordinates as 999 and 1001 (or 99 and 101 if your study area is small). Or transform the coordinates to the East of the boundary using +1000 as in example 1.

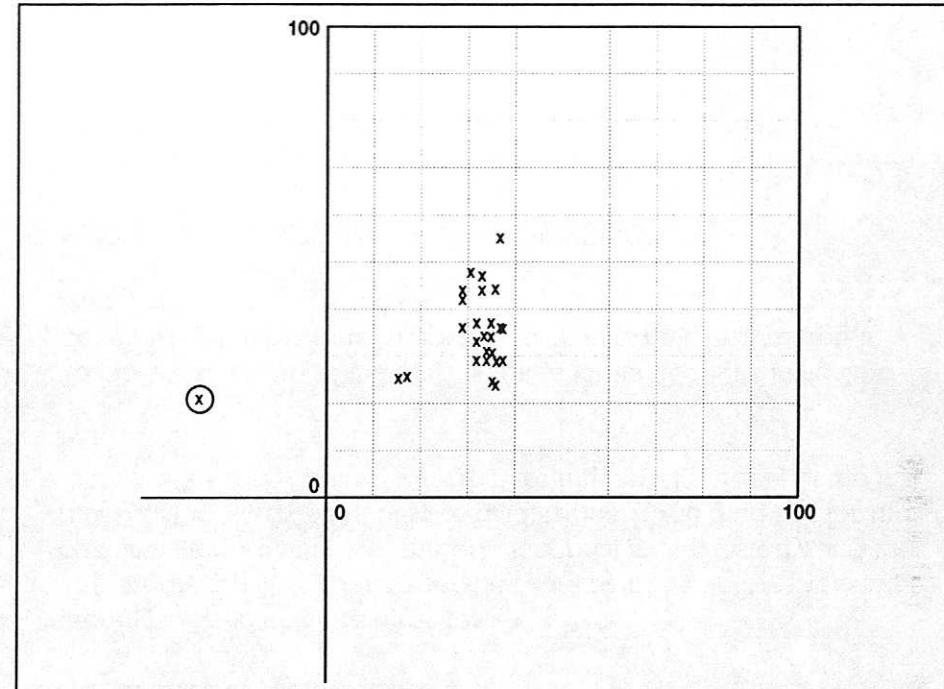


Figure 6. Fixes on a 0-99 coordinate system. The ringed location is outside the defined study area

## A.5 INPUTTING AND EDITING OUTLINE MAPS

For input, use option 1 of Main Menu 1 (then 2 in the submenu)

To edit, use option 2 Main Menu 1

This process is similar to the entry and editing of fix data. Consecutive pairs of coordinates are entered, and lines draw between these define each shape in the map.

- Map (and habitat) coordinates *do not* have to be integers. If the fix scaling is 10m, but you wish to plot a map feature's position to the nearest metre, you can use a decimal value, e.g. (23.4, 10) would be 4 metres east of (23.0, 10).
- You can alter the scale of a map if required, or to transform

coordinates which cross a grid boundary, by using the TRANSFORM procedure in option 3 of Main Menu 1 (p. 14).

- A background map is loaded automatically during data entry and editing and range analysis, if it is in the same directory as the file of fixes, and is named KARTA.BBC.

### **GETTING READY TO DIGITISE**

(If you are using a keyboard, skip this section)

If you intend to enter your data using a digitiser, the tablet should be set up before you start. RANGES V is capable of receiving input from 2 types of digitiser, these are Summagraphic BITPAD II and SUMMASKETCH III.

- **Setting up the Summagraphic BITPAD II digitiser tablet.**

The tablet should be connected to the RS232 (RS423) port, with its internal DIP switches set as follows:

Switch 1: 1-Off 2-Off 3-On 4-Off 5-Off 6-On 7-On 8-Off

Switch 2: 1-Off 2-Off 3-Off 4-Off 5-Off 6-Off 7-On 8-On

Switch 3: 1-Off 2-Off 3-Off 4-On 5-On 6-On 7-On 8-Off

To overcome a fault in early versions of the PS-2 operating system, X-ON/X-OFF is not supported. You may therefore need a lead which lacks a connection to pin 5 of the plug. Check this if there is no input from the tablet.

The tablet is "active" over the area framed by a groove. Your map should be fastened firmly (e.g.. with masking tape) so that shapes lie fully within the active part.

### **ENTERING THE DATA**

After choosing to start or edit a file, you first specify the correct filename(s) and then select the appropriate file type from the menu. In this case MAP OUTLINES.

- The next menu allows you to specify the mode of data input for input and editing.

**1 BITPAD II DIGITISER INPUT  
2 SUMMASKETCH III DIGITISER INPUT  
DEFAULT IS KEYBOARD**

**N NO GRID LINES**

**<RETURN> TO CONTINUE**

If you press ↲ the programme assumes that you intend to enter coordinates using the keyboard.

The data entry screen is similar to the one in entry of fixfiles. It is initiated by giving the GRID EDGE coordinates. For details of keyboard entry of coordinates, see p. 11.

- **Getting started with the digitiser**

The program will ask you to set the scale of the tablet by pressing a cursor button with the crosshair on the most southwesterly, and the most northeasterly point of your grid edges. It will then ask for the most southeasterly point, to correct for any misalignment of the map.

To move a new part of the map onto the tablet, RESET the scaling *before* filing the previous shape, or start a new file and merge it later using Main Menu option 2.

### **THE ROUTINE FOR KEYBOARD OR DIGITISER INPUT**

- During input, a list of coordinates appears on the data entry screen. You can scroll up and down through these during editing.

N.B. You cannot enter points south or west of your scaled area.

- There are 2 function keys available on the keyboard data entry

screen. **F1** gives the first coordinates, this is the easiest way to "close" a shape. **F9** terminates the shape.

- **When using the digitiser**

- ☛ Enter coordinates by pressing cursor **Button 1**

- Terminate a shape by pressing **Button 3**

- ☛ After terminating a shape, the details are shown on the top left of the screen. A menu below allows you to EDIT, FILE or OMIT the shape.

- ☛ If you FILE the shape, the next screen will ask if you wish to APPEND (add another shape) or FINISH. If you choose to OMIT rather than FILE a shape, it will be deleted from the screen.

- ☛ After you have finished entering all the shapes, there is a final summary screen. Here you can press **1** to alter scaling parameters if required (p. 12).

#### CONVERSION OF MAPS TO HABITAT FILES

This is possible providing that every shape in the map has been entered in a clockwise direction, without crossing lines (see p. 18). After conversion, all shapes will be filled with habitat colour as if they are closed.

The map can be converted using any text editor to change the appendix variable which codes for file type. Map files are coded "1" after the tilde and at the end of the appendix and habitat files are coded "2" at the same position.

#### A.6 INPUTTING AND EDITING HABITAT SHAPES

For input, use option 1 of Main Menu 1 (then 3 in the submenu)

To edit, use option 2 of Main Menu 1

Habitat shapes are entered by keyboard or digitiser in the same way as map outlines, with the important difference that *habitat shapes must be*

*entered in a clockwise sequence, and without lines that cross.* This routine automatically "closes" each shape by adding the first coordinates when you terminate the shape.

Labels for each habitat type are defined by you at the beginning of the routine. Later you select the required habitat type before entering the coordinates or adding more shapes. RANGES V displays a list of the habitat labels when you need them.

#### THE PROCEDURE FOR ENTERING HABITAT SHAPES

- ☛ You will be asked to type in habitat labels after giving the file name. They can be up to 5 letters or a number of any length including decimals. If you don't specify habitat labels you can still enter shapes. It is easy to add or change labels later using the EDIT routines. Note that the labels can be numbers (e.g.. density values), in which case habitat analysis will produce an average value for each range (see section 6.E).

- ☛ The next sub-menu is as shown above for MAP OUTLINES with an additional option, to add or change habitat colours.

1 BITPAD II DIGITISER INPUT  
2 SUMMASKETCH III DIGITISER INPUT  
**DEFAULT IS KEYBOARD**

**N NO GRID LINES**  
**C ADD/EDIT HABITAT COLOURS**

<RETURN> TO CONTINUE

If you select **C** you will be asked to assign colours to your habitat types before you enter any shapes. A colour chart is provided on screen (fig.7). Each colour is annotated with one or more habitat names as you select them. Text on the same screen explains how the tone of each colour can be modified using F-keys.

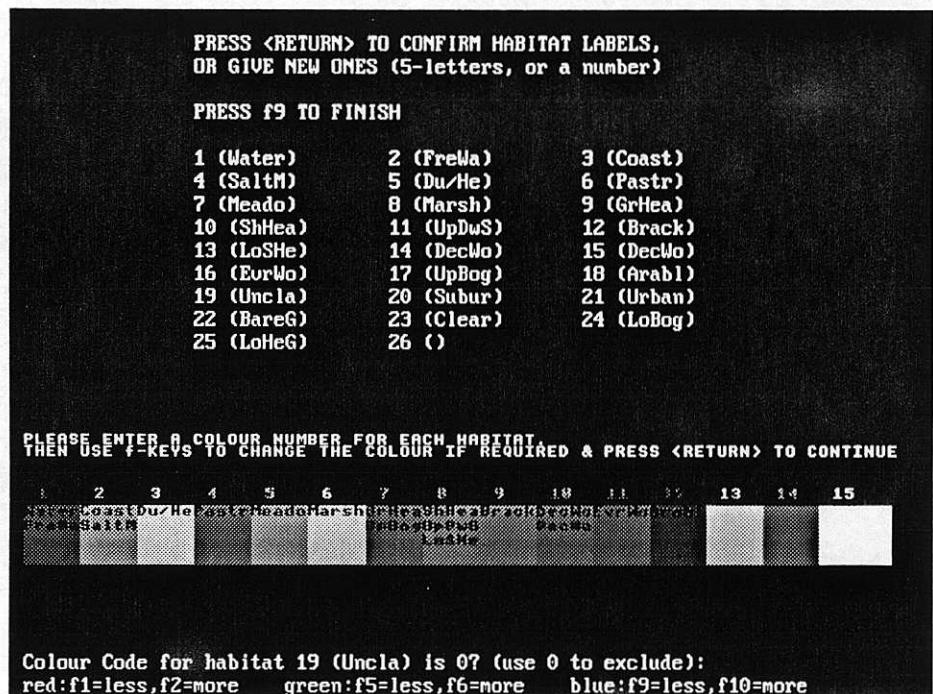


Figure 7. Confirmation of habitat labels and colours on editing BUZZARD\RASTER

- Next, you are prompted to specify the habitat type for the first shape, by confirming the current one with **F** or selecting a new type. Then the data entry screen is displayed and you can enter the coordinates. It is important to remember to enter shapes in a *clockwise direction, without crossing lines*.
- If one habitat in your map is an "island" within another, this must be digitised as a "hole" in the larger shape. Take a line in from an outer fix and then progress anti-clockwise round the hole. Then take the same line from the hole back to the outer edge. See fig 8.
- When you terminate a shape, by pressing **F9**, RANGES V automatically inserts a final coordinate which is the same as the first fix, hence closing the shape.

- After filing the shape by pressing **F**, options of appending with the same or another habitat type are provided. The area and peripheral distance of each shape are summarised at this point.

After you have finished entering, reviewing or editing the shapes in the input routine, the program provides a summary screen similar to that given for fix files, with options to change grid edge coordinates and scaling.

- The edit routine is the same as the input routine except that the submenu has an extra option **L** for editing the habitat labels.

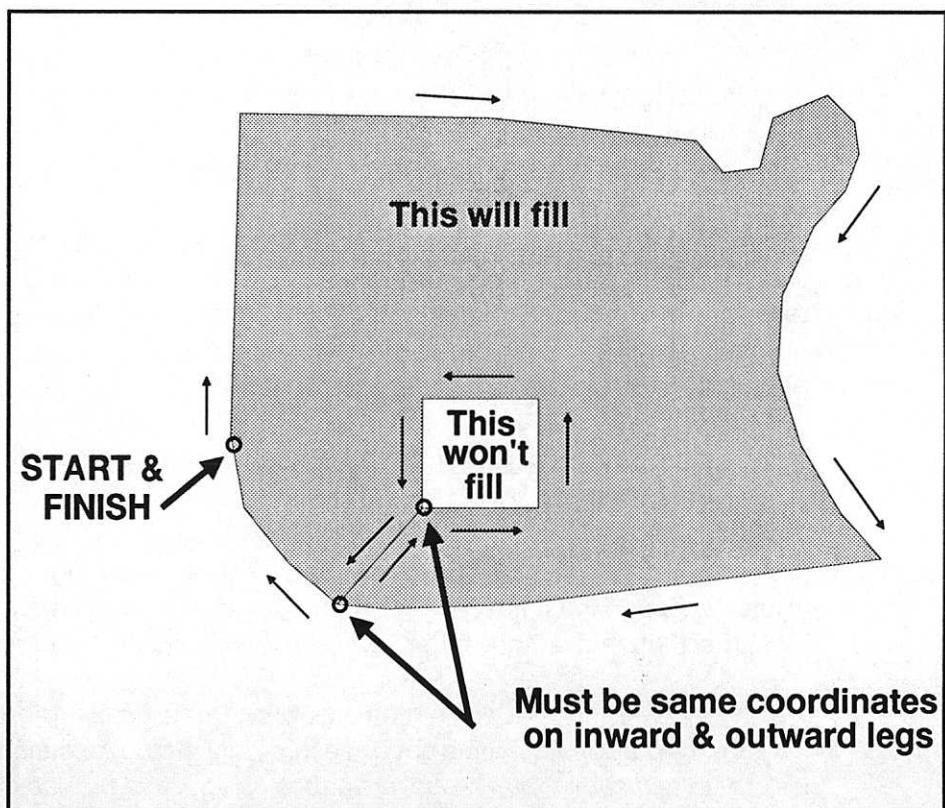


Figure 8. How to digitise an "island" of habitat, when entering habitat shapes

## A.7 INPUTTING AND EDITING HABITAT POINTS

For input, use option 1 of Main Menu 1 (then 4 in the submenu)

To edit, use option 2 of Main Menu 1

Input and editing of habitat points is identical to the routines for habitat shapes. The order of coordinate entry is not important as there are no shapes to be filled.

## A.8 EDITING RASTER MAPS

Use option 2 in Main menu 1

Colours and habitat labels on raster maps (e.g. maps produced from satellite imagery and imported to RANGES) can be edited if you wish to alter the appearance of the map. The procedure is the same as during import of raster maps (see section 5.B.4, p. 23).

The graphics of the map are not shown during editing. So you need to inspect the map using option 0 in Main Menu 7 (HABITAT ANALYSES) to decide what editing is required, prior to going into the EDIT menu.

NB. After editing is complete, the raster file is *saved under the same name*, unlike other file types in RANGES V. This is because only the appendix of such a large file is edited. So if you wish to save the file under a different name you should copy the file and then edit the copy.

## A.9 VIEWING FILES

Use option 4 of Main Menu 1

This option allows you to review a fixfile, map or habitat file without having to save it under a new name. It is displayed in the same format as the edit functions of options 1 and 2 in Main Menu 1. See p. 12.

- Raster files cannot be viewed with this option. To view these, use option 0 in Main Menu 7 (HABITAT ANALYSES).

- You can also view files in **Option 4 of Main Menu 2**, The File Manager (see p. 25). This types the file contents on the screen. It can therefore be used to look at files prior to import to RANGES, as well as RANGES files.

## B. IMPORT/EXPORT OF FILES

Use Main Menu 2- FILE MANAGER MENU

If you already have files of fix data, decide to do your editing in a spreadsheet, or want output for statistical analysis in another package, you may need to import and export files from RANGES V. You may also wish to print files for checking against original field notes.

Compatibility with other software has been enhanced by features that allow import and export of files in ASCII (text) format and as DXF (graphics) files. The file types which can be imported or exported from RANGES are shown in table 3, together with numbers denoting the main menu option where the import or export function is performed.

- NB:
1. The files exported as column text are spreadsheet-compatible.
  2. RANGES V can import values in types of format provided by most spreadsheets i.e., separated by commas (CSVs), tabs (TSVs) or spaces (SSVs).
  3. Option 4 (to view a file), in the FILE MANAGER (Main Menu 2) can be used to view any ASCII text file or DXF file suitable for import into RANGES V or any file produced by an export operation (see p. 22).

Table 3. File types for import and export in RANGES V

NB: All import functions are available in Main Menu Option 2. The export functions are available in various parts of the programme and are given in brackets.

IMPORT				EXPORT			
Column (text)	CSV etc. (text)	Graphics (DXF)	Raster map	Column (text)	Spreadsheet compatible (text)	Graphics (DXF)	Raster map
Fix	Fix	Fix	Gridascii	Fix (2)	Utilisation (3)	Fix (2)	Gridascii (2)
Vector map	Vector map	Vector map	Byte array	Vector map (2)	Interfix (3)	Vector map (2,5)	Byte array (2)
Vector habitat	Vector habitat	Vector habitat		Vector habitat (2)	Range structure statistics(3)	Vector habitat (2,5) (3)	
				Edge (2)	Fix-site distances (3)	Edge (2,5)	
					Overlap matrices (5)	Utilisation, increment, autocorrelation plots (4,6)	
					Dynamic interaction matrices (6)		
					Autocorrelation and fix-site (6)		
					Habitat matrices (7)		

## B.1 IMPORTING ASCII TEXT

### B.1.1 IMPORTING FIX FILES AS ASCII TEXT IN COLUMNS OR STRINGS

Use option 1 in the FILE MANAGER menu

#### THE PROCEDURE FOR IMPORTING

- Select 1. (TO IMPORT) from the FILE MANAGER menu.  
Type [filename] of file to be imported ↴.

N.B. If the extension is not .BBC, you must specify it, e.g. FIXES.TXT

If the file to be imported was produced by RANGES V and still has an appendix, it will be recognised and imported in the appropriate format.

For files from other sources, after pressing ↴ you can select the type of import procedure. You will be asked if the source file is:

T TEXT (ASCII)?  
G GRAPHICS (DXF)?  
R A RASTER MAP?

Then you are asked if the file contains:

F FIXES?  
M MAP DATA?  
H HABITAT DATA?

To import an ASCII text file use the following options:

Choose T for TEXT (ASCII)  
Choose F for FIXES

Type destination [filename] ↴.

N.B. There is no need to give an extension on this filename.

The following stages ask you for information about the positions of your variables (i.e. range variables, fix coordinates and FQVs) in each row of the file. You are shown the first line of the source file to help you to give the correct answers.

- First type the number of FQVs then ↵.
- The next screen display has some explanatory text and the following options:

**PLEASE CHOOSE TO SELECT VARIABLES:**

**0 BY THEIR ORDER IN EACH ROW**  
**1 BY THEIR START AND END POSITIONS**

Option 0 is easier to use, providing that the columns in the ASCII file are separated. All recently produced data sets are likely to be stored in this way. Fig. 9 gives an example of details for variable positions in a fix file being given using option 0. The second option is for data stored in columns without spaces between each value. With this option, each value is defined by the first and last possible positions of digits in each row.

eg. Column number:      1  2  3  4  5  6  7  8  9  1  
 Variable:                  X                  Y  
 Row 1:                    2  3  4        4  3  2        1  2

-with "option 1" the position of X in each row is 1 and Y is 2  
 -with "option 2" the position of X in each row is 1-3 and Y is 5-7

- After selecting the method of data entry, you will be prompted to define the position of each variable in turn. The prompts for FQVs are "qualifier 1, qualifier 2" etc.. Range variable (i.e. ID number, month, year, focal site coordinates) positions are given after coordinates and FQVs. If ID code positions are not given, the default puts all the coordinates into a single range.

```

 9 2 1 9 5 41 46 48 45 9 0 1

Please give X variable order in row: 8
Please give Y variable order in row: 9
Please give qualifier 1 order in row: 10
Please give qualifier 2 order in row: 11
Please give qualifier 3 order in row: 12

Animal identifiers, <RETURN> to finish
ID code order in row: 1
Identifier 2 order in row: 2
Identifier 3 order in row: 3
Identifier 4 order in row: 4
Identifier 5 order in row: 5
Identifier 6 order in row: 6
Identifier 7 order in row:

```

Fig 9. Providing information for import of a fix file: entering variable positions by their order in each row

- When import is complete, you are shown details of the file on a summary screen and given the option to alter &/or attach labels to the RANGE VARIABLES.
- Press ↵ for the 3<sup>rd</sup> screen which gives the convention for RANGE VARIABLE labels. You can press 1 to change them, otherwise press ↵.
- On the 4<sup>th</sup> screen you must label any FQVs. Appropriate label formats are listed.
- We recommend checking that the file has imported correctly by using option 4 (VIEW) in Main Menu 1. If there is a problem, the imported file can be examined by listing on the screen without a format check, in option 4 in Main Menu 2.

## B.1.2 IMPORTING MAP AND HABITAT FILES AS COLUMNS OF COORDINATES

Outline maps and habitat shapes or points can be imported as columns of ASCII text.

- Each row of a map file should contain an *X* and *Y* coordinate and there should be an empty line between each shape.
- Each row of a habitat file should have the appropriate habitat code before the *X* and *Y* coordinate. After import of habitat files you will be prompted to add habitat labels and may then use the editor to add colours (see p. 17–18).
- Note that habitat files will not function or be displayed correctly unless the coordinates have been entered clockwise.

