Simply Tagging

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Simply Tagging is used to estimate population size for both closed and open populations using mark-recapture methods. It also allows students to simulate data and explore the accuracy and reliability of mark-recapture.

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Simply Tagging

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1 Introduction to Simply Tagging

Simply Tagging is a Windows program that offers a range of analytical techniques to estimate population size, mortality and survival using mark-recapture methods. *Simply Tagging* has been designed for ease of use on PCs running under Windows. Data can be organised using Windows programs such as Excel and the output from *Simply Tagging* is displayed, exported and printed using standard Windows techniques. This results in a program that is easily used by both students and professional ecologists. It is particularly useful for ecological teaching because it also offers a data simulation module to generate data sets that can be used to test the reliability and accuracy of the methods available under different levels of capture probability and types of animal behaviour.

For installation instructions see
Installation
System requirements

For information about mark-recapture methods see
An introduction to mark-recapture methods

For getting started with data entry see
Summary for entering data
A simple example of data entry
Entering data

1.1 Installation

1. Place the *Simply Tagging* CD in your CD drive: the installation process should begin automatically - follow the on-screen instructions.
2. If the CD does not auto-play, browse the CD in Windows Explorer or My Documents and double-click file named Setup.exe in the root directory.
3. When installation is complete there will be a *Simply Tagging* group on your Start button/Programs menu, and a folder (directory), *C:\Program Files\Simply Tagging*, which holds the *Simply Tagging* program files. The program's demonstration data files will be stored in *My Documents\Simply Tagging Data*. An uninstall facility will also be created, in case you wish to remove the program.

1.2 System requirements

Simply Tagging runs on Windows 98, NT, 2000, ME, XP and Vista operating systems.

The SVGA screen must run at a minimum of 256 colours and there must be 2MB of free hard disk space. *Simply Tagging* does not limit the size of your data set.

1.3 Summary for entering data

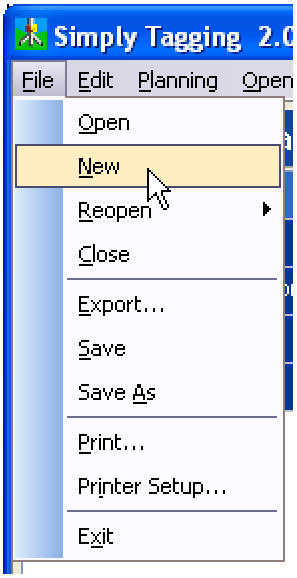
For full instructions about entering data and data set formats see Entering Data.

Data sets can be created both within and outside *Simply Tagging.* The data is stored in a simple CSV or comma delimited file

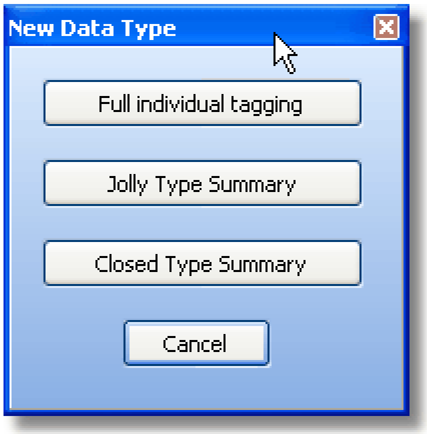
Some example data sets are supplied with the program. These will be installed with the program, in the folder *My Documents/Simply Tagging Data*.
DemoFull.csv is an example of a data set where individual capture histories have been entered.
Jolly_summary.csv is mark-recapture summary data organised for the Jolly-Seber method and
Closed_summary.csv holds the summary data needed for the closed methods. See a simple

example of data entry to show an example of the entry of closed summary data.

To create a new data set within *Simply Tagging* select **File: New** from the drop-down menus.



You will be presented with a window that offers 3 types of data for entry, Full individual tagging, Jolly-Seber summary and Closed summary.



Full individual tagging
If you have selected to enter the capture history of each individual you will be presented with an empty grid which you will need to fill in for every individual.
Instructions for data entry
Editing data
Subsetting your data by size or sex

Jolly-Seber summary
If you have selected to enter your data as a Jolly-Seber summary table then you will be asked to enter the number of samples taken, and will then be presented with an empty grid which you will need to fill.
Instructions for data entry
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Closed summary

Instructions for data entry
Editing data
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1.4 An introduction to mark-recapture methods

When an absolute estimate of population size is required, these methods are the main alternative approach to those based on the count of animals within a fixed unit of the habitat. They offer the advantage that accuracy does not depend on an assessment of the amount of habitat; their disadvantage is that accuracy does depend on capturing a large proportion of the population.

Seber (1982,1986) reviews the statistical theory that underlies the mark-recapture approach. Originally developed to estimate population size, capture-recapture methods are now frequently used for the estimation of birth, death and emigration rates. Lebreton *et al.* (1992) reviews methodologies for the estimation of survival rates. Populations can be classified as either open or closed. A closed population remains unchanged over the period of study whereas an open population changes because of some combination of birth, death and emigration. Reviews of methods applicable to closed and open populations are those of White *et al*. (1982) and of Pollock *et al*. (1990) respectively. Descriptions of the application of the methodology to particular animal groups are given by, try Nichols *et al.* (1981) for birds, by Burnham *et al.* (1987) for fish and by, Eberhardt *et al.* (1979) for marine mammals.

A mark-recapture method was first used for ecological study in 1896 by Petersen to estimate plaice, *Platichthys platessa*, populations; later, Lincoln (1930) independently developed the method to estimate waterfowl populations. The principle used to calculate population size in these early studies, in which the population was assumed closed, still applies. If a sample from a population is marked, returned to the original population and then, after complete mixing, re-sampled, the number of marked individuals in the second sample would have the same ratio to the total numbers in the second sample as the total of marked individuals originally released would have to the total population. A basic prerequisite to the use of these methods is a technique for marking the animals so that they can be released unharmed and unaffected into the wild and recognised again on recapture.

Various assumptions underlie all methods of capture-recapture analysis. If the particular animal does not fulfil one or more conditions it might be possible to allow for this to some extent, but a method of analysis should not be applied without ensuring, as far as is practicable, that its inherent assumptions are satisfied. Parsimony, the use of the smallest possible number of parameters to model a situation, is essential, so though assumptions can be avoided by adding further parameters to a model, this inevitably leads to an increase in the variability of parameter estimates (Cormack ,1979; Begon, 1983).

There are four assumptions common to most methods:

1. The marked animals are not affected (either in behaviour or life expectancy) by being marked, and the marks will not be lost.
2. The marked animals become completely mixed in the population.
3. The probability of capturing a marked animal is the same as that of capturing any member of the population; that is, the population is sampled randomly with respect to its mark status, age and sex. Termed 'equal catchability', this assumption has two aspects: firstly, that all individuals of the different age groups and of both sexes are sampled in the proportion in which they occur; secondly, that all the individuals are equally available for capture irrespective of their position in the habitat.
4. Sampling must be at discrete time intervals and the actual time involved in taking the samples must be small in relation to the total time.

The violation of these assumptions may invalidate the capture-recapture method. *Simply Tagging* offers tests for equal catchability.

See Methods for Closed Populations and
Methods for Open Populations.

1.5 Methods for open populations

A number of methods have been developed to estimate population parameters for open populations, of which the most general is the Jolly-Seber method. *Simply Tagging* offers both a full Jolly-Seber analysis and a reduced model in which probability of capture and survival are assumed to be constant over the period of the experiment. Before either of these methods is attempted, it is important to note that they are unlikely to produce good estimates unless a high proportion of the population is tagged. If you know that only a small proportion of the population will be captured, then closed methods should be used and your effort is best expended trying to ensure that the population can be assumed closed for the duration of the experiment.

1.5.1 Open population

An open population is one that can vary in size during the study. There may be births, deaths, or emigration.