## B.2 EXPORTING FIX, MAP, HABITAT AND RANGE OUTLINE (EDGE) FILES AS COLUMNS

Use option 2 of Main Menu 2

RANGES V files are in ASCII format, with values separated by spaces. They can therefore, be read and edited in word processing packages and text editors, or pulled into spreadsheets as space separated values.

- To export text columns you just have to enter the source and destination filenames and press ↴ at the RS menu.
- When files are exported from RANGES they have the extension .BBC.
- Each row of an exported *fix file* contains the following columns: ID, AGE, SEX, MONTH, YEAR, (focal) *X*, *Y*, (location) *X*, *Y*, qualifier 1,2,...,.
- Each row of an exported *map file* has just the *X*,*Y* coordinates and an exported *habitat file* has the habitat code and the coordinates. There is an empty line between shapes.

- Each row of an exported *edge file* is the same as a fix file without the FQVs, and with an empty line between shapes.
- To ensure suitable display in some MS-DOS based applications, RANGES V outputs both a carriage-return (ASCII 13) and a line-feed (ASCII 10) at the end of lines. These codes can cause problems when importing to some spreadsheets (e.g. MINITAB). Solutions are either to strip the ASCII 13 globally in an editor, or to import first into another spreadsheet (e.g. LOTUS 1-2-3 or EXCEL).
- If you export a fix or map file from RANGES V for editing in a spreadsheet and want to take it back into RANGES, keep the appendix for adding to the end of the file before re-importing.

## B.3 IMPORT AND EXPORT OF DXF FILES (GRAPHICS)

### B.3.1 IMPORT OF DXF FILES (GRAPHICS)

Use option 1 of Main Menu 2

The import routine asks you to specify whether the source file contains fix, map or habitat data.

- After importing the values, the programme allows confirmation or alteration of labels, e.g. habitat labels. Each POLYLINE ... SEQEND in the DXF file creates a new shape, with or without a label change. Each change in DXF label (if present) starts a new range or habitat type, which will be labelled 1,2 etc. in sequence.

### B.3.2 EXPORT OF DXF FILES (GRAPHICS)

Use option 2 from Main Menu 2

The ability to export graphics files means that screen-dumping (in RANGES IV) can now be superseded by importing DXF files produced by RANGES V into drawing or GIS packages (e.g.. ARC/

INFO, DRAW, AUTOCAD, FREELANCE) and then printing, if required, from these.

- Graphics output is available for fix data as points, squares or fix-fix lines. To choose between these output options in option 2 of Main Menu 2, select **A** from the RS menu.
- Graphics output is available for vector maps (as lines) and for edge files of range outlines (as lines and range centres). When exported as DXF files, the map, habitat and range outlines become polylines, labelled 6AF or 1SHAPE, 2SHAPE, as appropriate.
- There is graphics output in DXF format for incremental and utilisation plots (Main Menu 4) and for autocorrelation plots (Main Menu 6). To maximise compatibility with other packages these exports are in line format without text.

## B.4 IMPORT AND EXPORT OF RASTER MAPS

RANGES V can import and export raster maps, such as those prepared from satellite data or other remote sensing. Raster maps are a lattice of rectangles of equal size. They are stored in RANGES V as an array of single bytes, each of which codes for a habitat type. Files may be imported or exported in this form or in ARC/INFO gridascii format.

### VIEWING AND EDITING RASTER MAPS

It is not possible to view raster maps as byte arrays in the EDITING or FILE MANAGER menus. However, gridascii maps can be viewed in option 4 in the File Manager, prior to import, or after export from RANGES V (see p. 25).

In order to view a raster file, use option 0 in the HABITAT ANALYSES MENU (Main Menu 7).

Colours and habitat labels on the raster map can then be edited using option 2 in Main Menu 1.

### B.4.1 IMPORT OF RASTER FILES

*Use option 1 of Main Menu 2*

Before importing a raster map, you should have all the necessary details to hand. Imported raster files lack habitat labels and colours, so you will be asked to specify:

- labels (a number or 5 letters) for each habitat type
- colours for each label.

If you are importing a byte array, you will also need to provide:

- the number of rows and columns of data, if your map is not square
- the edge coordinates and scale for the map.

#### TO IMPORT A RASTER FILE

- First specify the file name, then choose **R** for RASTER MAP on the RS menu.
- On pressing ↴ a title screen appears with details of the file format which has been recognised by the programme (gridascii (ARC/INFO) or a byte array in rows by columns), and the filename. RANGES V recognises GRIDASCII files by the first label "ncols". If this is missing, and the file is recognised as a byte array, a "not square" warning may be generated.

If your map is square, import will commence when you press ↴. If it is not, RANGES will prompt you to enter the following information:

**THE NUMBER OF COLUMNS (E-W)  
THE NUMBER OF ROWS (N-S)**

During the import procedure, you should see a flashing message on the screen which reads e.g. Row 1 of 200, Row 2 of 200 etc.

- After import is complete, labels and colours must be attached to the values in the file. The next screen asks you to give or confirm *habitat labels*. Default labels of (VAR 1), (VAR 2) etc. are added if you do not specify any. On completion press **F9**.
- You can then assign colours using the colour chart provided (see fig. 7 p. 18). Each colour is annotated with one or more habitat names as you select them. Text on the same screen explains how the tone of each colour can be modified using function-keys.
- Lastly, a results screen displays the numbers of rasters filed, the source and destination filename and gives the opportunity to change the scaling parameters by pressing 1.

To change the scale, you first make any necessary changes to the GRID EDGE coordinates then type in the new scale.

#### **EXAMPLE**

To practise importing.

- First *export* the example file \RANGESV\BUZZARD\RASTER.BBC as a gridascii file. On export the scale will be automatically set to 1m.
- When you *re-import* this file the scale can be changed back to the original 100m.
- After import choose 1 to change scale and then:
  - divide the GRID EDGE COORDINATES by 100, i.e. remove "00" from each
  - give the new scale as 100.

#### **B.4.2 EXPORT OF RASTER FILES**

*Use option 2 of Main Menu 2*

When exporting, you first give the source filename, and are given the choice of 2 formats:

- 1 GRIDASCII (ARC/INFO) FORMAT?**
- 2 A BYTE ARRAY IN ROWS BY COLUMNS?**

Option 1 is for transferring data. Option 2 produces the data in a more compact format which saves disk space.

NB: gridascii files are exported with a scale of 1m.

As export proceeds you should see the same flashing screen message as on import.

- Press ↲ to exit when export is complete.

#### **C. MERGING AND SPLITTING FILES AND RANGES**

*Use option 3 of Main Menu 2*

Files can be MERGED so that each range remains separate. Alternatively, if each file contains data from the same animal, you can merge the ranges as well. For instance, animals A,B,C with A,C,D,E can be merged as A,B,C,A,C,D,E; or as A,B,C,D,E where fixes from A and C in the first file are combined with those in the second into single ranges.

To merge ranges you have to specify labels denoting the "same animal" (e.g. both ID and SEX if you have MALE 2 and FEMALE 2).

- You can merge all the fixes from *different* animals by first splitting the file into single range files. Then merge them again into one range. To do this first choose **A** for analysis options in the RS menu and press 1

to MERGE SETS OF FIXES FOR THE SAME ANIMALS. Then use a variable common to each file (e.g.. year) to merge A with B, then A&B with C, etc..

- It is also possible to use FQVs during file merging and splitting, for example to split a file so that only the morning fixes are saved in the new file.
- You can merge edge files of different types, (e.g. 100% convex polygons with 95% contours) to compare overlaps of different methods or for habitat analyses. The type of outline (edge) is coded at the end of each coordinate set. (See Appendix I for codes).
- The merge-fixes option operates both when given a batch of 2 files (e.g.. /FIXES1/FIXES2/) or when given only an initial file, in which case it will prompt for a second file.
- ***Saving time by making multiple split operations***

When you finish a file operation of this sort, you can press **F2** or **F3** to repeat it, e.g. with a different set of ranges selected within a large file. In this case, you are given the opportunity to select a new output file. This allows you to make multiple split operations from single files or batches (e.g. to remove 1 range at a time). NB. This only works for the files initially selected, not after pressing **1** to add new files during a run.

## D. VIEWING FILES

Use option 4 of Main Menu 2

Files can be viewed in this option without the format checks required to view in Main Menu 1. This means that it can be used to check files before import or after export. Fig. 10 shows a range edge file, produced in a RANGE ANALYSIS ROUTINE. Note that, because it has been output from RANGES V, it has an appendix. This gives the file format. For instance, variable 9 in the appendix has a value of 2, which denotes 2 ranges. (See p. 7 and Appendix 1 for more on file structure).

```

8 2 1 9 5 15 31
11 13.5 28.5 13.5 29.5 13.5 34.5 19.5 41.5 20.5 41.5 32.5 37.5 32.5 36.5 27.5 29
.5 16.5 17.5 15.5 17.5 13.5 27.5 15 31
-1 100.111
11 13.5 28.5 13.5 29.5 13.5 34.5 19.5 41.5 20.5 41.5 21.5 27.5 21.5 26.5 20.5 23
.5 19.5 23.5 14.5 26.5 13.5 27.5 15 31
-1 75.111
7 13.5 28.5 13.5 29.5 13.5 34.5 17.5 34.5 17.5 30.5 15.5 27.5 13.5 27.5 15 31
-1 50.111

1 2 2 9 5 35 34
9 32.5 26.5 34.5 53.5 35.5 53.5 62.5 47.5 62.5 46.5 43.5 30.5 39.5 28.5 33.5 25.
5 32.5 25.5 35 34
-1 100.111
10 32.5 26.5 33.5 33.5 34.5 34.5 40.5 37.5 43.5 37.5 43.5 31.5 43.5 30.5 39.5 28
.5 33.5 25.5 32.5 25.5 35 34
-1 75.111
8 33.5 32.5 33.5 33.5 34.5 34.5 35.5 34.5 39.5 33.5 39.5 30.5 39.5 28.5 38.5 28
5 35 34
-1 50.111
-1

~ 11 2 2 0 13 63 17 54 2 10 1 12 0 1 0 1 0 0 3 10 Y A M F 50/75/100/ 8-15 11
PRESS <SHIFT> TO CONTINUE

```

Figure 10. Display of a file of 50%, 75%, and 100% convex polygon edges for 2 ranges

# 6. DATA ANALYSES

---

## A. RANGE ANALYSES

Use Main Menu 3

### A.1 INTRODUCTION

A wide variety of different methods of range analysis have been published. These include:

- grid cell analyses
- minimum area convex polygons (MCPs, MAPs)
- peeled MCPs
- concave (restricted edge) polygons
- cluster analyses
- tessellation techniques
- bivariate normal ellipses
- contouring based on various kernel density estimators (including harmonic means).

Just as there is no single statistical test suitable for all types of analysis, so it has become clear that there is no "grand unifying range analysis". Ranges are analysed for a variety of reasons, including estimation of range sizes and habitat use for conservation projects, estimation of range structure and overlap for behavioural studies, and combinations of all these parameters for demographic modelling. The various techniques are useful for different purposes.

The different analysis techniques divide loosely into families, whose relationships and properties are outlined in the next few paragraphs. The special value of each technique is mentioned again at the start of the section dealing with its implementation in RANGES V.

The two main families of range analysis techniques are either primarily parametric, based on estimating fix density distributions, or non-

parametric, usually being based on a ranking process. The simplest parametric technique is the production of bivariate normal ellipses (Jennrich & Turner 1969). This assumes that the distribution of fix density is distributed normally on two axes (the simpler, circular case being an ellipse with equal axes) about the arithmetic mean  $x$  and  $y$  coordinates for all the fixes. The implicit assumptions of normality and that ranges are mono-nuclear are seldom met (White & Garrott 1990), but ellipses are still useful for estimates of range size when few fixes are available.

More sophisticated parametric techniques, use kernel estimators to allow for multinuclear fix distributions (Dixon & Chapman 1980, Donn & Rennolls 1983, Worton 1989). Fix density is estimated over a matrix of intersections of a grid, which is placed arbitrarily (i.e. without reference to the fix coordinate system) across the locations. Contours are then interpolated between the intersections. Fix-density-contouring confers shape that is lacking in ellipse models, but still includes assumptions about the density distribution that substantially affect the results.

Contouring on Gaussian kernels is mathematically more robust than harmonic mean contouring, and use of techniques such as least squares cross validation (Worton 1989) have potential for providing unique best-fit results. However, the assumptions of continuous density distribution still tend to "balloon" contours into unused areas that border high-use areas.

The non-parametric techniques are based on forming outlines that encompass linked locations. The simplest approach is to surround each location by a grid cell, that is the width of the tracking resolution. Finding the maximum area used in any one study period requires very large numbers of observations, so rules have been applied for joining the grid cells. The simplest rules join adjacent cells, named after appropriate moves in chess (Voight & Tinline 1980). However, these are only part of a larger set of distance-based rules that can use multinuclear

clustering (which includes tessellation) techniques, or join all the fixes within a particular distance of a range centre to produce a single outline. The latter, mononuclear case has value for constructing single-outline territories, whereas clustering is ideal for focusing on areas of high use in multinuclear ranges. Restricted-edge (concave) polygons (Harvey & Barbour 1965) are in effect a "half-way house" between the two approaches.

In RANGES V, the boundary strip, which is half the tracking resolution round each location, makes allowance for the real position of the fix being up to this distance on either side of the registered coordinates. Use of a boundary strip shows clearly the relationship between the different techniques. Thus, outlying locations in cluster or concave polygon analyses become isolated grid cells.

RANGES routines have now been used to examine area, shape and internal structure of many ranges from a variety of species. An extension of RANGES V has used jack-knifing to examine precision of cores for including the trajectory of animals that were tracked continuously, and repeatability of those cores, with increase in sample size (Robertson *et al* in press). The aim has been to define the best techniques for answering particular questions and to determine the minimum sample sizes required. This enables biological questions to be answered by using individual ranges as sample units for statistical tests, thereby avoiding the need to make assumptions about fix independence within each range (Kenward 1992, Aebischer *et al.* 1993).

In general, the more detail on shape and structure that is required, the more locations that are needed to define a range. The most stable ranges are ellipses, which often require just 8-10 fixes to give a stable index of area, assuming that consecutive fixes are independent in time. However, ellipses have the least precise trajectory inclusion. Density contouring improves on precision, and can give stable area estimates with only 15-20 fixes. Polygon peeling gives similar or better

precision, but requires larger samples of fixes (MCPs are typically stable after 30 fixes). Any of these techniques may be suitable for estimating habitat available to an animal, but only the latter two are likely to be useful for examining range overlaps. Cores from cluster polygons contain the highest density of trajectory, which is appropriate for examining habitat use and internal structure of ranges (e.g.. core:excursive ratios), but are also least stable, which makes them less suitable than an intermediate technique (contouring or peeled polygons) for studying sociality.

RANGES V implements all but one of the analyses used in more than 1 refereed publication. Only Fourier analysis (Anderson 1982) is not provided, because mathematical problems in implementing this approach are even worse than for Harmonic Mean Analysis (- see section 6.A.8 ). Contouring based on Gaussian kernels may well give results similar to contours from Fourier Analysis, or to the once-published approach of Donn & Rennolls (1983). Similarly, the polygon peeling techniques are slightly different to that of Hartigan (1987) but should give very comparable results. Cluster analysis should give results similar to those from Dirichlet tessellations (Wray *et al.* 1992), without the problems of setting limits to outer tiles.

## A.2 RANGE ANALYSES MENUS

All options in the RANGE ANALYSES menu lead to selection of data file(s) and then to a titled sub-menu. After choosing an option from this menu, you will progress, *via* at least one more submenu, to the analysis routine.

### THE RUN SPECIFICATIONS MENU

The RS menu is very similar in every range analysis routine, so it is described here. (N.B. It is also used in routines other than RANGE

ANALYSES, see p. 2). The options vary according to the routine being used but all range analyses routines will offer the following options.

- P PRINT RESULTS
- F FILE RESULTS
- N NON-STOP RUN
- O OVERLAY PLOTS
- E ENLARGED PLOTS
- R SELECT RANGES
- X SELECT FIXES

P PRINT RESULTS directs an ASCII text file from the results screen to a printer. NB. this is only suitable for printers which do not need a special driver (e.g. dot matrix type). It is generally more useful to use the next option to save text files and then print from a text editor. See p. 7 for more details on printing.

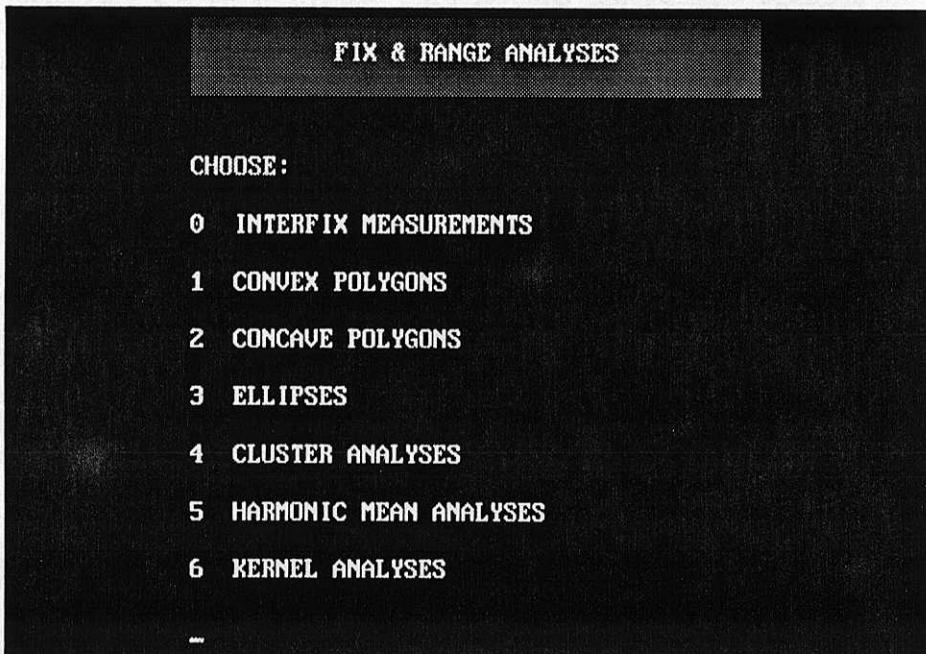


Figure 11. The first RANGE ANALYSES menu

- F FILE RESULTS outputs text file of range edges, utilisation distributions, distance values, areas and statistics. It is switched on automatically for INCREMENTAL AREA ANALYSES.
  - N NON-STOP RUN prevents the machine waiting for a key press after displaying the results for each range. It is useful for leaving long analysis runs.
  - O OVERLAY PLOTS will give an overlayed screen display for files with >1 range. Where possible, different colours and line patterns distinguish separate ranges. The scale is set to the edges defined in the appendix of the fix file.
  - E ENLARGED PLOTS expands the scale for each range to fill the top right hand corner of each screen. Selecting E turns OVERLAYS off and vice versa.
  - R SELECT RANGES is only available if there is >1 range in the fix file. Ranges can be selected by their rank (order in the set), sex, age, or start date. To make selection easier, the range IDs month and year and sex are listed with tables for age and sex.
  - X SELECT FIXES allows you to select fixes with particular FQV values (e.g. in a feeding habitat). FQV labels (see p. 10–11) and their range of values are listed to help you choose.
- There are two more options which become available in some of the routines.
- A ANALYSIS OPTIONS can be selected to access an additional submenu. For instance, in interfix distance measurement you can use the dispersal detector, or you can change the default grid settings in contour analyses.
  - M MATRIX OUTPUT files matrices if required when producing contours in HARMONIC MEAN and KERNEL ANALYSES.

## A.3 INTERFIX MEASUREMENTS

Use option 0, Main Menu 3

These are useful for providing plots and summary statistics from continuous recording sessions. Other applications include the estimation of indices of daily movements for animals tracked intermittently, and the investigation of dispersal.

After typing in the data filenames, you will be shown the INTERFIX MEASUREMENTS menu. The second paragraph of the menu is displayed after selection of options 1 or 2. Here, "SITE" refers to the focal site defined in the RANGE VARIABLES (see p. 10-11).

- 0 Headings
- 1 Distances
- 2 Times
- 3 Speeds

PRESS S FOR SITE-TO-FIX VALUES, OR  
CHOOSE HOW MANY FIX-FIX VALUES AT A TIME:

(eg. 3 for day-distance with 3 fixes/day, <RETURN> for value to each consecutive fix, A for total from 1st to last fix)

The results screen (apart from dispersal detection-see next page) will show a plot of each animals movements, a table of the interfix measurements, and summary statistics when appropriate.

Any of the example fix files (BUZZARD, FIXFILE etc.) can be used to try out this option.

### A.3.1 DISTANCES

#### FIX-TO-FIX VALUES

When choosing fix-to-fix values for data from continuous monitoring, you would probably select for 1 fix at a time. This would give an estimate of each consecutive distance travelled.

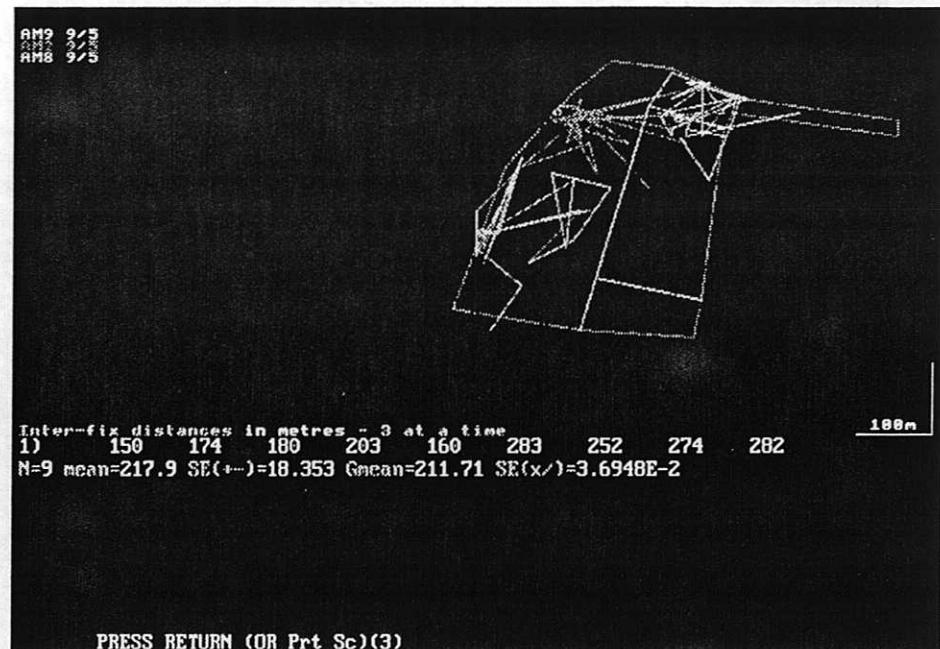


Figure 12. Interfix distances (3 at a time ) for 3 squirrels in SQUIRREL\FIXFILE

If you recorded the same number of fixes each day this number can be specified as a fix-to-fix value to get an estimate of distance moved per day. For example, FIXFILE in the SQUIRREL example directory contains fixes which were sampled 3 times a day. By selecting for 3 fixes at a time, you get a rough index of the daily movement (fig. 12).

The program actually uses four fixes if three were taken each day, because it assumes that the first fix in each sequence is a night-rest (or day-rest) position, and thus estimates the distance from rest to rest. If the data do not start with the first rest site, the first day-distance is to the first fix on the second day.

#### SITE-TO-FIX VALUES

When measuring distance from a focal site, the output file includes the fix coordinates as well as the focal site. The file is therefore saved in the

same column format as a fix file, with the distance added as an extra FQV, in the first FQV position. The distance-from-site may be a useful FQV in further analyses, for example to estimate sociality coefficients for locations that were not at a nest. If you wish to re-import the output file for range analyses, you must first remove the appendix using a text editor.

#### • *Dispersal detection*

To use dispersal detection, remember that the question you are asking is "when did dispersal occur?". The process will therefore only work for ranges which have been given FQVs which indicate time.

- ☛ You can use dispersal detection by selecting **S** for SITE-TO-FIX VALUES and then **A** for the ANALYSIS OPTIONS menu which is shown below:

**TO PLOT TIME VALUES:**

**FROM THE FIRST FIX, PRESS <RETURN>  
FROM THE START OF THE YEAR, PRESS 1**

**TO RECOGNISE DISPERSAL BEYOND A CERTAIN DISTANCE,  
GIVE THE DISTANCE IN METRES, ELSE PRESS <RETURN>**

**FOR DISPERSAL DETECTION BASED ON FIX DISTRIBUTION  
PRESS 1, 5 OR 9(=10) TO SET ALPHA LEVEL,  
OR <RETURN> FOR FASTER PROCESSING**

- ☛ Either of the time values can be used in dispersal detection. Pressing 1, gives time as Julian days from the start of the year. The default, ↓, gives the date of the first fix as "0".
- ☛ Next, you set minimum distance to recognise dispersal.
- ☛ Then give an alpha (probability) level (1 for 1%, 5 for 5% and 9 for 10%) if you want a *stochastic detector* (see Explanatory note). Or

#### **Explanatory note: stochastic dispersal detection**

This starts with the first 3 fixes, and estimates their arithmetic mean centre (Ac), and their confidence limit for distance from the Ac, using the relevant probability level. It then estimates the arithmetic mean for the next n fixes in the data set, where n is usually 3 (but see below), and defines the "dispersal" vector (i.e. probable direction of dispersal) between these. Dispersal is recognised if the orthogonal distances of the n fixes along this vector are all outside the confidence limit for the first N (i.e. 3). If not, N increments by 1, and the process repeats through the set of fixes.

The use of a dispersal vector means that dispersal will not be recognised erroneously if an animal makes consecutive excursions in different directions. However, dispersal may be recognised late if the animal makes an initial movement in one direction, and then departs in another direction. The estimation is only rigorous with N+n fixes where n > 3. Missing values in the dataset (recorded as -9,-9), are assumed to represent occasions when the animal was sought but not found, and was outside the confidence limit for the current N. Dispersal is, therefore, recognised with a minimum of 4 (3+1) fixes if the last fix is -9,-9. It is advisable to set a minimum distance as well as a probability level. This will prevent premature detection of dispersal (e.g. when a bird leaves a nest after several records there, instead of leaving the natal area).

select a distance without a stochastic detector. The latter sets the routine to calculate when this distance from a focal site was first exceeded.

After running DISPERSAL DETECTION, the screen will display a distance/time plot with a vertical red line just after the appropriate fix. The sequence number of that fix with its date in Julian days will be at the end of a list of mean distances. The distance vs time plot colours fixes according to date, by hour for plots of less than a day, by day for plots of 1-30 days, by week for 31-60 days and by 6-month period for longer plots. The colours are a guideline only, and are not corrected for leap-years. (N.B. 2,000 is not a leap year).

### A.3.2 HEADINGS, TIMES AND SPEEDS

When you choose these options, the analysis results are given as headings in 360°, times in minutes, and speeds in metres/hour.

## A.4 CONVEX POLYGONS

Use option 1 in the RANGE ANALYSES menu

Convex polygons have external angles which are all greater than 180°. Minimum convex polygons (MCPs) are the smallest of such polygons which can be drawn around a set of fixes. The outermost of these, which includes 100% of the fixes, has been widely used to define ranges. It is therefore useful for comparisons, even though its area and shape are heavily influenced by outlying fixes (Harris *et al* 1990).

- Single boundaries for core territories can be defined by plotting convex polygons around given proportion(s) of the fixes. These mononuclear peeled polygons show areas of highest fix density by excluding a proportion of fixes furthest from a range centre (Kenward, 1987).
  - Data on range area and structure can be displayed, printed or filed for subsequent analyses.
- ☞ After data filenames have been typed in, the CONVEX POLYGONS menu will be displayed. This menu is similar in all other range analyses options :

#### CHOOSE:

- 0 Outer (100%) edges
- 1 Selected edges & statistics
- 2 Core edges at 5% intervals
- % utilisation plots
- 3 Incremental area analysis

- ☞ If you select 1 or 2, a sub-menu appears later in the routine for selecting a range centre:

#### SELECT CORES WHICH EXCLUDE FIXES FURTHEST FROM THE:

- 0 Focal site
- 1 Harmonic mean fix (Hc)
- 2 Kernel fix (Kc)
- 3 Arithmetic mean (Ac)
- 4 Recalculated Ac (RAc)

#### Explanatory note: range centre definition

The *arithmetic mean* of all the *x* and *y* coordinates defines the "centre of activity" *sensu* Hayne (1949).

The *harmonic mean fix* is the fix where the inverse reciprocal mean distance to all the other fixes is a minimum (Spencer & Barrett, 1984). The *kernel fix* is the equivalent Gaussian kernel estimator (Worton, 1989).

The latter two provide more robust estimators than the simple arithmetic mean.

Option 4 focuses on the area of densest fixes by recalculating the arithmetic mean position after excluding each furthest fix.

### A.4.1 OPTION 0: OUTER 100% EDGES

This option gives a rapid estimation of a convex polygon around all the fixes in a range. If you choose to file data, you will be offered the option of filing edges and also distances from a selected range centre to each fix. These are in column format suitable for input to a spreadsheet. Each row contains the distance preceded by the 7 range variables and followed by the FQVs.

#### A.4.2 OPTION 1: SELECTED EDGES & STATISTICS

This option allows you to examine range structure and to define core areas. By excluding fixes furthest from the chosen activity centre, areas with the highest density of fixes are identified i.e. those used most by the animal. N.B. if the range is multinuclear (i.e. has more than 1 core area) the home range is better described by *cluster analyses* (p. 35). See the introduction to Range Analyses p. 26–27 for more details.

- After making viewing and output selections from the RS menu (see p. 2, 27–28), you can choose one or more values for the percentage of fixes to be included in the polygon(s), as shown below:

##### RANGE EDGE DISPLAYS AND FILING:

**SELECT RANGE EDGE % (S) BETWEEN 5% AND 100%  
WITH <RETURN> TO FINISH  
OR PRESS <RETURN> NOW FOR 100% EDGES**

Note that the default on ↵ is for 100% edges. When you enter the polygon percentages, you need to press ↵ after each number then ↵ ↵ to finish. If you just leave spaces between them, the program will only read the first number typed. This screen will appear in all routines which require you to specify the edge percentages.

- Finally, you choose the method for calculating the range centre (see p. 31).

The results screen (fig.13) shows core range area(s), range span, and the mean, median, and maximum distance of fixes from the selected range centre. Polygon edges for different range percentages are shown in different colours. Edges can be filed for use in habitat and range overlap analysis.

- As well as filing edges from this option, you can also save range areas and statistics. These are in column format suitable for spreadsheets.

Each row has the 7 range variables, followed by X,Y coordinates for the range centre, followed by 5 range statistics (see Appendix 1 for details), followed by as many areas as there were core percentages.

#### A.4.3 OPTION 2: CORE EDGES AT 5% INTERVALS AND UTILISATION PLOTS

This option provides plots which help to decide which fixes are part of a core, and which are outliers.

The analysis produces a results screen (fig.14) which shows a map of the range edges, a table showing the area and % of total area of each % polygon, and a graph of utilisation distribution.

- You can choose to save both edge (polygon) and utilisation files. In this case all the edges from 20–100% are saved at 5% intervals, a total of 17 sets.
- Utilisation files can be plotted in UTILISATION AND INCREMENT PLOTS (Main Menu 4) p. 41.

#### CORE RANGES

Graphs of utilisation distribution can be used to assess (by eye) whether a sharp discontinuity in area, after the elimination of outlying fixes, indicates a core range. Better estimation may be possible if the utilisation file is saved and plotted in Main Menu 4 (see above). See p. 41 for details about utilisation plots.

#### A.4.4 OPTION 3: INCREMENTAL AREA ANALYSIS

Details on incremental area analysis are given on p. 43–44.

- Saving the file is obligatory (F is always selected on the RS menu), because you need to examine it in Main Menu 4.

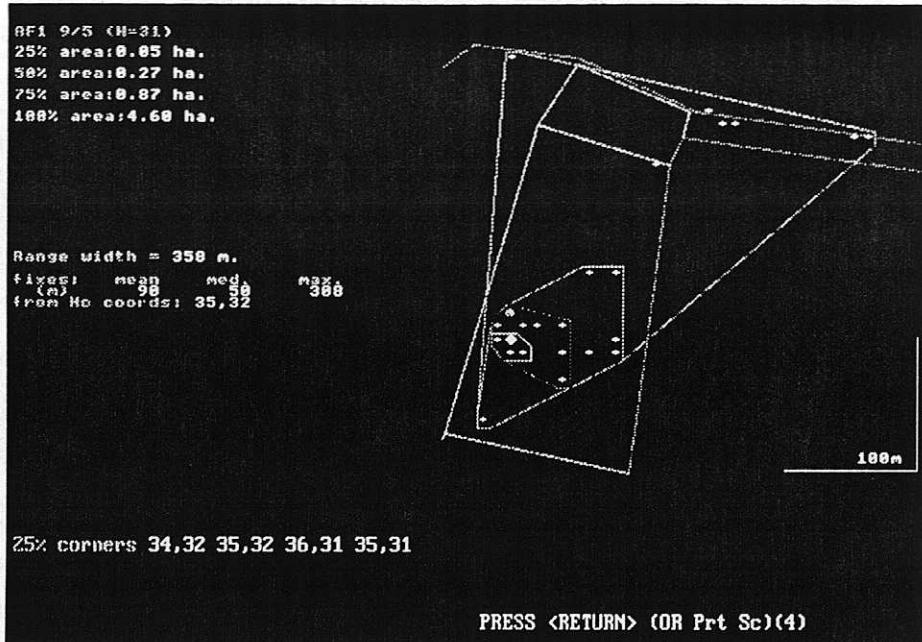


Figure 13. Convex polygons at 25%, 50%, 75% and 100% for AF1 in SQUIRRELFILE

- During incremental runs, the option to expand single ranges is not available on the RS Menu. This is because the routine cannot estimate the size of the complete range, and thus scale the screen correctly, from the few fixes it reads at the start of the run.

## A.5 CONCAVE POLYGONS

*Use option 2 in the RANGE ANALYSES menu*

Concave polygons (or "restricted edge polygons"), can be used to eliminate large areas which are not visited, such as lakes at the edges of areas used by terrestrial animals. Lines are only drawn between edge fixes if they are shorter than a selected fraction of the range width. This makes the range concave where there are large gaps between edge fixes.

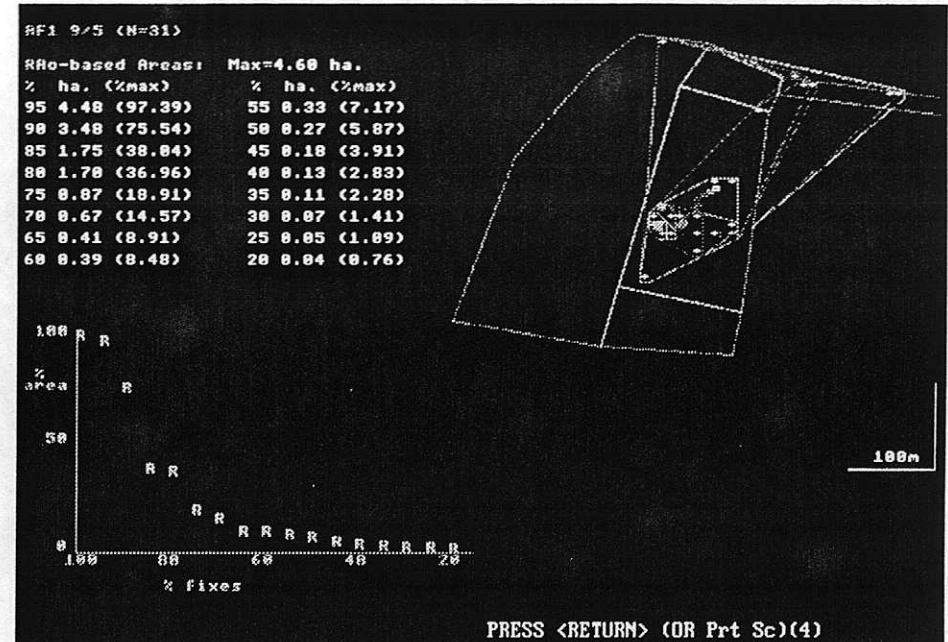


Figure 14. Convex polygons at 5% intervals for AE1 in SQUIRREL.FIXFILE with utilisation analysis

### **Explanatory note**

RANGES V creates concave polygons by starting with the fix at the extreme southwest and proceeding clockwise. It starts a new polygon if the separation between fixes is greater than the range-width fraction. Outlying fixes occupy small squares which are formed by applying a boundary strip to the fix. The squares are thus equivalent to a grid cell with side lengths defined by the resolution of the tracking technique (see Explanatory note, p. 13, for further details on fix resolution).

The concave polygons menu is displayed after the data files have been chosen. It is shown below:

**CHOOSE:**

- 1 Selected edges only**
- 3 Incremental area analysis**

- Note that option 2, which gives utilisation distribution in other range analyses, is not available for concave polygons. This is because all the fixes are included in the analyses. However, a process analogous to utilisation plotting can be obtained by progressively reducing the width fraction used to set the minimum edge length.

#### A.5.1 OPTION 1: SELECTED EDGES ONLY

The edges of concave polygons are selected by specifying the *edge length* as (whole) metres or as a fraction of the maximum range width. The edge length is standardised for all animals in the file if you use metres.

The screen for selecting the maximum edge length for concave polygons occurs after the RS Menu. This means that these can be changed easily between runs. It looks like this:

**PRESS <RETURN> TO RESTRICT POLYGON EDGE LENGTHS TO 0.5x  
MAXIMUM RANGE WIDTH, OR GIVE ANOTHER DECIMAL, OR SET A  
MAXIMUM NUMBER OF METRES:**

#### OUTPUT OF GRID CELLS

If you select a fraction (or length) that is smaller than the distance between fixes, and have your fix resolution set to this distance, the output is of *single grid cells* (e.g., set 5 metres for a run with the example FIXFILE in the SQUIRREL directory, in which the resolution is 10 m). Figures 15 and 16 show the same range plotted with different restrictions on polygon edge length. If you set the length equal to your resolution

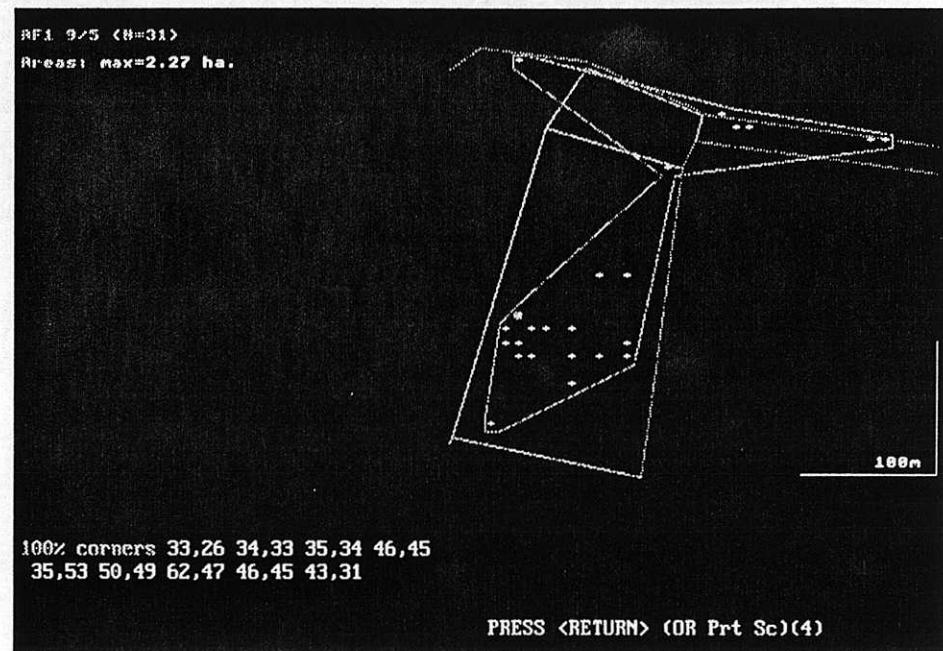


Figure 15. Concave polygon with edges restricted to 0.5x maximum range width for AF1 in SQUIRREL\FIXFILE

(i.e. 10 m for FIXFILE), adjacent occupied grid cells are joined using the "Rook's" rule (i.e. adjacent horizontal and vertical cells join, but not adjacent diagonal cells). To use this approach for distances of less than 1 metre between fixes, you will need to multiply your distances using the transform option (3 of Main Menu 1, see p. 14).

#### A.5.2 OPTION 3: INCREMENTAL ANALYSES

In this option saving the file is obligatory . See p. 32 .

Note that incremental plots of concave polygons tend to require more fixes to reach an asymptote than those from convex polygons. This is because ranges can fragment.