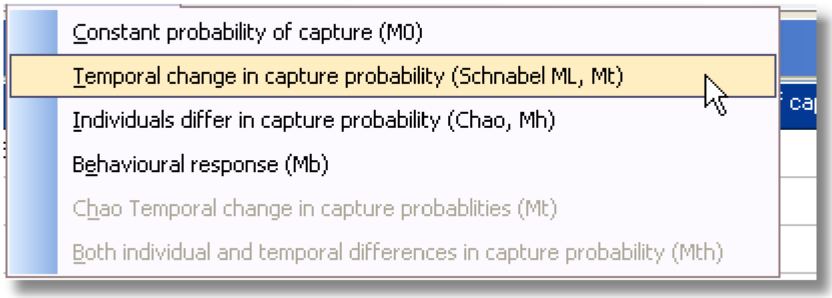
See also Closed population

1.6 Methods for closed populations

These methods assume that the population does not change over the period of study, which is termed a closed population. It is therefore essential that this period is short compared to life expectancy. Further, individuals must not be able to enter or leave the study area. Methods in which the probability of capture is not assumed constant require a series of occasions (at least two) on which animals previously marked are recaptured, marked again, and released. The methods available within *Simply Tagging* are generalised for 2 to 500 sampling occasions. Some methods require full individual data, while others only require summary data that can be generated by batch tagging methods.

The simplest experiment has only two sampling occasions, on the first of which animals are captured, marked and released, and on the second, captured and the number of marked and unmarked animals recorded. From such data the Petersen-Lincoln method is used to calculate population size.

Within *Simply Tagging* these calculations will be obtained on the **Closed methods** menu, selecting **Temporal change in capture probability (Schnabel ML, Mt)**, as when only two samples are available this method will calculate a simple Petersen-Lincoln estimate.



Simply Tagging uses the nomenclature and approach developed by Gary White, David Anderson, Kenneth Burnham and David Otis in which a number of models, each of which makes different assumptions about the probability of capture both through time and between individuals, are considered. Each model can be selected in turn from the **Closed methods** drop-down menu, and their results compared.

Closed methods available:

Model M0:	Constant probability of capture
Model Mt:	Maximum likelihood Schnabel census (Petersen-Lincoln index if samples = 2)
Model Mt:	Chao method
Model Mh:	Individual variation in probability of capture
Model Mb:	Behavioural changes following capture
Model Mth:	Temporal changes in catchability and individual heterogeneity

1.6.1 Closed population

This is the term used for a population which has a fixed size over the period of study. There is no death, birth or emigration within the study area. This assumption offers great advantages, but, can only be justified if the study is undertaken over a brief period of time (or you are estimating gods or other immortals).

Part

II

2 References

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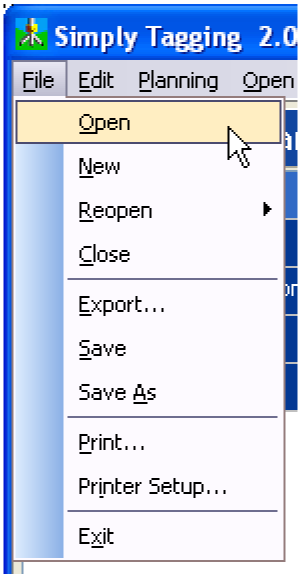
Part
III

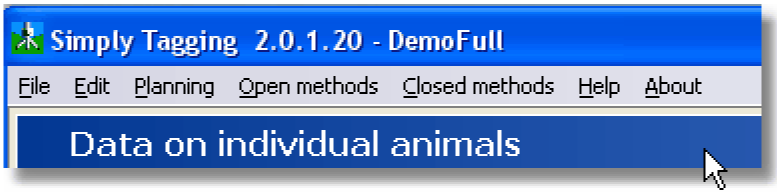
3 Main Windows

3.1 The Main Form

When the program is started, you will be presented with a blank working area.
From the **File** menu choose **Open** to load an existing data set, or Reopen to load one that you have used previously. The program will "remember" the 6 most recently-used data files.



Once a data set is loaded or a new data set created, methods can be selected from the drop-down menus, and the calculations for each method will be displayed in individual tabbed pages. The title of the data set is displayed in the top bar of the program.