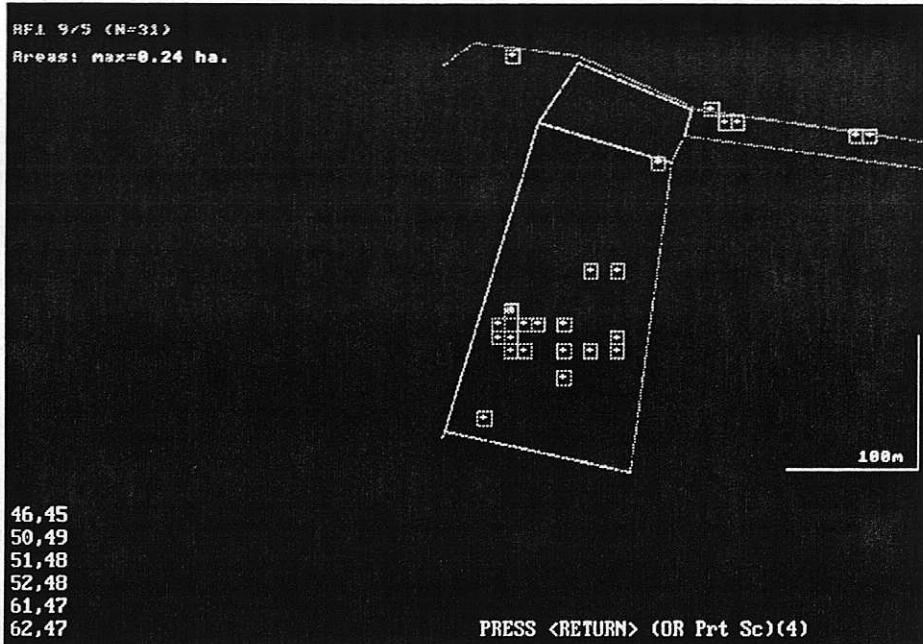


Figure 16. Grid cells for AF1 in SQUIRRELFILE, from concave polygon analysis with edges restricted to 5m

## A.6 ELLIPSES

Use option 3 in the RANGE ANALYSES menu

Ellipses, usually estimated to include 95% of the fix density distribution, are another longstanding technique. They do not define range shape well but require few fixes to reach a maximum area estimate and are therefore useful for identifying habitat available to animals that cannot be tracked frequently.

- The ELLIPSES menu is the same as for CONVEX POLYGONS (see p. 31) except that it is unnecessary to choose a range centre.
- Analysis results include *utilisation distribution* plots. Note that ellipses have a smooth utilisation distribution because they are based purely

on a normal distribution. The smoothing that this entails also leads to rapid achievement of an asymptote in incremental analyses, often with as few as 10 fixes. However, if several successive fixes add to a core area following a number of outliers, the estimated ellipse areas may fall after the initial increase.

- The range statistics include the ratio of the standard deviation of the fixes along the major and minor axes of the ellipse (see explanatory note) as an index of range asymmetry.

## A.7 CLUSTER ANALYSES

Use option 4 in the RANGE ANALYSES menu

Cluster analysis is particularly good for eliminating outliers and separating range cores. This can identify patchiness in range use, for instance where the study animal forages in several separate areas. Convex polygons are used to provide an outline around these cores.

The CLUSTER ANALYSES menu offers the same options as for convex polygons (section 6.A.4, p. 31). However, there are two methods of

### Explanatory note: ellipses

Ellipses are plotted using the original Jennrich & Turner (1969) approach. Assuming a bivariate normal distribution of the fix locations, their variance and covariance are used to estimate their density about major and minor axes centred on the arithmetic mean coordinates. The major axis is inclined at  $\theta$  degrees to the horizontal.

Whereas convex polygon cores are based on shapes that include the required percentage of fixes, ellipses enclose a proportion of the bivariate normal density distribution. They may therefore include more or less than the appropriate percentage of fixes. The outermost ellipse is estimated to include 99% of the density distribution because the 100% ellipse would be at infinity.

### Explanatory note

The analysis starts the first cluster by identifying the two fixes which are closest together and have the nearest 3rd fix. It then finds the fix nearest to one in this initial cluster. If this is less than the distance to the 3rd fix in any other potential cluster, the 4th fix joins the original cluster. If not a new cluster forms. If two clusters have nearest neighbours at equal distances, the fix which joins, is the one which minimises the distance to all fixes in the cluster. If the nearest neighbour is already assigned to another cluster, the two clusters join. When the required percentage of fixes has been assigned, convex polygons are drawn around each cluster and their areas summed (Kenward 1987).

running the analysis because there are two ways of defining the distance of a fix from a cluster:

1. Nearest neighbour rule. This uses the distance of a fix from the nearest fix in the cluster.
2. Centroid rule. This uses the mean distance of the fix to all other the fixes in the cluster.

When you set the Run Specifications in any of the options (0,1,2,3), you therefore have the additional choice: **A ANALYSIS OPTIONS**. If you select this the following screen is displayed:

**PRESS 1 FOR CENTROID JOINING PRIORITY  
OR <RETURN> FOR NEAREST NEIGHBOUR JOINING PRIORITY**

Nearest neighbour joining priority is the default if you do not use the analysis options. N.B.: this default generally appears to produce the best results; this is probably because animals tend to return to a location from which they make a foray.

After selecting the joining priority, you can choose the required range edges as in the other analysis routines.

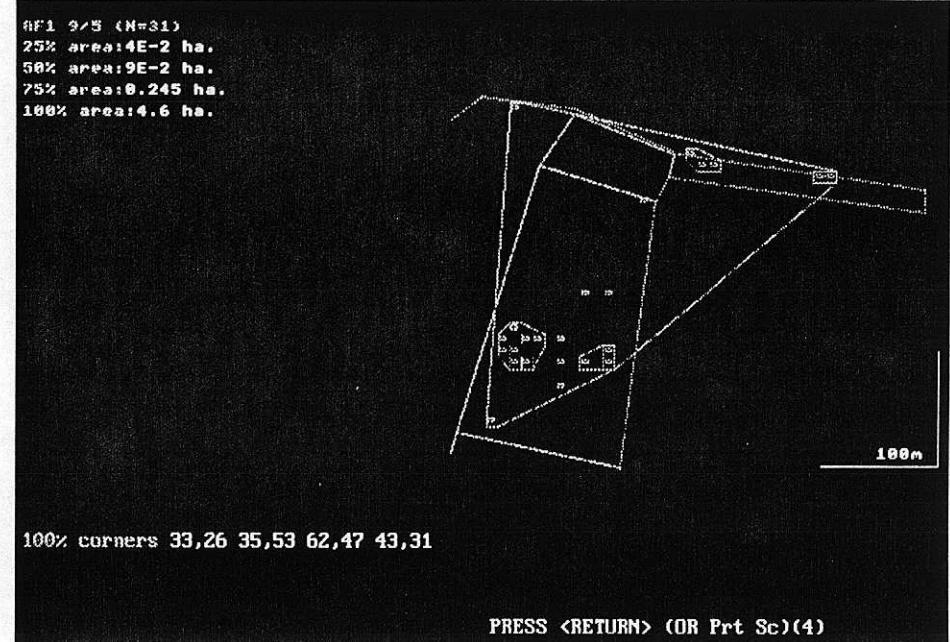


Figure 17. Analysis results screen: 25%, 50%, 75% and 100% polygons for AF1 in SQUIRRELFILE by cluster analysis

The results screens are similar to those for convex polygons, except that in options 1 & 2 the statistics include the number of range nuclei for each % polygon. See fig. 17. The utilisation plot can be used to identify core ranges as in convex polygons (see p. 32).

## A.8 HARMONIC MEAN ANALYSES

*Use option 5 of the RANGE ANALYSES menu*

The harmonic mean model of Dixon & Chapman (1980) estimates the fix density distribution (equivalent to the probability of encountering the animal) at intersections of an arbitrary grid. The density function used is the reciprocal of the mean inverse distances of all the fixes from each intersection i.e.  $n/ \sum d_i$ .

Contours containing a specified percentage of fixes are then interpolated across the grid. For further reading on harmonic mean analyses see Dixon and Chapman (1980), Spencer and Barrett (1984) and White and Garrott (1990).

The menu for this analysis option is shown below:

- CHOOSE:**
- 0 Fixes, Hc & statistics
  - 1 Selected % contours only
  - 2 Contours at 5% intervals & utilisation plots
  - 3 Incremental area analysis

#### A.8.1 OPTION 0: FIXES, HC & STATISTICS

This runs far more quickly than the other options because the programme does not have to calculate a matrix of fix density values (see below). It provides the coordinates of the Hc (Harmonic mean fix, see p. 31) and its distance from the focal site. Range structure statistics include the dispersal, spread, skewness and kurtosis (Spencer and Barrett 1984).

#### A.8.2 OPTIONS 1, 2 & 3: (CONTOURING)

After selecting any of the contouring options (1, 2, & 3), the RS menu (see p. 27–28 for more details) allows you to access ANALYSIS OPTIONS (by selecting **A**) and to output MATRIX files (by selecting **M**).

In option 2 you select edges in the same way as in convex polygons.

#### MATRIX FILES

The programme estimates a matrix of fix density values at intersections on an arbitrary grid. As matrix estimation is time-consuming, you can choose to output matrices for use in repeated analyses. If you select **M** in the RS menu, you will be asked to give a filename. This matrix file can be loaded

instead of a fix file in future analyses. In this case the first screen shows the analysis method that was used to create it. If you select **F2** for further analyses after the first run has finished, the matrix will also be loaded automatically. You can then select either option 1 or 2 from the harmonic mean analyses sub-menu. If you choose **A** from the RS menu while using this facility, you only have to choose contour percentages because the other options relate to calculation of the matrix.

#### ANALYSIS OPTIONS

In Harmonic Mean analyses, as in other areas of RANGES V, you can save time and keep the defaults by not selecting ANALYSES OPTIONS. If you do select **A** the following choices will be displayed:

**PRESS <RETURN> FOR CONTOURS FITTED TO FIXES**  
(with 100% contour through outermost fix)  
**PRESS 1 FOR CONTOURS MODELLED ON THE**  
**FIX DENSITY ALONE** (with 99% outer contour)

#### SHOULD FIXES BE:

- 0 Centred between grid intersections (NB grid-size effects)
- 1 unmodified (NB resolution-scale effects)

#### GRID SIZE

By default, the grid has 40 x 40 cells. Press **<RETURN>** to confirm this size. Give a lower value (eg 20 for a 20 x 20 grid) for a faster run with lower accuracy, or give another value of up to 50.

**PRESS 1 TO FREEZE GRID**  
(even if some contours extend beyond it)  
**OR <RETURN> FOR EDGE DETECTION AND RESCALING**

#### EXPLANATION OF ANALYSIS OPTIONS

##### 1. Contours fitted to fixes vs contours modelled on fix density alone.

Contours may be fitted to include the selected proportion of fixes, in the same way that edges are fitted in polygon analyses. However, contours can also be fitted by using the fix density distribution alone, as in ellipse

analyses. In this case, the contours estimate the probability of including a particular proportion of fixes and may include more or less than the proportion of fixes recorded.

This option is included in the contouring routines (harmonic mean and kernel options) for consistency with the approach used in plotting ellipses and in other packages. As explained in the section on ellipses, the outermost line (in this case a contour) is at 99%, because the fix density at 100% would be infinitely small.

## 2. Fixes centred between grid intersections vs unmodified fixes

The original approach for this analysis is used if you select option 1. The density matrix for harmonic mean contouring is estimated by summing  $1/d$  (i.e. the inverse distance of the fixes) from each density-grid intersection. This truncates  $1/d$  at the minimum tracking resolution. Unfortunately,  $1/d$  tends to infinity with increasing fix proximity to intersections. Therefore, Dixon & Chapman (1980) set  $1/d$  to a maximum of 1, for fixes with an assumed tracking accuracy of 1m.

The results of this implementation depend on the use of an appropriate tracking resolution (see the Explanatory Note). The default (by pressing ↵) uses the method of Spencer and Barrett (1984) to avoid the necessity of having a correct resolution. It does this by treating fixes as if they were centred between the four nearest grid intersections. This produces reasonable contours for poorly defined data, but the analysis becomes sensitive to the distance between intersections.

## 3. Grid size

Contouring is most detailed when there are small distances between grid intersections, i.e. many grid cells. Therefore, RANGES V has a default 40x40 grid. Grids with fewer cells will give faster analysis runs but less detail. There is an upper limit of 50x50 because of memory constraints.

## 4. Freezing the grid vs edge detection and rescaling

You can freeze the grid in analysis options. However, the outer contour may extend beyond the grid edges and be truncated. The default slightly increases the run time because it checks that the contours do not extend beyond the edge of the grid at the start of each range. If they do, the grid will re-scale automatically until all the contours are complete.

## CONVERSION TO POLYGONS

When contour edges are filed, they have to be converted to a continuous polygon at the end of a run. If the non-stop run is selected, this process occurs immediately after the run; otherwise a key must be pressed to continue the conversion.

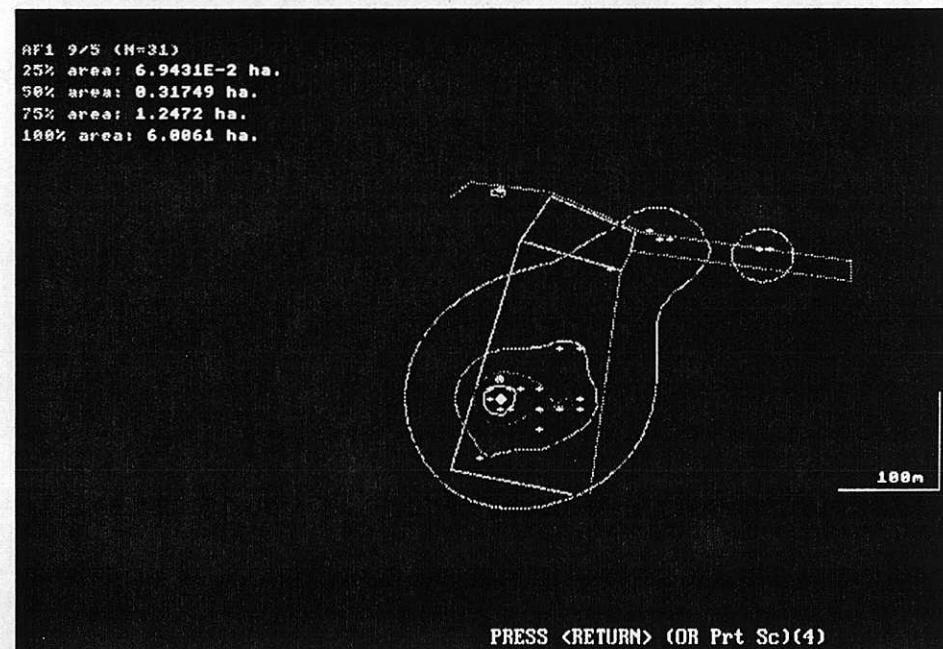


Figure 18. Analysis results screen: 25%, 50%, 75% & 95% harmonic mean contours for AF1 in FIXFILE\SQUIRREL

## Explanatory note: resolution-scale and grid size effects in harmonic mean contouring

All implementations of harmonic mean contouring are likely to give slightly different results for the same set of data. At least, this is due to differences in the scale of the grid used to estimate fix density, and to movement at the grid's origin (southwest corner). In the original implementation by Dixon and Chapman (1980), the grid was scaled with 10 units of tracking resolution between intersections. This was assuming a relatively high tracking accuracy for their hare data. The squirrels in SQUIRREL\FIXFILE and blackbirds in BLAKBIRD\BLACKFIX were tracked with 3-element Yagi antennas from distances of less than 100 m, so it is reasonable to claim a 10 m tracking resolution. For the buzzards in BUZZARD\BUZZARDS that were usually tracked from within 2 km using a 6-element Yagi, 100 m is appropriate. The range widths in those example files are 100-360 m, 110-330 m and 900-4500 m, respectively, as can be seen by choosing Convex Polygons in Range Analyses and then selecting Range Area Statistics. The ranges therefore had widths of 10-36, 11-33 and 9-45 resolution units, so that intervals of 10 resolution units between grid intersections would give very coarse contour plots. Values greater than 100 resolution units across a range are only found for very mobile species, tracked to 100 m accuracy over large ranges.

If the number of grid intersections is held constant, the number of resolution units per intersection changes from range to range. It is quite usual for the area being covered in a particular season to vary 5-fold between individuals. A 5-fold increase in range size causes a 5-fold increase in the number of resolution units between grid intersections. The effect of this on centred and uncentred fixes can be seen by changing the scale in the file BUZZARDS. Computations in Harmonic Mean analyses are based on units of tracking resolution, so rather than multiply all distances by 5, it is convenient to keep area estimates comparable by changing only the tracking resolution. To do this, create a new file with the EDITING option (Main Menu 2): select the merge function (option 3), specify BUZZARDS as the input file and BUZ20 for output. Make no changes until you get to the scale menu, and then change only the tracking resolution, from 100 m to 20 m. Whereas a 1200 m north-south spread covers 12 resolution units of 100 m in BUZZARDS, BUZ20 covers 60 units, equivalent to 6000 m at 100 m resolution.

### Effect on uncentred (unmodified) fixes

Go to Harmonic Mean analysis in Range Analyses, select BUZZARDS as the input file, Contours at 5% intervals and utilisation plots (option 2) and press A on the RS menu. Choose unmodified fixes and a 50x50 grid. When the first range has been processed, note that the area estimated for the 95% contour is 99 ha. Now repeat the process (unmodified fixes, 50x50 grid) for BUZ20. Note how contours tend to

draw round individual fixes, and the 95% area estimate is reduced to 43 ha. With 5 times as many resolution units,  $l/d$  is decreasing with distance from grid intersections 5 times as fast as in BUZZARDS, which emphasises the influence of nearby fixes on the score at each intersection.

If you make a new file (BUZ5) by claiming a 5 m resolution for the tracking, the 95% area estimate falls to just 15 ha for a 50x50 grid, compared with 42 ha for a 40x40 grid! Much of this difference is caused by re-scaling of the grid, which has moved the intersections, such that most fixes lie close to intersections on the 50x50 grid. With 5 m tracking resolution, there are about 10 resolution units per intersection interval (as in the original implementation). This means that moving the origin by 5 units could cause the maximum contribution of a fix to the density function at its nearest intersection to vary between 1 (the maximum value of  $l/d$ ) and 0.141 ( $1/\sqrt{50}$ , the diagonal distance from a corner to the centre between intersections).

### Effect of grid size on fixes centred between grid intersections

To avoid the problems with scale and origin-movement of the grid, Spencer & Barrett (1984) suggested that all fixes be relocated by the analysis to the centre between the nearest four intersections. If you try BUZZARDS and BUZ20 (and BUZ5), with fix-centring (the default), the 95% area should in each case be 51 ha for the 50x50 grid. Unfortunately, the centring process means that the  $l/d$  contribution of fixes to the density function at nearby intersections goes up in discrete steps that depend on grid-size, and there is still a different estimate for a 40x40 grid (65 ha), rising to 91 ha for a 20x20 grid. It is therefore accepted practice to specify a standard grid size, for example of 25x25 (Larkin & Halkin 1994), to maximise comparability within and between different species. Implementations may differ in whether the quoted size includes or excludes a "contour-completion" boundary. In RANGES V, the proportion of grid covering the maximum east-west or north-south range dimension is 70%, so a (frozen) 36x36 grid gives 25 intersections across the range itself. Implementations may differ in whether the quoted size includes or excludes a "contour-completion" boundary.

### In conclusion

Harmonic mean analyses with fix centring are sensitive to grid size, and the original approach (unmodified fixes) is sensitive to grid movement and assumptions about the tracking resolution. These problems stem from the need to truncate the contribution of  $l/d$  to the density matrix for fixes close to grid intersections. Note that the Gaussian estimator used in other Kernel Analyses does not require truncation and therefore avoids these pitfalls.

## ANALYSIS RESULTS

The results screens for options 1 & 2 are similar to those for convex polygons. See fig. 18.

## A.9 KERNEL ANALYSES

Use option 6 of the RANGE ANALYSES menu

Strictly speaking, kernel analyses include the harmonic mean approach. Worton (1989) introduced the concept of using a function with a negative exponential term for fix distances. This is a mathematically robust kernel that produces more consistent results than harmonic mean contouring.

Fix densities at grid intersections are derived using a bivariate normal kernel estimator. This is less grid-dependent than the harmonic mean function. There is therefore no need to centre fixes in grid cells, and the result is quite similar for 10x10 and 40x40 grids.

- After the data filenames have been entered, the programme displays a sub-menu with options identical to those for HARMONIC MEAN ANALYSES (see p. 37).
- The RS menu is the same as for HARMONIC MEAN ANALYSES, including the option of saving the matrix file. The only exception is that the Analysis options omit the choice of whether to centre fixes in grid cells; instead, you can choose a *smoothing factor*.

### SMOOTHING FACTOR:

Press <RETURN>for SD/Sixth root N),  
or choose a multiple of this (0.1 [tight] - 2 [loose]),  
or press L for Least Squares Cross Validation

- You are then given the sub-menu, shown below

0 for fixed kernels  
1 for tail-weighting (adaptive)  
2 for core-weighting

## ANALYSIS RESULTS

The results screens (fig. 19) are generally similar to that displayed in HARMONIC MEAN ANALYSES (see p. 38).

If you have chosen to use least squares cross validation the message "OPTIMISING THE SMOOTHING CONSTANT" appears while the programme is running and the value of the *smoothing factor* (*h*) is then displayed. If the constant is shown "x1", the process has not found an optimum value and has taken the default.

### Explanatory note: smoothing factor multiple

The initial choice of smoothing factor multiple is standard deviation  $/N^{1/6}$  where  $N$  is the sample of fixes. It can be multiplied by 0.2 to 2 to vary the effect. Values less than 1 will fit contours more neatly to high density areas of the matrix and values greater than 1 will cause contours to flow more into low density areas.

Least squares cross validation provides an objective method of choosing an optimal smoothing factor. It starts at 0.25x the smoothing factor multiple and then increments by steps of 0.05 until the values of the multiple reaches 1. The optimal value is used if a minimum least squares value is found, if not the original smoothing factor multiple is used.