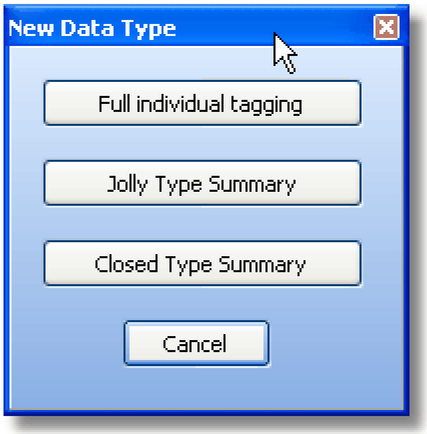


Along the top bar are a number of drop-down menus. These work in the same way as any other standard Windows program.

File: To open, save, export and print data sets.
Edit: To cut copy and paste to and from the active window.
Planning: To create simulated data.
Open methods: To undertake calculations on populations that can change in size during the study period.
Closed methods: To undertake calculations for populations that are assumed to have remained constant during the coarse of the study.
Help: To enter the Help system.
About: Details about the program version.

3.2 New Data Type

This dialog box is used to select the type of data you wish to enter.

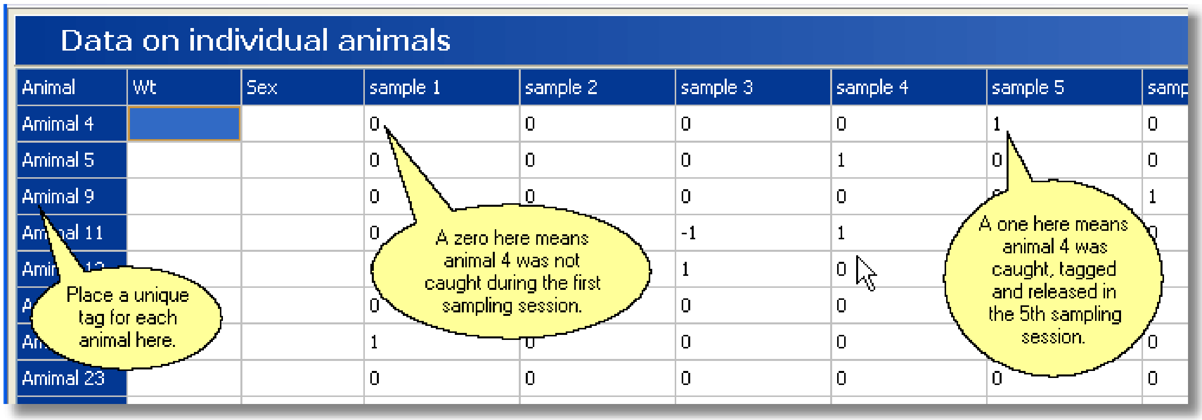


See Entering Data for more information on these different data formats.

3.3 Full Data - tab

This screen shows data sets that comprise the recapture history of each individual animal over all the samples taken. An entry of 1 in the grid indicates that an animal was captured in the sample, a 0 (zero) that it was not captured, and a -1 that it was captured and killed before release.
See entering full individual data for more information.

A brief summary of the grid layout is shown below.



Data on individual animals

Animal	Wt	Sex	sample 1	sample 2	sample 3	sample 4	sample 5	samp
Amimal 4			0	0	0	0	1	0
Amimal 5			0	0	0	1	0	0
Amimal 9			0	0	0	0		1
Am al 11			0		-1	1		0
Amir					1	0		
A			0		0	0		
An			1	0	0	0		0
Amimal 23			0	0	0	0	0	0

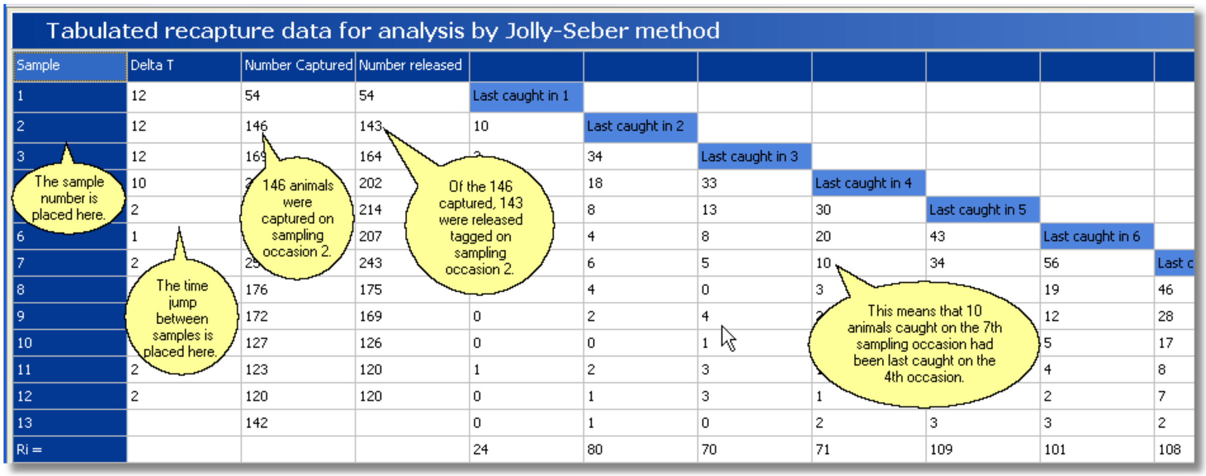
The data can be printed by selecting **File: Print** with this window open.

A cell can be edited by clicking into it in the normal spreadsheet fashion.

3.4 Jolly Summary - tab

This tab displays the data set as a Jolly-Seber summary table. It will be created automatically by *Simply Tagging* if you have entered or opened a full individual tagging data set. Alternatively, you can enter data into this table.
Instructions for entering Jolly Seber summary data.
Editing data

A brief example of the data structure is shown below.



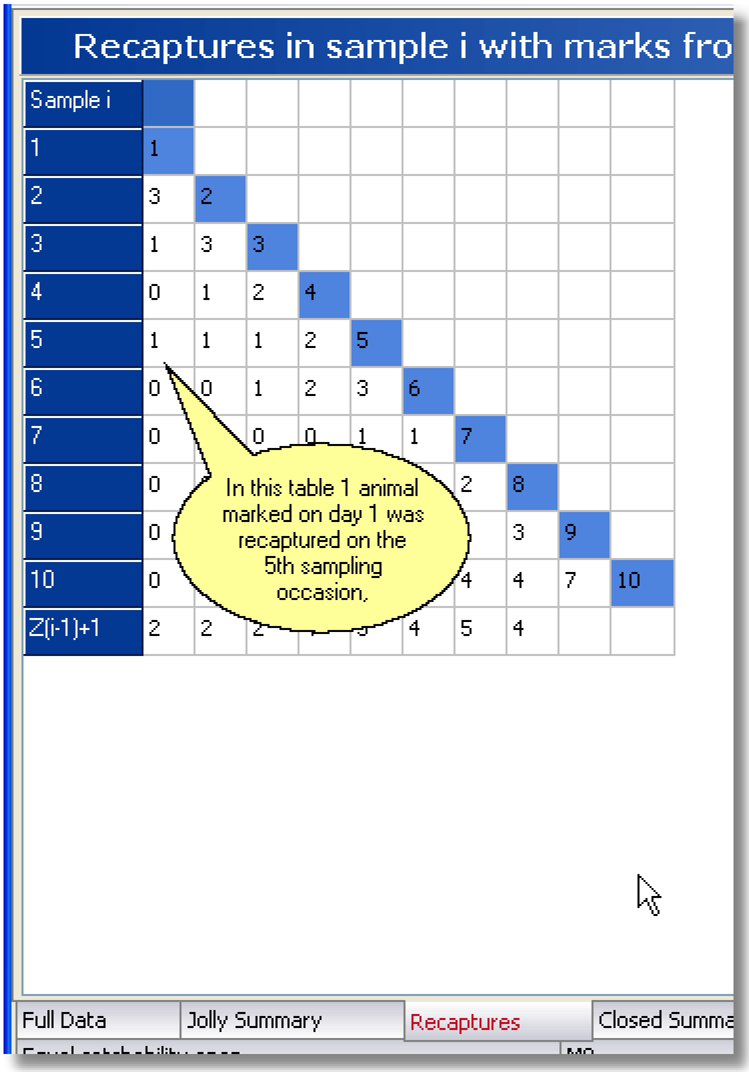
Tabulated recapture data for analysis by Jolly-Seber method