### Explanatory note: fixed vs adaptive kernels

The adaptive kernel technique estimates values for the density matrix, and then weights them to smooth the density gradient in the tail of the distribution (see Worton 1989). This approach initially appeared promising, but may produce unacceptable expansion of the outermost contours. To emphasise the core of the distribution, an inverse of the original weighting function has been provided. In adaptive kernel analyses, it is difficult to predict contour positions before a run has finished. Even with edge checking, the outer contour may be truncated slightly at the grid edge. However, the effect is slight (i.e. <5% of the area).

## B. UTILISATION AND INCREMENT PLOTS

Use option 4 of the Main Menu

This part of the program is for use with utilisation and increment files produced in Main Menu 3 - RANGE ANALYSES.

When you type in your filename for this plot, the programme will recognise it as a utilisation, or incremental file.

The RS menu that follows includes the option **M** TO SET MEANS AND LIMITS. Selecting this gives a multi-range plot. This shows the mean values (and 95% confidence limits, for utilisation distributions) for all ranges in the file. If instead, you use the *default*, the incremental area or utilisation distribution plots are displayed for each range in sequence through the file.

- Note that you can also get DXF graphics output by selecting **G** in the RS menu. This file can contain plots for several ranges, offset from each other.

The routine produces a graph for increment plots and a graph followed by a table for utilisation files.

### B.1 UTILISATION PLOTS

Examination of utilisation plots (Ford & Krumme 1979) provides a method of deciding on the percentage of fixes which define a core range. A perfect, objective core estimation technique has still to be developed, but this method can give a good indication.

#### Explanatory note: calculation of utilisation plots

The means and confidence limits are estimated using logarithms for area values and arc-sine transformation for percentages or proportions.

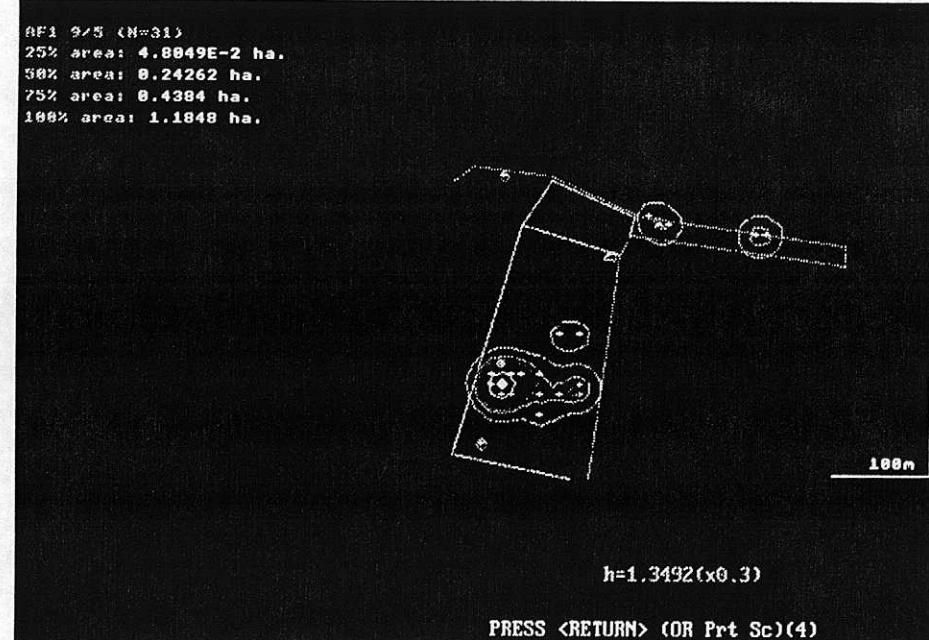


Figure 19. Selected contours produced by kernel analysis with an optimised smoothing constant (x0.3 of the initial choice) for AF1 in SQUIRREL\FIXFILE

- The utilisation distributions of ranges can be examined singly, or as multiple plots.

### SINGLE RANGES (THE DEFAULT)

If there are a few fixes far from the range centre, the slope of the plot is initially steep, but becomes shallower when only the core fixes remain. This *slope discontinuity*, if present, is a useful indicator of how many fixes constitute the core. Discontinuity tends to be most marked in cluster analysis, which is particularly effective for eliminating outliers, but is reduced by the smoothing in contour models

#### • Examples of interpretations of plots

1. A range without clear slope discontinuity, and a maximum size similar to the core range for other animals. This indicates that no excursive activity was recorded for that animal.
2. No slope discontinuity in a plot produced from cluster analyses, but discontinuity in a peeled convex polygon plot produced from the same range. This suggests that this range also lacks outlying fixes, but has >1 well-defined core.

### THE MULTI-RANGE PLOT (SELECTED WITH M IN THE RS MENU)

This can also be used to indicate range cores. A multi range plot and its statistics are shown in figs. 20 and 21. If all the animals are behaving similarly, the variance in range size tends to a minimum at the percentage of fixes which excludes most of the excursive activity. This is because range cores of different animals tend to be more similar in size than their excursive areas.

To help detect this effect, multi-range analyses also display a second graph (fig. 22) which shows the S.E. as a proportion of the mean area for each core % (the coefficient of variation).

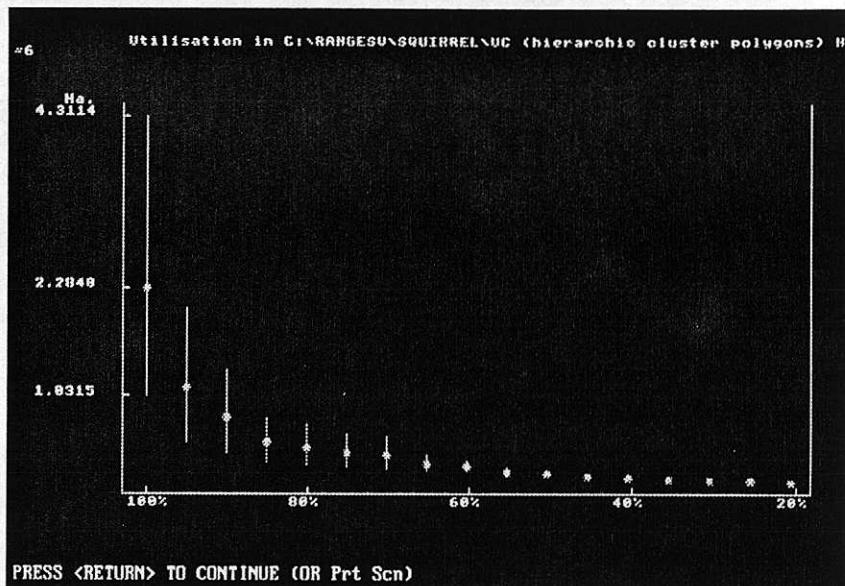


Figure 20. Multirange utilisation plot of SQUIRRELUC

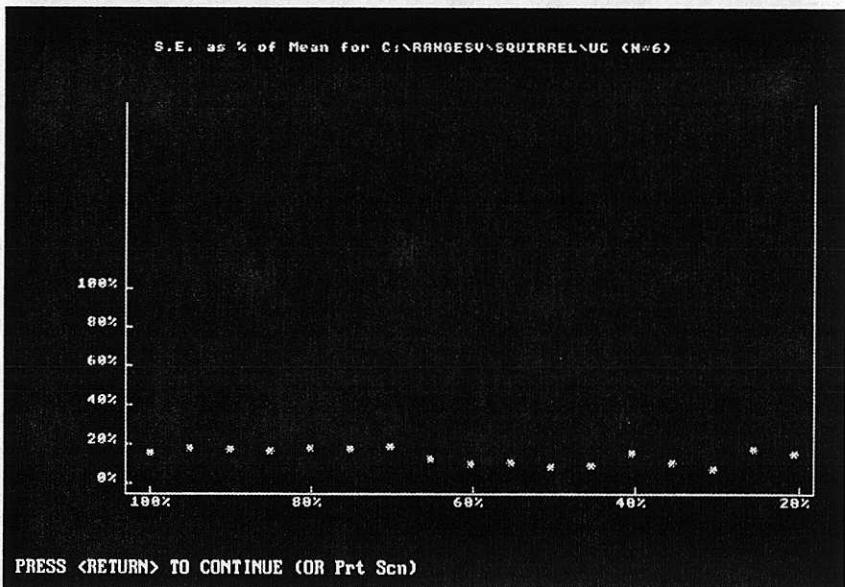


Figure 21. Coefficient of variation for each core % of the multirange utilisation plot of SQUIRRELUC

%	area (ha)	nmax	95% C.L.	se/mean	nuclei	part-area	S-fixes	S-area
188	2.20	188.00	187-189	0.16	1.17	8.95	1.00	1.00
98	2.20	200.00	199-201	0.17	1.22	8.95	1.00	1.00
95	2.49	241.00	239-253	0.17	1.22	8.95	1.00	1.00
90	2.44	231.00	229-250	0.18	1.22	8.95	1.00	1.00
78	2.25	195.00	193-200	0.19	1.22	8.95	1.00	1.00
65	2.24	133.00	131-135	0.19	1.22	8.95	1.00	1.00
60	2.28	133.00	131-135	0.19	1.22	8.95	1.00	1.00
50	2.12	100.00	98-102	0.19	1.22	8.95	1.00	1.00
45	2.12	99.00	97-101	0.19	1.22	8.95	1.00	1.00
35	2.12	99.00	97-101	0.19	1.22	8.95	1.00	1.00
25	2.12	99.00	97-101	0.19	1.22	8.95	1.00	1.00
20	2.12	99.00	97-101	0.19	1.22	8.95	1.00	1.00
15	2.12	99.00	97-101	0.19	1.22	8.95	1.00	1.00
10	2.12	99.00	97-101	0.19	1.22	8.95	1.00	1.00
5	2.12	99.00	97-101	0.19	1.22	8.95	1.00	1.00
0	2.12	99.00	97-101	0.19	1.22	8.95	1.00	1.00
PRESS <RETURN> TO EXIT								

Figure 22. Statistics for the multirange utilisation plot of SQUIRREL\UC

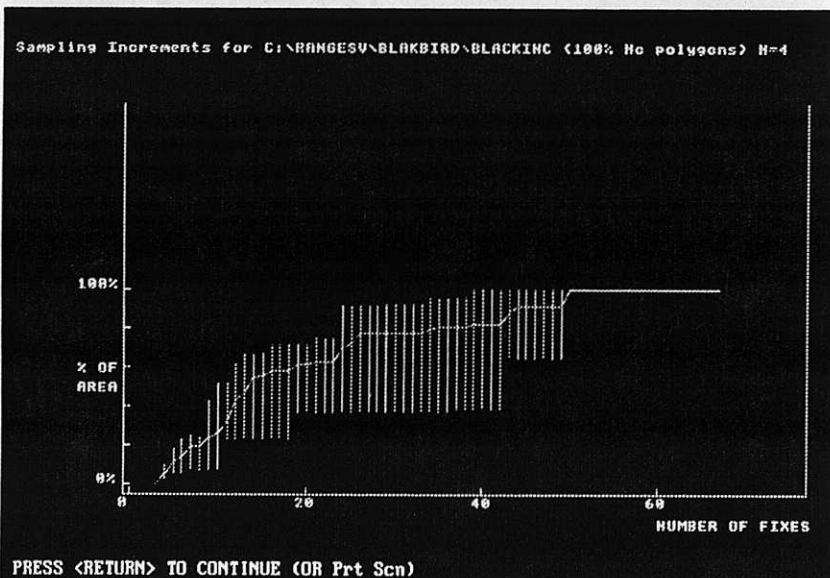


Figure 23. Multi-range plot of sampling increments for BLAKBIRD\BLACKINC (100% Fc polygons) N=4

### Explanatory note: cluster statistics

These give you the number of nuclei, the partial area, and Simpsons' index of diversity for numbers of fixes, and areas, in the cluster.

Partial area is 
$$\frac{\Sigma \text{area of separate cluster polygons}}{\text{area of a single polygon around all the nuclei}}$$

This gives an index of patchiness which is 1 for a single nucleus and less than 1 for a patchy range.

Simpsons index is a means of comparing clusters. A high value indicates that areas, or numbers of fixes, differ greatly between clusters.

### STATISTICS

Both single and multi-range plots are followed by a screen showing the mean values and percentage of total area in the core, for each percentage of fixes. These provide indices of excursive activity.

Utilisation files produced by *cluster analysis* also list cluster statistics for each core percentage (see fig. 22).

### B.2 INCREMENTAL AREA PLOTS

With this option, you can examine how the range area changes as successive fixes are added. In a pilot study, this helps to decide how many fixes are needed to define each range.

- Note that all cores, and outer polygons based on density estimates (ellipses and contours) may decrease in size after an initial increase. This happens when an increase in density of core fixes reduces the influence of outliers.
- Multiple plots show the spread of values as vertical bars (fig. 23).

### **Explanatory note: how incremental plots are created**

An outline is drawn around the first three fixes. Successive fixes are plotted one by one, and an outline drawn each time, until all the fixes in the range have been added.

## **C. OVERLAP ANALYSES**

*Use option 5 on the Main Menu*

The OVERLAP ANALYSES menu is shown below:

### **CHOOSE:**

#### **0 TO DISPLAY/PLOT OVERLAP OUTLINES**

##### **TO MAKE AN OVERLAP MATRIX:**

- 1 OVERLAPPING RANGE OUTLINES**
- 2 OVERLAPPING FIXES ON OUTLINES**

#### **3 TO EXAMINE AN OVERLAP MATRIX**

**NB.**      **0 & 1 RUN ONLY WITH EDGE FILES**

**2 RUNS WITH EDGE AND FIX FILES**

**3 RUNS ONLY WITH OUTPUT FROM 1 & 2**

### **C.1 OPTION 0: TO DISPLAY/PLOT OVERLAP OUTLINES**

This can be used for displaying polygon or isoline outlines from edge files, and for filing selected edges for further analysis or export.

The display function makes it possible to see the habitat within a range or the extent of overlap between ranges (fig. 24). Ranges can be differentiated by different colours and line types, which can be set to your preference.

- ☞ After entering the edge filename, and the map filename if required, the RS menu (see pp. 2, 27–28) appears, including the options:

**F FILE EDGE COORDINATES**

**G FILE EDGE GRAPHICS**

**S SELECT EDGES**

**R SELECT RANGES**

Note that option **S** will only be present for files with multiple cores for each range, and **R** is only available for files with >1 range. **R** can be used to produce overlap outlines from a limited number of ranges in your file.

- A DXF file can be produced by choosing to file *edge graphics*. If you use a background map of outlines or habitat shapes, the edge and map graphics will file together, with the scale bar as shown on the screen. The screen coordinates are used which are usually convenient for import to graphics packages. If you want DXF files with the original coordinate values for fixes, maps and range edges, these should be exported from the File Manager (see p. 22).

- ☞ The next screen will depend on whether you have chosen to display a habitat (coloured) map or not. Note that if you have a map named "KARTA" (as in the example directory SQUIRREL), this will plot by default. This can be avoided either by changing its name or by giving a non-existent filename.

### **PLOTTING RANGES WITHOUT A MAP, OR WITH AN OUTLINE MAP**

Here there are two choices which allow you to choose how to display the ranges:

**PRESS 1 FOR DOTTING THE FIRST AGE CATEGORY  
OR <RETURN> FOR DOTTING ACCORDING TO SEQUENCE**

**PRESS 1 FOR ONE COLOUR PER SEX, OR  
<RETURN> FOR INDIVIDUAL COLOUR SHADING**

- Note that if you press ↲, for dotting according to sequence, this *only* works if **E** to enlarge, has been selected in the RS menu. If this has not been selected, all the ranges will plot as solid lines. If it has been selected, the ranges will plot in the following sequence: solid; dashed; dotted; dot-dashed.

The colouring default is to plot each range with a different colour. There are six colours available for each sex, and these are plotted with lines that change after each sequence of six through solid, dashed, dotted, to dot-dashed. This means that you can distinguish 24 individuals of each sex.

By selecting 1 in the second option, you can select one colour for each sex.

#### **PLOTTING RANGES WITH A HABITAT MAP**

With a habitat (coloured) map, range edges are always plotted as thick lines in the last colour of the 15-colour palette. This is a good reason to leave this colour as white, or as another bright colour.

- Here a screen is displayed which gives the options of setting the required line types.

RANGE OUTLINES CAN BE  
DOTTED TO SHOW AGE OR SEX

PRESS 1 FOR DOTTING THE FIRST AGE CATEGORY  
OR 2 FOR SOLID LINE FEMALE & DOTTED MALE  
OR <RETURN> FOR DOTTING ACCORDING TO SEQUENCE

Pressing ↲ gives the default, a repeating sequence of solid, dashed, dotted, and dot-dashed lines to distinguish consecutive animals.

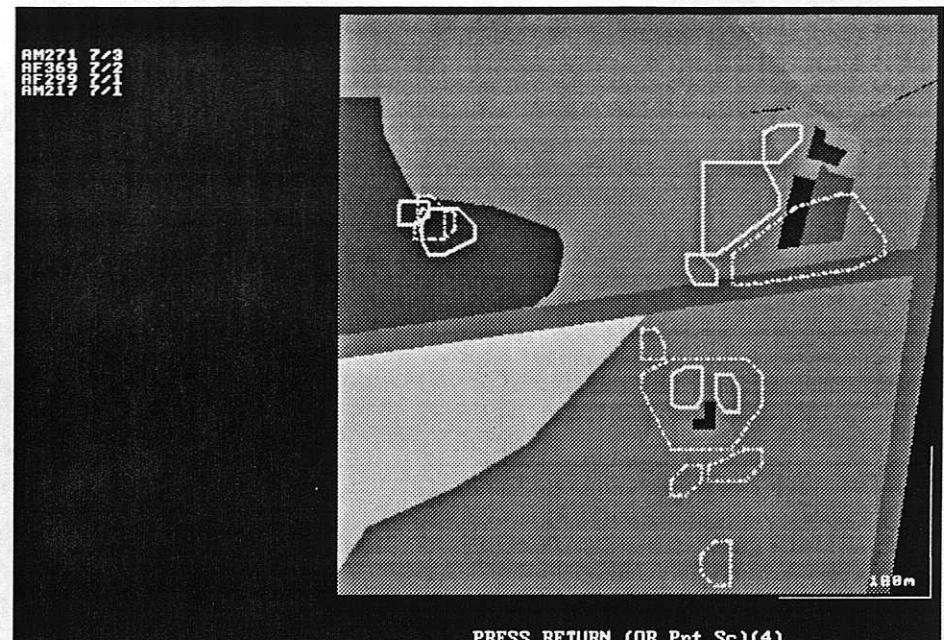


Figure 24. Overlap plots for BLACKBIRD\BLACKCLU

## **C.2 OPTIONS 1 & 2: TO MAKE AN OVERLAP MATRIX**

### **C.2.1 OPTION 1: OVERLAPPING RANGE OUTLINES**

This produces a matrix of the percentage overlap of range B on A, and of A on B, for each pair of ranges. A routine scans the pixels in the 'window' that contains each range. The screen display shows each pair of ranges. The first range is plotted in white and the second overlaid in black.

Note that calculation of overlaps for complex contoured shapes can be a slow process. This is because the routine must allow for any possible scale or shape. If a contour contains a "hole", this is plotted separately and its overlap subtracted from the overlap of the outer shape.

The RS menu gives the option **R** TO SELECT RANGES. This allows you to compare specific animals without having to split the fix file in file manager.

At the end of the processing of both options 1 & 2, the input and output filenames are displayed with the title of the process that has just run. The matrix file is *always saved* for use in further analyses. It can be displayed using overlap analysis option 3 (fig. 25).

### C.2.2 OPTION 2: OVERLAPPING FIXES ON OUTLINES

This option estimates the proportion of fixes from one file which fall within the edges of another file. It is much faster than the assessment of area overlaps.

### C.3 OPTION 3: TO EXAMINE AN OVERLAP MATRIX

To examine a matrix you have created, or to look at an overlap distribution (fig. 26), first enter your matrix filename then select either **D** for SUM DISTRIBUTION or **M** for VIEW MATRIX from the RS menu. Note that these selections are mutually exclusive. Therefore, **M** and **D** toggle on the menu. This allows the selected options to remain selected through repeated runs.

The **P** TO PRINT option is also very useful in this option to provide hard copies of the matrices.

#### SELECTING RANGES

Ranges can be selected by pressing **R** in the RS menu. With this option you will be asked to choose between the following categories:

- 1 RANGES WHICH OVERLAP OTHERS**
- 2 RANGES WHICH ARE OVERLAPPED**
- 3 BOTH CATEGORIES TOGETHER**

OUTPUT FROM 90% hierachic cluster polygons FILE C:\RANGES\BLAKBIRD\BLA90MAT  
RANGE AREAS IN ROWS ARE OVERLAPPED BY RANGE AREAS IN COLUMNS

AM271	AF369	AF299	AM217
AM271	100.0	10.8	0.0
AF369	10.7	100.0	0.0
AF299	0.0	0.0	100.0
AM217	5.4	6.0	13.8

PRESS <RETURN> TO EXIT ..