Sample	Delta T	Number Captured	Number released							
1	12	54	54	Last caught in 1						
2	12	146	143	10	Last caught in 2					
3	12	169	164	[illegible]	34	Last caught in 3				
[illegible]	10	[illegible]	202	[illegible]	18	33	Last caught in 4			
[illegible]	2	[illegible]	214	[illegible]	8	13	30	Last caught in 5		
6	1	[illegible]	207	[illegible]	4	8	20	43	Last caught in 6	
7	2	[illegible]	243	[illegible]	6	5	10	34	56	Last c
8	[illegible]	176	175	[illegible]	4	0	3	[illegible]	19	46
9	[illegible]	172	169	0	2	4	[illegible]	[illegible]	12	28
10	[illegible]	127	126	0	0	1	[illegible]	[illegible]	5	17
11	2	123	120	1	2	3	[illegible]	[illegible]	4	8
12	2	120	120	0	1	3	1	[illegible]	2	7
13		142		0	1	0	2	3	3	2
Ri =				24	80	70	71	109	101	108

3.5 Recaptures - tab

The Recaptures tab is generated by the Jolly-Seber method for open populations.

It displays the standard table of the total number of marked individuals recaptured on a given day bearing marks from a previous day.



Recaptures in sample i with marks fro

Sample i										
1	1									
2	3	2								
3	1	3	3							
4	0	1	2	4						
5	1	1	1	2	5					
6	0	0	1	2	3	6				
7	0		0	0	1	1	7			
8	0						2	8		
9	0							3	9	
10	0						4	4	7	10
Z(i-1)+1	2	2	2		3	4	5	4		

In this table 1 animal marked on day 1 was recaptured on the 5th sampling occasion.

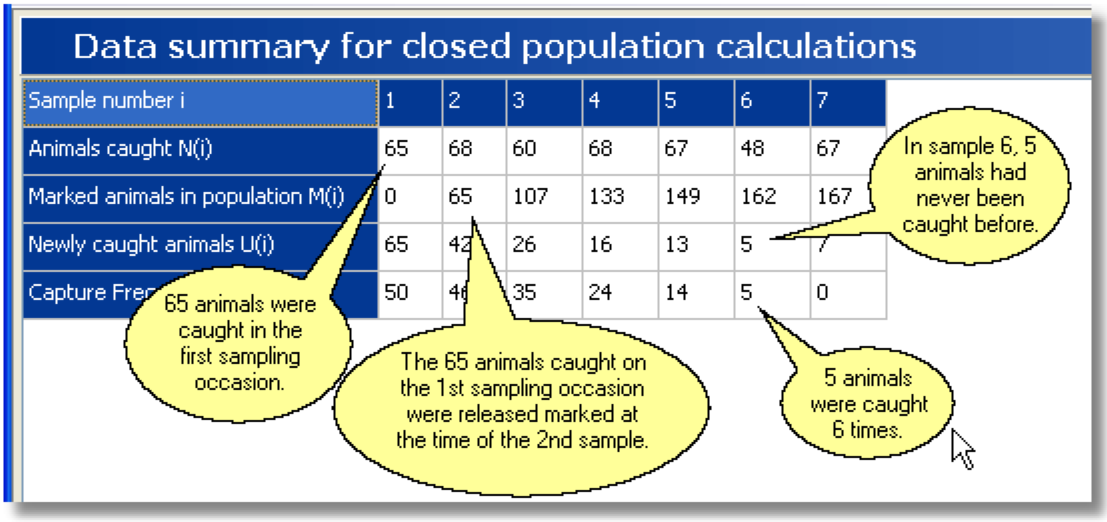
For example the column labelled 1 holds the number of animals caught on day 1 that were recaptured on the sampling occasion given by the row number.

The final row gives the calculated Z(i) numbers - these are the numbers of individuals marked before sample i which were not caught in sample i but were subsequently captured (yes it is a little confusing).

The table can be printed by selecting **File: Print** with the window open.

3.6 Closed Summary - tab

This window displays the data in the standard format used for the analysis of closed populations.