Figure 25. Overlap matrix for BLAKBIRD\BLACKCLU

PERCENTAGE OVERLAP OF RANGE AREAS ON RANGE AREAS  
FROM 90% hierachic cluster polygons FILE C:\RANGES\BLAKBIRD\BLA90MAT

4 PAIRS WITHOUT OVERLAP

>0-	10-	20-	30-	40-	50-	60-	70-	80-	90-
10%	20%	30%	40%	50%	60%	70%	80%	90%	100%
4	3	0	0	0	0	0	0	0	1

Average for 8 overlappers = 20.36%

PRESS <RETURN> TO EXIT ..

Figure 26. Summary distribution for range overlap for BLAKBIRD\BLACKCLU

After making a first choice, the menu is shown again, giving the chance to make another selection or to exit.

#### VIEWING A MATRIX

The overlap matrix shows the percentage of areas in rows overlapped by those in columns (fig. 25).

#### SUM DISTRIBUTION

Here the percentage overlaps for all ranges in the file are summarised in a table (fig. 26). This gives the number of ranges in the 0-10% overlap group, the 10-20% group etc..

## D. INTERACTION ANALYSES

Use option 6 in the Main Menu

The general purpose of these routines is to analyse spatial interactions between animals or between patterns of locations (spatial and temporal) for individual animals. The INTERACTION ANALYSES menu (fig. 27) includes 4 different techniques.

- All the results can be filed in spread-sheet format for further analyses, and autocorrelation plots can also be saved as DXF files to produce figures in graphics packages.

### D.1 OPTION 0 “AUTOCORRELATIONS”

Autocorrelation analysis examines the way that distances between fixes change with sampling intervals. It is, therefore, useful for estimating the optimal time interval to use between recording consecutive fixes.

- As time intervals are integral to the analysis, suitable fix files must include correctly labelled time FQVs (see p. 10–11).

#### THE PROCEDURE FOR RUNNING AUTOCORRELATIONS

- ☛ After the name of the required fix file has been entered, the RS menu is displayed.
- ☛ If you select A for analysis options the following options are given:

IF DATA ARE FROM SEPARATED SESSIONS OF  
CONTINUOUS RECORDING, GIVE THE MINIMUM  
INTERVALS IN HOURS BETWEEN SESSIONS.  
FOR OTHER DATA FORMATS, PRESS <RETURN>

PRESS <RETURN> FOR 5-MINUTE SAMPLE INTERVALS  
OR GIVE ANOTHER TIME INTERVAL (IN MINUTES)

PRESS RETURN TO PLOT FOR UP TO 48 HOURS,  
OR GIVE ANOTHER VALUE IN HOURS

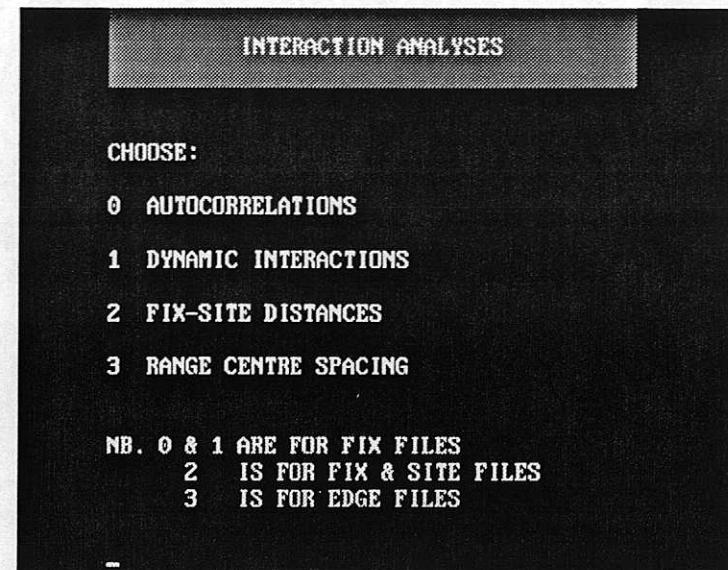


Figure 27. Interactions analyses menu

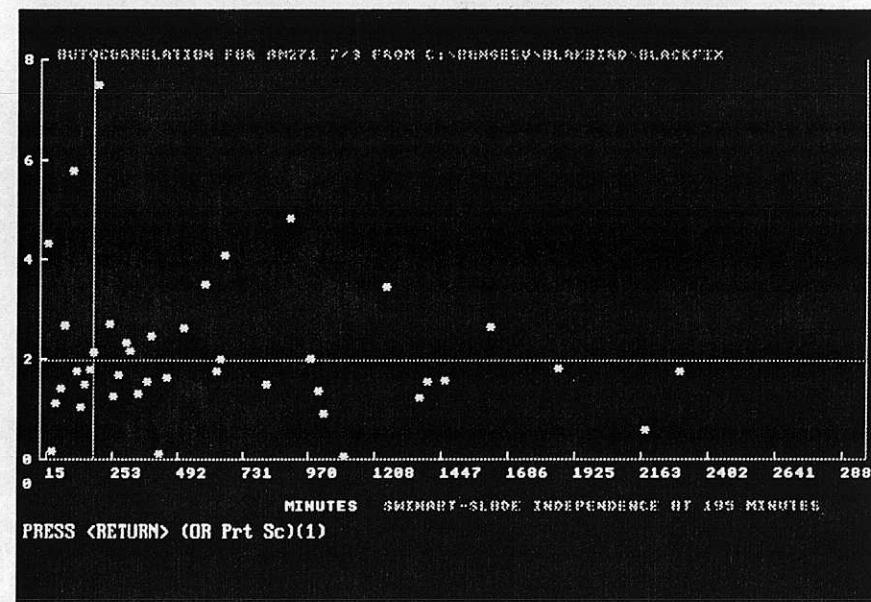


Figure 28. Autocorrelation plot with 15 minute sample intervals for BLACKBIRD\BLACKFIX

### Explanatory note

Following the format used by the originators of the technique (Swihart & Slade 1985), the programme plots increasing sampling intervals in minutes on the *x*-axis and Schoener's index on the *y*-axis (fig. 28).

Schoener's index indicates the degree of independence between distance and time. If the value of the index is low, this indicates a high correlation between distance and time, e.g., because during short sampling intervals the animal did not have time to move far before it was next located.

Sampling intervals are by default in multiples of 5 minutes. The programme works through the sequence of fixes from start to finish for each set of sampling intervals. It then tests for correlations between distance and time for this set. First it tests for all fixes from 2.5 to 7.5 minutes apart. It then tests for those between 7.5 to 12.5 minutes apart and so on up to the default maximum of 48 hours apart.

As sampling intervals between fixes increase on the *x* axis, the distances between the fixes usually become less correlated with time, so the value of Schoener's index becomes greater. The originators proposed that the sampling interval at which 3 consecutive values on the *y* axis are higher than 1.96 represents the time at which distances between fixes no longer depend appreciably on time. A line is drawn across the graph at this level. If your aim is to base range estimates on as few fixes as possible, this method can estimate the minimal interval to use between taking consecutive fixes.

In practice, independence levels for many animals never consistently reach 1.96. Quite often, the index peaks and then declines again, showing that the animal's locations tend to become correlated again after a particular time interval. In this case, the time to reach the peak may be taken as the optimal interval for sampling locations with minimal data redundancy.

The first section allows you to change the default, which assumes that the whole data set is continuous. If you specify 8 hours as the minimum time between sessions, the routine would only use intervals between consecutive locations of less than 8 hours. If there are gaps between recording sessions, you are advised to define a minimum time interval between consecutive sessions. This prevents gaps between recording sessions being interpreted as an animal failing to move.

The second section allows you to alter the length of the sample interval. This is by default based on multiples of 5 minutes (5, 10, 15 etc.). Choosing an appropriate interval is important. If, for example, fixes have been taken approximately one hour apart, there may be too few fixes to estimate in Schoener's index using 5 minute sampling intervals (i.e., 57.5 to 62.5, 62.5 to 67.5 etc.). However, good results may be obtained with 30 minute sampling intervals (i.e., 45 to 75 etc.).

The third section allows you to set the total length of time of the recording period to be used in the analysis. The default is to plot the estimate for 48 hours.

- The default values are appropriate for examining 24-hour timetabling. However, you may wish to set shorter times than these defaults. For example, if data are in runs of 1 hour observations, you would probably choose 1 minute intervals for a 1 hour plot (which would also automatically eliminate gaps of >1 h between observation sessions). Alternatively, if you had continuous records during 16 hours of daylight, you might want to make independence estimates within each day. To do this you could use a 16-hour plot (perhaps with 15 minute intervals) but omit non-movement for 8 hours at roost.

## D.2 OPTION 1: DYNAMIC INTERACTIONS

This analysis routine gives a single "cohesion" index, for the tendency of pairs of animals to be close together at the same time. The index tends to be most consistent if based on the geometric mean distances.

## THE PROCEDURE FOR ANALYSING DYNAMIC INTERACTIONS

- After selecting a fix file for DYNAMIC INTERACTION analyses, the following menu is displayed.

### CALCULATE INTERACTIONS FOR:

- 0 ALL ANIMALS
- 1 OVERLAP-QUADRAT ANIMALS?
- 2 RANGE-OVERLAP ANIMALS?  
(NEEDS RANGE-OVERLAP MATRIX)
- 3 ANIMALS AT THE SAME FOCAL SITE?

**Option 0** in this menu is only relevant if all the animals share overlapping ranges, for example through being a single family. If many families are combined in a file, option 3 can be used to confine the analysis to those at the same den or other focal site.

**Option 1** uses a quadrat around the W E S and N limits of ranges to select animals which have overlapping quadrats for estimation of range overlaps.

**Option 2** examines animals with ranges which overlap, and requires the input of a range overlap matrix created in main menu options 3 and 5 (see p. 45).

- After choosing one of these options, the RS menu is shown.
- Method of defining same-time locations (observations).*
- Pressing **A** for ANALYSIS OPTIONS in the RS menu gives the following choices:

### ARE SAME-TIME OBSERVATIONS DEFINED BY:

- 0 THE SEQUENCE OF FIXES?
- 1 TIME VARIABLES WHICH QUALIFY FIXES?

**Option 0** (the default) is appropriate if there are equal numbers of fixes for each animal, recorded at roughly the same time on each occasion (i.e. by repeated sampling round all the tagged animals).

**Option 1** is based on FQVs which define times.

If you use the default, the analysis will still work if a few animal locations were scored as missing (-9,-9). The missing values merely reduce  $n$  for all pairs involving that animal. If you use time FQVs, you will be asked how many minutes should be allowed between "same time" fixes before they should be treated as missing and excluded from the analysis.

- Selection of a sample of  $nxn$  to increase speed of analysis*

The programme can select at random (boot-strapping) to give a smaller sample within the set  $n \times n$ . This is useful to make analyses of large datasets run faster. Estimation of median distances between animals involves ranking observations. This becomes slow when large numbers of fixes ( $n$ ) produce even larger numbers  $n \times n$ .

Selection of a sample from  $n \times n$  occurs automatically to limit sample size if  $n \times n$  is greater than 5000. The option shown below makes it possible to give a sample size for datasets with  $n \times n$  of <5000. For instance, if each animal had 60 fixes, the following prompt would be given.

**THE MAXIMUM RANDOMISATION SAMPLE SIZE IS 3600.  
CHOOSE ANOTHER (500-3600) OR PRESS <RETURN>**

Note that you cannot select less than 500.

- Pressing **F** in the Run Specifications menu allows you to file the results of the analyses. If you choose to file results, you will be given the following options after giving the output filename:

**PRESS 1 TO FILE ALL DISTANCE ESTIMATES,  
OR PRESS <RETURN> TO FILE SUMMARIES.**

#### Explanatory note

Animals shown to share large areas in overlap analyses (6.C) may seldom encounter each other because they rarely visit the same place at the same time. Macdonald *et al* (1980) called this analysis by overlapping range outlines "static interaction" and they proposed the examination of "dynamic interaction" by looking at fixes taken at the same time. The original publication provided a test of whether 2 individuals showed significant attraction or avoidance, but this depended on two assumptions. Firstly, that fixes are statistically independent and secondly, that their distribution fitted a parametric model. RANGES V avoids assumptions about independence and distributions of fixes between single pairs of individuals. The programme provides a single statistic for each range, or in the case of Dynamic Interaction analyses, each pair of ranges, so that tests are based on ranges and not fixes (Kenward 1992, Aebischer *et al* 1993).

The RANGES V method for investigating dynamic interactions is described in Kenward *et al* (1993). The observed and possible distances between animals are compared. The mean, geometric mean and median distances are estimated between the  $n$  observed pairs of same-time fixes for animal 1 and 2. Then the equivalent values are estimated for the  $n \times n$  possible distances if animal 2 could be at any of its  $n$  used positions when animal 1 was at each of its used positions. The observed and possible distances are compared using Jacob's Index (Jacobs 1974). This gives a value of 0 if the observed and possible distances were the same, rising towards +1 if observed distances were small relative to possible distances (because the animals were usually together) or falling towards -1 if animals tended to avoid each other. This gives a single index for each pair of animals.

Summaries include range variable labels to identify each pair of animals, followed by numbers of fix pairs, followed by summary statistics. These are: number of observations, sum, sum of squares, sum of logs, sum of log squares and median. These are given first for observed distances and then for possible distances. The cohesion indices are then listed for the arithmetic mean, geometric mean and medians.

There are the same number of these variables for each pair of animals, which makes the output file suitable for exporting to a spread-sheet for further analysis.

If you press 1 the file will also contain a complete list of all observed and possible distances, ranked by size. This can be used for custom-designed analysis of distance distributions, but takes up a lot of file space.

#### D.3 OPTION 2: FIX-SITE DISTANCES

This option allows you to estimate whether an animal has been tending to approach or avoid sites associated with other animals, such as nests or scent marks. To use it, you require a fix file and a site file. The latter can have been prepared either as a fix or a habitat file. Habitat files may also be used to refine the analysis by defining boundaries for random sampling operations.

- After giving the fix input filename you will be asked to define how far from the sites a fix or random point can be before it should be excluded from the analysis. The options are given in the following menu:

##### DEFINE BOUNDARIES FOR SPACING ESTIMATES BY:

- 0 NEAREST-NEIGHBOUR (N-N) DISTANCES IN FILE?
- 1 PROVIDING A MAP/EDGE FILE FOR THE SITES?
- 2 SITE-CENTRED CIRCLES WITH N-N RADII?

Option 0 defines a boundary strip round all the sites, based on nearest neighbour distances between sites. This is the option to use if you know

of all the sites within one area, for example all the nests within a study area (fig. 30).

#### Explanatory note

The routine starts by producing a single sample of nearest-site distances for a set of random locations. It then estimates the observed distances of each fix from the nearest site for each set of fixes. The process is very similar to that used for DYNAMIC INTERACTIONS. Jacobs' Index is again used to estimate the arithmetic mean, geometric mean and median distances. The output is also the same, with options given in the RS menu for summaries or all distances.

**Option 1** uses a *habitat* or range edge (referred to in the menu as map/edge) file to define the boundaries. You will be prompted for a SITE EDGE file, and must select a habitat or edge file. If the site file was a fix file, you can prepare suitable edge files as polygons in RANGE ANALYSES (see p. 26–40). These files must have the boundary strip set to the appropriate size (p. 13 & 33).

The display during the analysis shows the area for random sampling in white; fixes or random points are only included in the analysis if they fall within this area. This option may be appropriate if your study area contained edge areas which had been searched and found to contain no sites.

**Option 2** is useful for isolated sites.

- ☛ If you choose *option 1*, then pressing **A** in the RS menu gives the opportunity to select the size of the "randomisation sample" (the number of random locations used in the analysis) see p. 49.
- ☛ If you choose *options 0 or 2*, and then press **A** in the RS menu, you are allowed to set the size of the "randomisation sample" as above. However, first you are given the following options:

#### BASE BOUNDARY-STRIPS/RADIJI ON:

- 0 HALF MEAN N-N DISTANCES?**
- 1 HALF MAXIMUM N-N DISTANCES?**
- 2 HALF MINIMUM N-N DISTANCES?**
- 3 SUPPRESSED**

The choice here depends on whether you are testing for attraction to sites, or avoidance of sites. When testing for attraction, the conservative approach is to use a small boundary around them, perhaps with option 2 or the very conservative boundary suppression of option 3. When testing for avoidance, the conservative approach is to use a large boundary, perhaps with option 1. Option 0 (the default) may be slightly biased in either direction, but is useful for an initial run, to check whether significant attraction or avoidance is likely. An example produced using option 0 is shown in fig. 29.

## D.4 OPTION 3: RANGE-CENTRE SPACING

The final interaction analysis provides tests for spacing of range-centres, using conventional nearest-neighbour analysis (Clarke & Evans 1954). The minimum input required is a range-edge file containing convex polygons, ellipses or contours (concave polygons and cluster analysis outlines lack centres). See section 6.A. on RANGE ANALYSES for details on creating these polygon files.

- ☛ A sub-menu on the first screen gives two options for defining boundaries for the assessment area:

#### DEFINE BOUNDARIES FOR SPACING ESTIMATES BY:

- 0 NEAREST-NEIGHBOUR (N-N) DISTANCES IN FILE?**
- 1 PROVIDING AN MAP/EDGE FILE FOR THE SITES?**

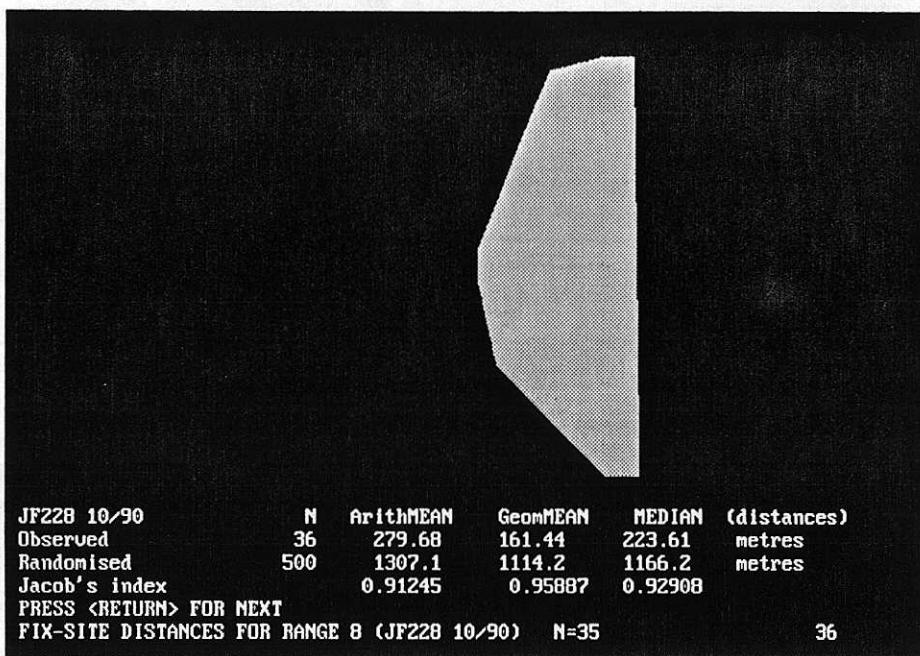


Figure 29. Fix-site distances of JF228 in BUZZARD B90FIX, in relation to nest sites in B90NEST

- If you select option 0, and then **A** for analysis options in the RS menu, you are given the option of selecting the boundary setting. These analysis options are the same as the first 3 in "Fix-site distances", p. 50.

**0 HALF MEAN N-N DISTANCES?  
1 HALF MAXIMUM N-N DISTANCES?  
2 HALF MINIMUM N-N DISTANCES?**

A large boundary (selected with option 1) gives conservative test results, but a test with the boundary based on the mean nearest-neighbour spacing is probably closest to the approach used by the original authors.

- Choosing **A** in the RS menu, for either method of defining boundaries, allows you to choose whether to set the number of random locations used in the analyses (the "randomisation sample") see p. 49.

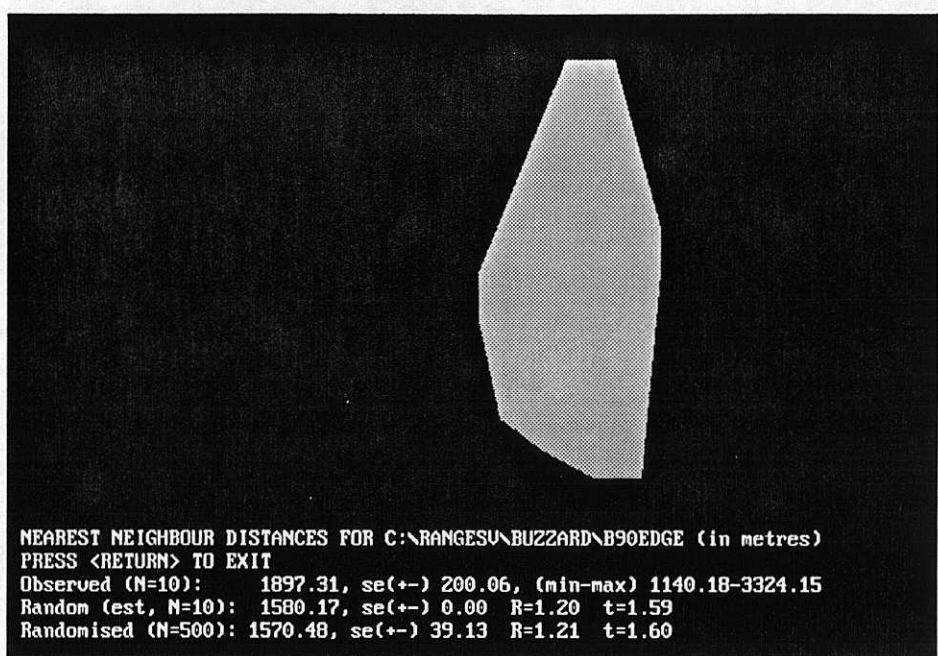


Figure 30. Nearest-neighbour distances to show range centre spacing for BUZZARD\B90EDGE

The results indicate whether centres are more regularly spaced both than an expected normal distribution, and also than a spacing based (by default) on 1000 random locations. In each case, as in the original publication, Student's t is used to test for significantly regular spacing. These results are displayed on the final screen (fig. 30) and can be filed or printed (by prior selection in the RS menu).

## E. HABITAT ANALYSES

*Use option 7 in the main menu*

Habitat analyses in RANGES V can use data from vector (line) or raster maps (e.g., remote sensed imagery). Habitat can be assessed for the whole map or in rectangular or circular sub-sections. Maps can also be used together with fix and edge files to give estimates of habitat use/ availability. The results can be saved to output files which are suitable for export to spreadsheets for further analysis.

- **The use of colour in habitat analyses**

Habitat analyses run in colour on VGA-based systems. Colours may be added to maps when they are imported, or by editing existing maps in main menu option 1. If colours are not selected, arbitrary colours are assigned from an existing palette. The system is limited to 15 colours (plus black, which is reserved for unclassified habitats).

If you have more than 15 habitat categories, some could be combined (which you would probably need to do anyway to simplify analyses) by giving them the same colour; the habitat content of both will then list under the name of the first habitat.

- **Import and use of raster maps**

Raster maps must first be imported in Main Menu 2 (see p. 23), at which time they should be given labels and colours (which can be edited in Main Menu 1). If you want to inspect a raster map, use option 0 of HABITAT ANALYSES. The whole map can be viewed at once if it is up to 400 rasters wide. Larger maps can be viewed in sections. To view them in full, use option 0 in the OVERLAP ANALYSIS menu (p. 44). In this option you must set coordinates to display the map and select E to ENLARGE in the RS menu. It is also essential to select an edge file (any will do).

- **Calculation of area of ranges and other map sections**

In all analyses, the area of ranges and other map sections is calculated from edge data, and compared with estimates produced by counting pixels to estimate the error in the pixel-based technique. After the analysis run, this error is shown on the screen adjacent to the calculated area. The error is typically less than 1%, but can tend towards 5% for very narrow ranges.

If habitats overlap, total percentage values will be greater than 100. If the total value is greater than 100% when they do not overlap, this is due to

pixel counting error. You can correct this using a simple calculation: multiply each observed value  $O_i$  by  $100 / \sum O_i$ .

- If habitat labels are numbers, they are assumed to represent density values. Output from the analysis will give an estimate of overall density in each range, in addition to the proportion and area of habitat type. For instance, if half the range was given habitat label 1.8 and the other half 0.6, the overall value would be 1.2.

- **Output files**

Output files contain 7 range label variables, and one of the following:

- the range area and the proportion of each habitat in the range
- the number of fixes and the proportion of each habitat at the fixes
- both, in sequence, when fix and edge analyses are combined.

The core values for range edges are also given. For edge files with more than one core the sequence is repeated.

The labels of the habitats used in the analysis are listed, in order, in the file appendix of the output file.

## **THE PROCEDURE FOR RUNNING HABITAT ANALYSES**

- The main menu for habitat analyses is shown below:

```
0 TO FIND HABITAT CONTENT OF A MAP
1 TO FIND HABITAT CONTENT OF RANGES
2 TO COUNT POINT SITES WITHIN RANGES
3 TO FIND HABITAT AT RANGE FIXES
4 COMBINED FIX & EDGE ANALYSES
```

Note that the maps referred to in this section can be either rasters or the vector-based habitat files created in the DATA ENTRY/EDIT MENU.

## **E.1 OPTION 0: TO FIND HABITAT CONTENT OF A MAP**

This option leads to a submenu which gives the opportunity to assess the whole map (fig 31), or habitat in sections round specific parts of the map, such as nests or dens.

- ☛ These choices appear in a submenu:

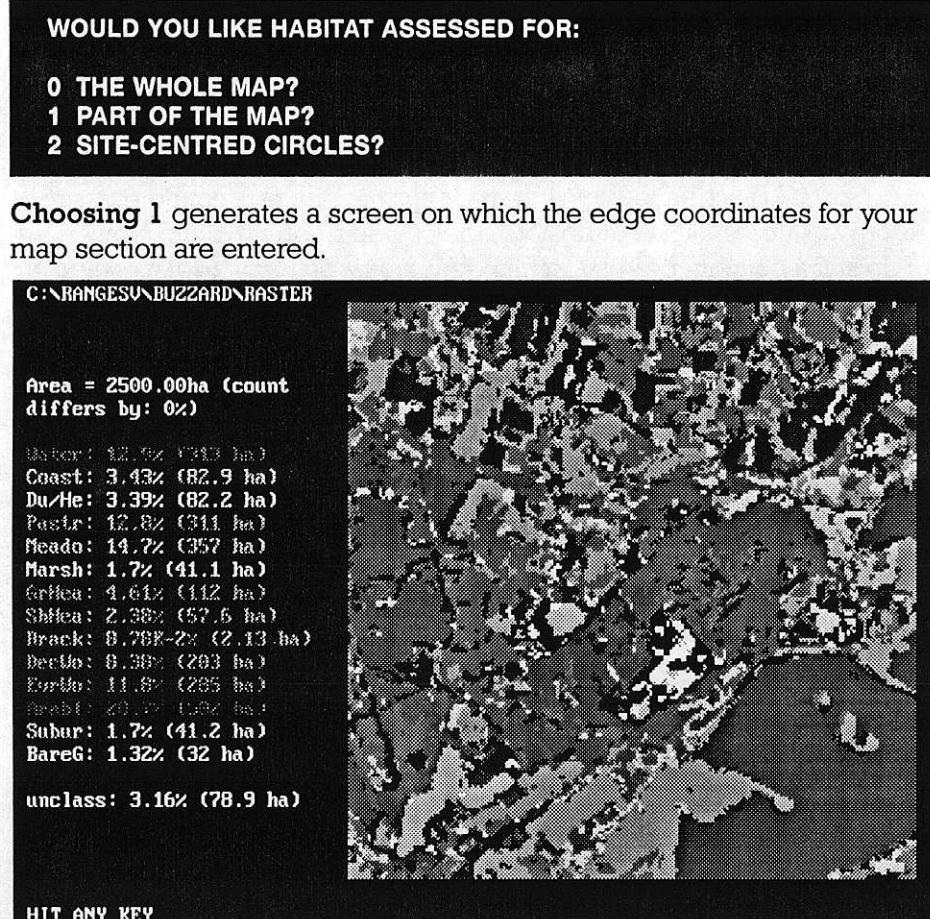


Figure 31. Habitat analysis of a raster map BUZZARD\RASTER

Choosing 2 gives a screen on which you are prompted for coordinates for the centres of circles and their radii.

- ☛ After the analysis for a map section or site-centred circle is complete, pressing ↙ takes you back to the previous screen with the opportunity to make further selections. Press F to finish.

## **E.2 OPTION 1: TO FIND HABITAT CONTENT OF RANGES**

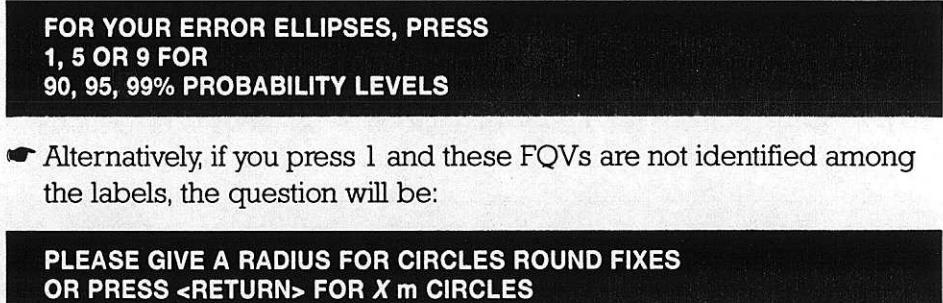
In this option you need to enter a range edge file and a habitat file. See fig. 32 for an example. A for analysis options in the RS menu gives you the choice to print summaries of the results.

## **E.3 OPTION 2: TO COUNT POINT SITES WITHIN RANGES**

This is the same as option 1, except that it uses files of habitat points rather than areas.

## **E.4 OPTION 3: TO FIND HABITAT AT RANGE FIXES**

If you choose option 3 and the fixes have associated error ellipses, such that the FQVs include X-VAR (x-variance), Y-VAR (y-variance) and COVAR (covariance), you will then be provided with an additional prompt, shown below:



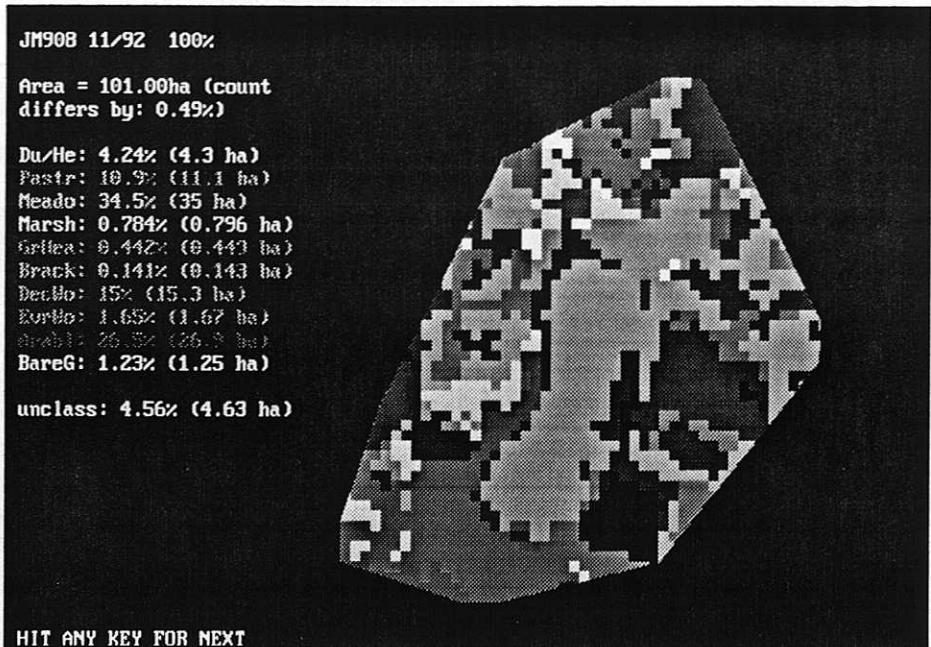


Figure 32. Habitat analysis for JM 908 from BUZZARD\BUZZEDGE and the habitat map BUZZARD\RASTER

X in this menu is half the tracking resolution in the specified file. The results of using this last option with an example file are shown in fig. 33.

This option is particularly useful for providing an average value round fixes on raster maps. Individual rasters may have been categorised inaccurately but the general area may be correct. The routine could also be used for a simple form of edge detection near fixes, by gradually increasing the assessment circle round each fix.

## E.5 OPTION 4: COMBINED FIX & EDGE ANALYSES

This assesses habitat in ranges and at fixes during the same run. After the analysis run, the display shows the preference or avoidance of habitat at fixes (with Jacob's index, values +1 to -1), compared with habitat in the range as a whole.

## E.6 THE RS MENU FOR ALL OPTIONS IN HABITAT ANALYSIS

ANALYSES options are available in the RS menu for options 1, 2, 3 and 4 in the HABITAT ANALYSES MENU. For options 1, 2 and 3, selecting A gives you the chance to print summaries of the data. For 3 and 4 (where you are assessing range fixes) you are given an additional sub-menu which allows you to choose whether to assess habitat at points at fixes or ellipses round them.

The sub-menu is shown below.

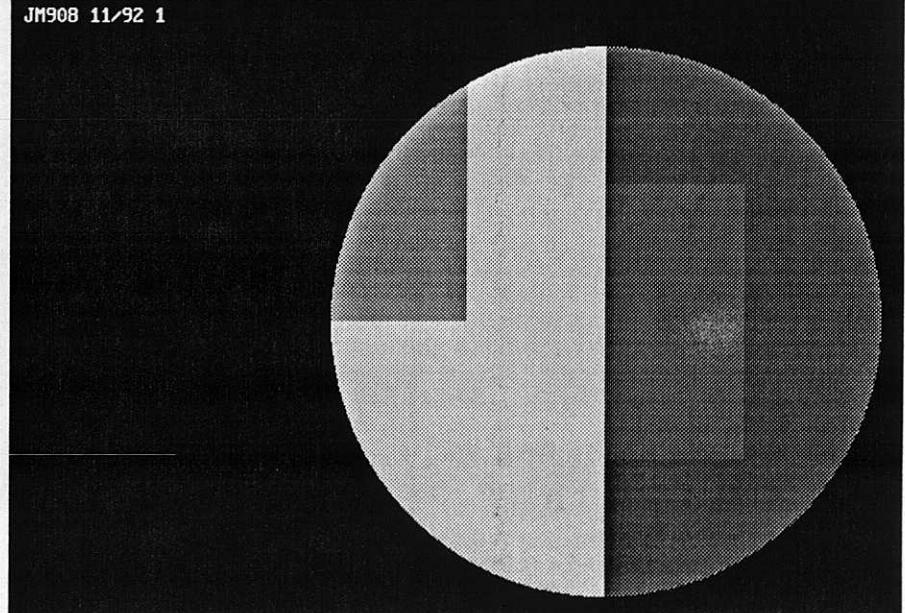
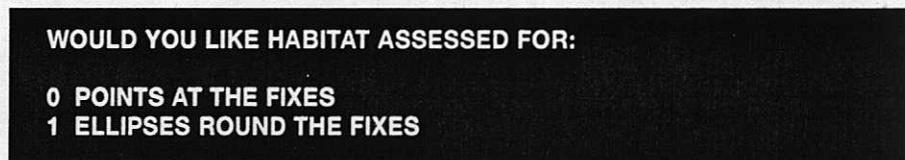


Figure 33. Habitat analysis for a 50m circle around a fix from BUZZARD\BUZZARDS and the habitat map BUZZARD\RASTER

menu provides an analysis option to save time by counting only the rasters and not pixels.

**PRESS 1 TO COUNT RASTERS WITHOUT COLOUR PLOTS**

(for shapes <400 rasters wide: faster but less accurate)

**PRESS <RETURN> FOR PIXEL PLOTTING & COUNTING**

#### Explanatory note

Raster maps only show on the screen in habitat analysis if the section chosen for display has no more than 400 rasters in width or height. This is because this maximum corresponds to one pixel per raster. With map sections larger than 400 across, habitat contents are automatically assessed by counting rasters in the map file. When analysing large maps, the screen plot is drawn without colour in order to speed processing. When map sections are less than 400 rasters in width or height, rasters are drawn as habitat squares. For smaller maps, pixel counting is feasible and is the most accurate way of assessing habitat content of the map. Note that analyses to assess areas of habitat round fixes are slow if run by pixel counting, but much faster if the option to count only rasters is used.

## 7. BIBLIOGRAPHY

---

- Aebischer, N.J., Robertson, P.A. & Kenward, R.E.** 1993. Compositional analysis of habitat use from animal radio-tracking data. *Ecology*, **74**, 1313-1325.
- Anderson, D.J.** 1982. The home range: a new non-parametric estimation technique. *Ecology*, **63**, 103-112.
- Clarke, P.J. & Evans, F.C.** 1954. Distance to nearest neighbour as a measure of spatial relationships in populations. *Ecology*, **35**, 445-453.
- Dixon, K.R. & Chapman, J.A.** 1980. Harmonic mean measure of animal activity areas. *Ecology*, **61**, 1040-1047.
- Don, B.A.C. & Rennolls, K.** 1983. A home range model incorporating biological attraction points. *Journal of Animal Ecology*, **52**, 69-81.
- Ford, G. & Krumme, D.W.** 1979. The analysis of space use patterns. *Journal of Theoretical Biology*, **76**, 125-155.
- Hartigan, J.A.** 1987. Estimation of a convex density contour in two dimensions. *Journal of the American Statistical Association*, **82**, 267-270.
- Harvey, M.J. & Barbour, R.W.** 1965. Home range of *Microtus ochrogaster* as determined by a modified minimum area method. *Journal of Mammalogy*, **46**, 398-402.
- Harris, S., Cresswell, W.J., Forde, P.G., Trewella, W.J., Woollard, T. & Wray, S.** 1990. Home-range analysis using radio-tracking data - a review of problems and techniques particularly as applied to the study of mammals. *Mammal Review*, **20**, 97-123.
- Hayne, D.W.** 1949. Calculation of size of home range. *Journal of Mammalogy*, **30**, 1-18.
- Jacobs, J.** 1974. Quantitative measurements of food selection. *Oecologia*, **14**, 413-417.
- Jamsa, K.** 1991. *DOS: the complete reference*. 3rd Ed. London: Osborne McGraw-Hill.
- Jennrich, R.J. & Turner, F.B.** 1969. Measurement of non-circular home range. *Journal of Theoretical Biology*, **22**, 227-237.
- Kenward, R.E.** 1987. *Wildlife radio tagging: equipment, field techniques and data analysis*. London: Academic Press.
- Kenward, R.E.** 1992. Quantity versus quality: programmed collection and analysis of radio-tracking data. In: *Wildlife telemetry: remote monitoring and tracking of animals*, edited by I.G. Priede and S.M. Swift, 231-246. Chichester: Ellis Horwood.
- Kenward, R.E., Marcstrom, V. & Karlstrom, M.** 1993. Post-nestling behaviour in goshawks, *Accipiter gentilis*. II. Sex differences in sociality and nest switching. *Animal Behaviour*, **46**, 371-378.
- Larkin, R.P. & Halkin, D.** 1994. A review of software packages for estimating animal home ranges. *Wildlife Society Bulletin*, **22**, 274-287.
- Macdonald, D.W., Ball, F.G. & Hough, N.G.** 1980. The evaluation of home range size and configuration using radio tracking data. In: *A handbook on biotelemetry and radio tracking*, edited by C.J. Amlaner and D.W. Macdonald, 405-424. Oxford: Pergamon Press.
- P.A. Robertson, N.J. Aebischer, R.E. Kenward, I.K. Hanski, & N.P. Williams** (in press). Simulation and jack-knifing assessment of home-range estimators based on underlying trajectories.
- Spencer, W.D. & Barrett, R.H.** 1984. An evaluation of the harmonic mean method for evaluating carnivore activity areas. *Acta Zoologica Fennica*, **171**, 255-259.
- Swihart, R.K. & Slade, N.A.** 1985. Testing for independence of observations in animal movements. *Ecology*, **66**, 1176-1184.

**Voight, D.R. & Tinline, R.R.** 1980. Strategies for analysing radio-tracking data. In: *A handbook on biotelemetry and radio tracking*, edited by Amlaner, C.J. & Macdonald, D.W. 387-404. Oxford: Pergamon Press.

**White, G.C. & Garrott, R.A.** 1990. *Analysis of wildlife tracking data*. New York Academic Press.

**Worton, B.J.** 1989. Kernel methods for estimating the utilisation distribution in home range studies. *Ecology*, **70**, 164-168.

**Wray, S., Cresswell, W.J. & Rogers, D.** 1992. Dirichlet tessellations: a new, non-parametric approach to home range analysis. In: *Wildlife telemetry: remote monitoring and trading of animals*, edited by I.G. Priede & S.M. Swift, 247-255. Chchester: Ellis Horwood.

# APPENDIX 1. DATA FILE STRUCTURE IN RANGES V

---

Except for raster maps, data files in RANGES V are of ASCII (text) characters, with values separated by spaces (ASCII character 32). All files have sets of data followed by an appendix. The appendix defines the file type and details of analyses which prepared it, contains labels for animal identifiers and fix-qualifying variables, gives maximum and minimum values of coordinates and fix qualifiers, and other values needed in analyses. This information is given as an appendix, rather than a header, because the amount of information is unknown until the end of an analysis, at which point it is easier to change the length of an appendix than a header. Appendices always start with a tilde (~, ASCII 126), which enables routines to find the start of the appendix relatively quickly by reading backwards from the end of the file. The value following the tilde (variable 1) is a code for the type of file, and is repeated at the end of the appendix: to confirm that the file is from RANGES V, both values should be the same. A second code for file type is given in variable 14 of the appendix. The appendix values denoting each file type are given on Table 2.

RANGES V stores data before the appendix in 14 different formats. These are as follows.

1. fixes
2. vector maps
3. raster maps
4. contour matrices
5. fix-fix and fix-site values
6. temporal autocorrelation values
7. dynamic interaction and fix-site analysis scores
8. site-site analysis scores
9. range area and statistic values
10. range edge polygons
11. area utilisation values
12. area increment values
13. range overlap matrices
14. habitat-use scores

The simplest files, for raster and vector maps, are described first, followed by the slightly more complex format of a file containing location coordinates (fixes), which serves as a model for all the other types.

## 1.1 RASTER MAP FILES AND THEIR APPENDICES

Each data byte in a raster map is a square block of habitat, with  $x$  blocks in a horizontal row and  $y$  vertical rows to form a rectangular map, giving a total of  $x \cdot y$  bytes before the start of the appendix. The first 20 values in the appendix of any file are numbers (separated by spaces), followed by a variable number of space-separated alphanumeric strings. The 20 numeric variables in raster files are (1) file type (which should be "3"), (2) number of habitat labels, (3) number of habitat colours (should equal value of variable 2), (4) number of bearing sites (if file used as map for field entry of data), (5) westmost coordinate, (6) eastmost coordinate, (7) southmost coordinate, (8) northmost coordinate, (9) number of bytes across row, (10) number of metres per coordinate unit, (11) not used (set to 0), (12) number of rows, (13) number of categories used in analyses, (14-20) not use (set to 0). Then come the 5-character habitat labels, and the same number of strings of the form  $aa/bb/cc$ , where  $aa$ ,  $bb$  and  $cc$  define RGB colour values. If there are bearing sites, each has a name, and after the names are the same number of  $xx/yy$  strings, where  $xx$  and  $yy$  are the east and north coordinates of each site. If there are no bearing sites, 2 single dash symbols (-) replace the names and coordinates.

A rather impoverished raster map appendix, without bearing sites, would be:  
~ 3 4 4 0 3440 3490 200 2050 1000 100 1000 4 0 0 0 0 0 0 0 SANDS ROCKS  
SCRUB WATER 64/64/16 64/16/0 0/32/0 0/0/32 3

Note the initial tilde, followed by the file type (3) which is repeated at the end of the file. This map has only 4 habitats, with edges 3440E 3490W 200S 2050N, and 1000 rasters east-west and north-south. With 100 metres per coordinate unit, it can be calculated that there are 5000 metres east-west and north-south, so each raster is 5 metres across and is square. The habitats, sands, rocks, scrub and water are coloured yellow, red, green and blue.

## 1.2 VECTOR MAP FILES AND THEIR APPENDICES

Vector maps contain lines which define shapes. If no names or colours are defined for such maps (such that the first 3 appendix variables are 1 0 0), they

serve only as outline maps. The format for each shape is a set of *x,y* coordinate values followed by -1 *a*, where *a* is a value corresponding to the order of the habitat label, or is set -1 in line maps. There is a final -1 -1 after all the shapes, before the header. If shapes are to be filled and treated as habitat blocks, they must not have lines that cross and must proceed clockwise from the first coordinate pair to the last. Vector maps have similar appendices to raster maps, except that variable (9) is the maximum number of coordinate pairs in a shape. This value is used by RANGES V for memory allocation.

### 1.3 FIX FILES

Files of location data (fixes) have a label of 7 values on the first line. The label should be an identity number, followed by 2 values which for convenience are called age and sex codes (but could be something different), followed by two date codes (which for convenience are referred to as month and year), followed by *x,y* coordinates for a nest, den or other site feature in the range (or -9 -9 if there is none). The value of the age and sex variables used in a range, refers to their position in the sequence of age and sex labels in the appendix. This label line is followed by sets of *x,y* coordinate values and any fix-qualifiers (or -9 for missing values), terminating the range by -1 -1.

Fix file appendix values are (1) file type (=0), (2) number of age labels, (3) number of sex labels, (4) number of fix-qualifying variables, (5) westmost coordinate, (6) eastmost coordinate, (7) southmost coordinate, (8) northmost coordinate, (9) number of ranges in file (10) number of metres per coordinate unit, (11), whether the nest, den or other site is to be included with the other fixes (=1) or not (=0), (12) the maximum number of fixes/range, (13) not used (set to 0), (14-19) not used, (20) the tracking resolution in metres, which sets the size of any boundary strip. There follow single character name labels, single-character sex labels, short labels for fix-qualifying variables, and strings which give maximum and minimum values for fix qualifiers. Fix qualifier labels YY, MO, DD, HH, MI, SS are reserved for years, months, days, hours, minutes, seconds, respectively, and may be added together to give 4 or 6 label digits. For example, HHMI would refer to an hour-minute qualifier with units 1035, 503, etc (note that values may omit leading zeros but no others: 1 January 2001 would be 10101). Non-time labels must have 5 characters. The labels MARAD, MIRAD, THETA and

X-VAR, Y-VAR, COVAR should only be used to define fix accuracy ellipses (the value need not be given after each fix for an accuracy circle, because its radius can be set during analysis runs).

Thus a minimal fix file would be :

```
23 2 2 11 93 250 115
234 135 6 0 -9 -9 15 30 250 115 23 59 -1 -1

2 3 1 11 93 250 115
250 115 23 55 -1 -1

-1
~ 0 3 2 2 100 300 100 300 2 10 0 3 0 0 0 0 0 0 10 JY A M F HH MI 6-23 0-59 0
```

The file starts with the range of Y(earling) F(emale) number 23 in November 1993, with nest at 250E, 115N and first fix 234E, 135N at 6:00 in the morning, second fix missing at 15:30 and third fix in its nest at 23:59. The second animal, AM2 has only 1 fix.

All subsequent file types start each range with a 7-value label for each range, followed by the relevant values for each range and then the appendix.

### 1.4 CONTOUR GRID FILES

Contour files, with type (appendix value 1) set as 5, have the set of fixes for each range followed by the values in the *d x d* square grid which contains fix density values. The appendix values are the same as in the equivalent raw fix file, with some additions. Thus variable (14) has value 0 for a harmonic mean-based grid with cell-centred fixes, 1 for a similar grid with uncentred fixes, 2 for a grid from bivariate normal kernel estimation, and 3 for one from adaptive kernel estimation. In the last 2 cases, variable (15) is the contour smoothing factor, and in all 4 cases variable (16) is *d*, the number of cells across the grid.

### 1.5 FIX-FIX AND FIX-SITE FILES

These files coded 8 and 9 are in column format for import to spreadsheets. After the range label and coordinates for each fix, the fix-fix or fix-site value is given followed by any fix qualifying variables.

## **1.6 AUTOCORRELATION FILES**

These are coded 80. After the range label variables, the values of the time (in seconds) and the independence index are given in pairs, followed by -1 to terminate each range.

## **1.7 DYNAMIC INTERACTION, AND FIX-SITE FILES**

These are in spreadsheet format, coded 81-82 in the appendix. After range label variables, the variables are the number of observations (fix-pairs, fixes or range centres) followed by sums, sums of squares and means (arithmetic and geometric) together with medians, first for observed distances and then for possible distances. If selected, the file also contain complete lists of all observed and possible distances, ranked by size.

## **1.8 SITE-SITE FILES**

The files from nearest-neighbour analysis of range-centre spacing are coded 83. They contain a single row of 15 variables, plus the appendix. The 15 variables are the number of observations and the mean, sum, sum of squares and standard error for their nearest neighbour distances, followed by the area covered, the expected mean and standard error for a regular distribution in it and Student's t for the difference from the observed value, followed by the number of random pairs, their sum, sum of squares, standard error and t value.

## **1.9 RANGE AREA AND STATISTICS FILES**

These are coded 70-79 and have one row of data for each range. In each row, the 7 range variables are followed by 7 range statistics and then as many area values as there were percentage cores for each range (% values are in the appendix). The first two range statistics are the x and y coordinates for the range centre (or 0 and 0 for cluster analysis). The other 5 range statistics differ between analyses. For convex polygons, they are the maximum range diagonal, followed by the mean, median and maximum distance of fixes from the centre, followed by 0. For ellipses, they are theta, the correlation coefficient, the standard deviations on the major and minor axes, and the asymmetry ratio. For clusters, they are the number of nuclei, partial area and

Simpson's index for fix and area diversity, followed by 0. For harmonic mean and other kernel analyses they are the range spread and the density score at the central fix, with the dispersion, skewness and kurtosis of the density distribution.

## **1.10 RANGE EDGE FILES**

After the range label, polygons representing file edges start with a single value  $n$  to define the number of coordinate pairs in the shape, followed by the  $n$  pairs, followed by an extra pair of coordinates which are the range centre (if present, or 0 for cluster analyses and concave polygons). If there are "holes" in isopleths, the initial value is negative ( $-n$ ). There may be several polygons to each core, but each core terminates with -1  $a,b$ , where  $a$  is the percentage value of the core (1-100), and  $b$  identifies the type of polygon: 1 for outer convex polygons, 11 for peeled convex polygons, 12 for cluster polygons, 14 for concave polygons, 16 for ellipses, 18 for harmonic mean isolines and 19 for kernel isolines. The different edge files can now be merged if one wants, for instance, to investigate overlap of polygons on ellipses, but one can still identify the origin of individual cores.

In edge files, and the overlap or habitat analysis files made from them, variable (18) is the number of edge cores per range (which is always either 1 or 17 for files from RANGES IV, but can be up to 99 for RANGES V. Values for the cores are stored as a single string  $a/b/c$ , or 20-99/ or 20/100/ following the age and sex labels (fix qualifier labels being relevant only the fix files). File type values (variable 1) are 10-19 and variable (14); these identify the precise type of edge (see Table 1).

## **1.11 AREA UTILISATION FILES**

These are in spreadsheet format, coded 20-29 and 0-4, using appendix variables (1) and (14) in the same way as among edge files. On each line, the range label is followed by 7 variables. The first of these is the core value (100%, 95%, 90%...20%), followed by its area. In most analyses these values are followed by 5 zeros, but in cluster analysis the second variable is the number of cores, followed by the indices of patchiness, fix diversity and area diversity in the cores.

## 1.12 AREA INCREMENT FILES

Variable (1) codes are 50-59. After the label line, values are areas for each fix added after the third, with -1 to terminate each range.

## 1.13 OVERLAP MATRIX FILES

Variable (1) codes are 30-39. Variable (16) is set to 0 for overlaps of cores on cores, and 1 for fixes on cores. Each range label is followed by n percentage overlap values, where n is number of ranges filed.

## 1.14 HABITAT USE FILES

Variable (1) codes are 40-49. After the label line, values are core%, area/fx number and use(%) of each habitat type. The appendix contains the labels for each habitat, in the order used.

## 1.15 RANGES COLUMN FORMAT FOR FIXES, VECTOR MAPS AND EDGES

When these files are available in column format for export to spreadsheets, they are given codes in the appendix of the normal value for each plus 100. Thus column format for fix files is 100. This fix file format is used for porting fix files to and from the field data entry programme FIELDER, on PSION palmtop computers.

Table 1. Values for the file appendix variables (1) and (14) which indicate file types

File types	Variables (1)	Variables (14)
Fixes	0	0
Vector line maps	1	0
Vector habitat shapes	2	0
Raster habitats	3	0
Contour matrices:		
harmonic, centred	5	0
uncentred	5	1
kernel, bivariate	5	2
adaptive	5	3
Fix-centre distances:		
nest	8	1
harmonic mean fix	8	2
kernel centre fix	8	3
arithmetic mean (ac)	8	4
Interfix values:		
headings	9	1
distances	9	2
times	9	3
speeds	9	4
Fix-site values:		
headings	9	5
distances	9	6
Range polygons:		
convex, outer	10	0
convex, peeled, centre on:		
nest	11	1
harmonic mean fix	11	2
kernel centre fix	11	3
arithmetic mean	11	4
recalculated ac	11	5
convex cluster based:		
hierarchic, nn priority	12	0
ce priority	12	1
concave	14	0
ellipses:		
Jennrich-Turner plain	16	0
harmonic mean contours:		
centred	18	0
uncentred	18	1
kernel contours:		
bivariate	19	2
adaptive	19	3

The coding system for the following file types is similar to that used for range edge polygons. These filetypes include area utilisations (20-29), overlap matrices (30-39), habitat use files (40-49) and area increments (50-59), and range statistics with areas (70-79). Autocorrelations are coded as 80, dynamic interactions as 81, fix-site files as 82, and site-site analyses as 83. Fix files in column format from field data entry are coded 100, other column export files have 100 added to their compact form (eg 101 for maps).

## APPENDIX 2. EXAMPLE FILES

---

There are files of example data in 3 directories. All files have the .BBC extension. The examples are real data.

### 2.1 SQUIRREL DIRECTORY

This contains data files for the grey squirrel *Sciurus carolinensis*.

FIXFILE is 6 grey squirrel ranges. These have 3 FQVs, for days (in sequence from 1 to 10), hours and minutes.

KARTA is a map of habitat shapes. They are displayed as outlines during RANGE ANALYSES or when editing fix files, and in colour with OVERLAP ANALYSES option 0 or during HABITAT ANALYSES.

#### *Output from RANGE ANALYSES*

The range edge files were all produced from FIXFILE. They can be used in OVERLAP ANALYSES, HABITAT ANALYSES and option 3 (RANGE CENTRE SPACING) in INTERACTION ANALYSES.

The utilisation & incremental plots can be examined in option 4 of the main menu.

E100	Outer (100%) convex polygons
EN75	Single core edge file, 75% nest centred polygons
EC90	Single core edge file, 90% cluster analyses polygons
ECALL	Multi-core edge file, 20-100% cluster analyses polygons
EH90	Single core edge file, 90% harmonic mean contours

UC	Utilisation distributions from cluster analyses polygons
I	Incremental outer convex polygons
GKM	is a grid intersection matrix from kernel analysis for a single range

FIXES, FIXCOL, FIX1, FIXI are files required for the DEMO.

### 2.2 BLACKBIRD DIRECTORY

This contains 4 files: BLACKFIX, BLA90CLU, BLACKINC and KARTA.

BLACKFIX is location data from 4 neighbouring adult blackbirds *Turdus merula*: 2 males and 2 females. Two of the birds are paired, with the female incubating.

KARTA is a map outline file of the blackbird study area.

BLA90CLU is a 90% cluster edge file. In OVERLAP ANALYSES option 0, this shows how the first 2 birds forage in separate ranges but go to a communal roost at night. The mate of the sitting female, which continues to incubate, also goes to the communal roost.

The core ranges of the pair overlap extensively, but INTERACTIONS ANALYSES show that they have a relatively weak DYNAMIC INTERACTION (option 1). This is also true of the other birds if fixes are selected for the hours 9-15, when they are not visiting the roost.

The ranges contain about 60 fixes taken at intervals of 1-2 hours, but an INCREMENTAL PLOT of BLACKINC (prepared from convex polygons) shows that maximum range sizes were recorded after about 25 fixes (apart from the nesting female which was rarely recorded foraging).

If INTERACTIONS ANALYSES are used for an AUTOCORRELATION plot (option 0), preferably using the RS menu A-Analysis option to select a 30-60 minute interval, it can be seen that fixes had low spatio-temporal correlation after about 4 hours. This means that they could have been taken about half as frequently to get an estimate of range size. It is interesting that spatio-temporal correlation tends to increase again after 12-16 hours, perhaps because the birds time-table back to their roost.

## **2.3 BUZZARD DIRECTORY**

This contains 7 files.

BUZZARDS is 10 standard ranges recorded in autumn from 5 common buzzards *Buteo buteo*, one with a tag still running after 3 years.

BUZZEDGE contains convex polygon ranges from BUZZARDS with nests as their centre. They can be inspected in OVERLAP ANALYSES option 0.

B90FIX is a set of autumn ranges of juvenile buzzards.

B90NEST is a file of nest sites in the buzzard study area. (These were entered as a fix file, but could also have been habitat points).

B90MAP is an outline map of the study area as one habitat shape.

RASTER is a 5x5 km section from ITE's Landcover map of Great Britain. It contains 15 classes of habitat data from Landsat imagery (i.e. 15 of the 25 categories in the original map data). This map can be used to test the HABITAT ANALYSES options using any of the fix or edge files in this directory.

MATRIX is a percentage overlap matrix calculated from an outer polygons file of the 10 ranges in BUZZARDS.

Using the INTERACTIONS ANALYSES option, FIX-SITE ANALYSIS (option 2) you can see whether the young buzzards in B90FIX tended to be attracted to or avoid nest areas in B90NEST. It appears that most birds prefer to be near nests. However, this mainly results from avoidance of heathland in the study area both for nesting and foraging. If analysis is confined to fixes that lie within circles around nests, the tendency to favour areas near nests is weaker, but note that at least one bird still shows a strong attraction to the natal site.

INTERACTIONS ANALYSES of RANGE CENTRE SPACING (option 3) with B90EDGE gives values around 2.0 for Student's t, indicating that spacing was relatively regular.

# APPENDIX 3. TERMS AND CONVENTIONS

---

## 3.1 CONVENTIONS

Bullet points (•) indicate important items in the text.

→ Denotes a step in a routine.

↓ means RETURN (enter), pressing this at a menu gives the default

Text which you are asked to type is shown in **bold**.

When files are listed for selection they are arranged in order of their creation, with the most recent at the end of the list.

Background maps are shown faintly with bright fixes and edges superimposed.

## 3.2 GLOSSARY OF TERMS

**Accuracy ellipses** are generated round fixes from bearing data by some packages (e.g. LOCATE II).

**Arithmetic mean** is the mean  $x$  and  $y$  coordinates for a set of fixes.

**Autocorrelation analysis** estimates the degree of spatio-temporal dependence of fixes.

**ASCII** is American Standard Code for Information Interchange, used to turn bytes into text characters.

**Bivariate ellipses** are based on fix distributions along a major and a minor axis.

**Boundary strips** round fixes in polygons have a width of half the tracking resolution.

**Byte arrays** are RANGES V storage format for raster maps; each byte codes for 1 raster.

**Centroid distance** is from a fix to all the fixes in a cluster.

**Cluster analysis** joins fixes in groups based on the distances between them.

**Core** denotes one or more high areas of high fix density in a range.

**CSV** files are composed of Comma Separated Values (other separators are Break/Space and Tab).

**Density matrix** values are estimated at intersections of an arbitrary grid for contouring.

**Digitiser tablets** may be used to input vector map data. **Dispersal detection** provides an objective estimate of when animals leave an area.

**DXF-files** provide graphics input and output in the AUTOCAD Data eXchange Format.

**Edge** denotes an outline estimated round fixes as a polygon or by contouring.

**Ellipses** include circles.

**Ellipse asymmetry** is the ratio of the standard deviations along the major and minor axes.

**Fix** denotes  $x,y$  coordinates of a location, often with associated qualifying variables.

**Fix centring** is computed during harmonic mean contouring to remove fix resolution effects.

**Fix Qualifying Variables (FQVs)** are time, activity, habitat, values associated with  $x,y$  coordinates.

**Fix resolution** is the smallest distance that can be recorded between adjacent fixes.

**Focal site** denotes an attraction point in a range, such a den or nest.

**Grid cells** are as wide as the fix resolution.

**Grid edges** are the eastmost, westmost, northmost and southmost coordinates in sets of fixes.

**Gridascii files** are used by ARC/INFO for transferring raster map data.

**Habitat points** are  $x,y$  coordinates associated with habitat codes for different trees, etc.

**Habitat shapes** are formed from a clockwise set of  $x,y$  values with the same start and end point.

**Harmonic mean analyses** are based on the inverse reciprocal mean of distances.

**Incremental analysis** estimates the change in range area as successive fixes are added.

**Isolines** of equal fix density are created during contour analysis and converted to polygons.

**Jacob's index** has values between -1 and +1 to indicate attraction versus avoidance.

**Kernel analyses** are based on estimating fix density as functions of distance.

**Kurtosis** indicates spread in the density distribution during kernel analyses (e.g. harmonic mean).

**Nearest neighbour locations** are those closest to a single site or fix in a cluster.

**Outlier fixes** are those beyond the main distribution of fixes.

**Overlap matrices** are formed as % overlaps of range A on B and B on A.

**Partial area** is the summed area of clusters divided by a single area encompassing all clusters.

**Polygons** are formed by joining edge lines round a set of fixes.

**Range variables** are 7 values that code ID, age, sex, month, year and focal site coordinates.

**Raster maps** are composed of equal-size rectangles with different habitat codes.

**Schoener's index** increases from 0 with decreasing spatio-temporal dependence between fixes.

**Skew** in the fix density distribution is estimated during kernel analyses (e.g. harmonic means).

**Simpson's index** increases from 1 with increasing diversity between clusters.

**Smoothing factor** modulates the density function in kernel analyses to improve fit of contours.

**Span** of a range, is the maximum diagonal dimension of a polygon enclosing all points.

**Spread** of a range is the grand mean of distances between all the fixes.

**Tracking resolution** is the smallest distance that can be recorded between adjacent fixes.

**Utilisation plots** are of range area against increase in fix density until all are included.

**Vector maps** are composed of lines and closed shapes defined by a sequence of  $x,y$  coordinates.

**Width** of a range is the maximum diagonal dimension of a polygon enclosing all the fixes.



**Centre for  
Ecology &  
Hydrology** Institute of Freshwater Ecology  
Institute of Hydrology  
Institute of Terrestrial Ecology  
Institute of Virology & Environmental Microbiology

Natural Environment Research Council