Data summary for closed population calculations

Sample number i	1	2	3	4	5	6	7
Animals caught N(i)	65	68	60	68	67	48	67
Marked animals in population M(i)	0	65	107	133	149	162	167
Newly caught animals U(i)	65	42	26	16	13	5	7
Capture Fre	50	46	35	24	14	5	0

65 animals were caught in the first sampling occasion.

The 65 animals caught on the 1st sampling occasion were released marked at the time of the 2nd sample.

In sample 6, 5 animals had never been caught before.

5 animals were caught 6 times.

For more details of the structure of the data and how to enter new data, see entering data in a closed summary table.

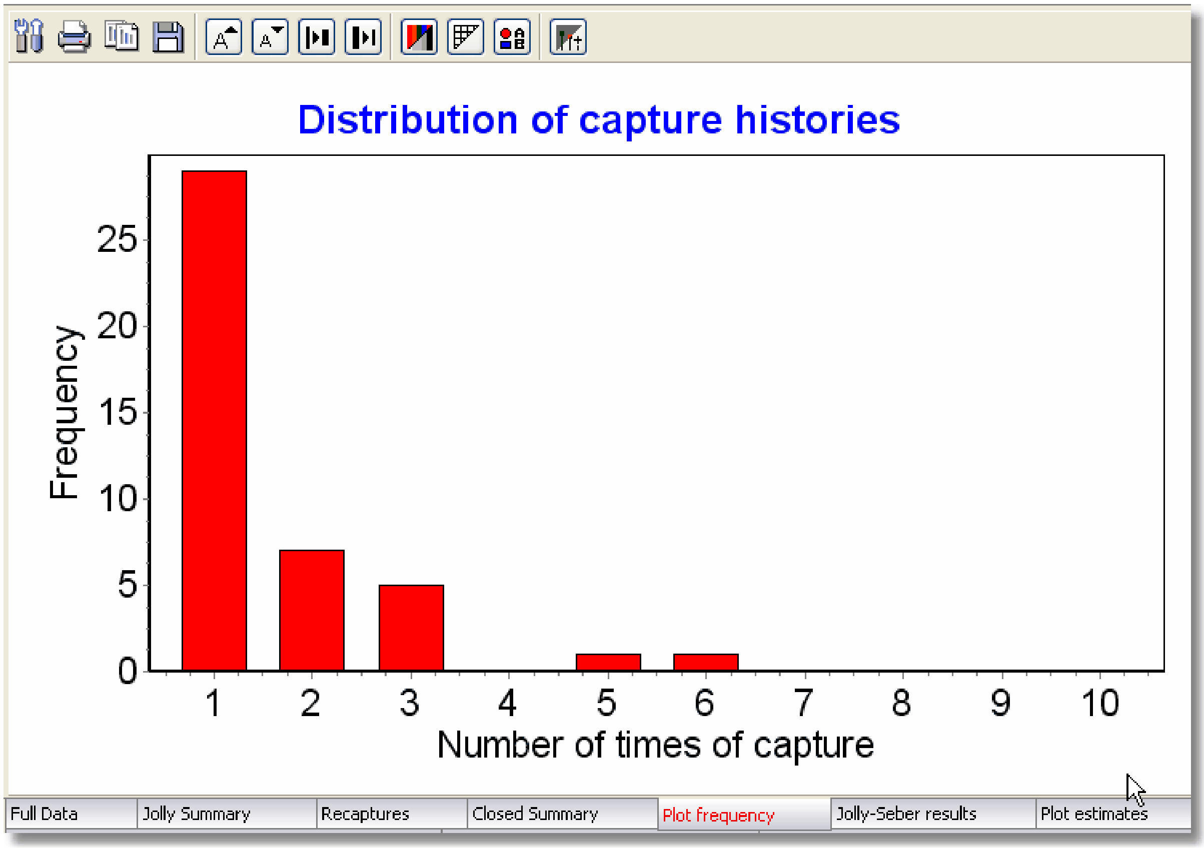
The data can be printed by selecting **File: Print** while this window is open.

Any data cell can be edited by clicking on it and typing in standard spreadsheet fashion.

3.7 Plot frequency - tab

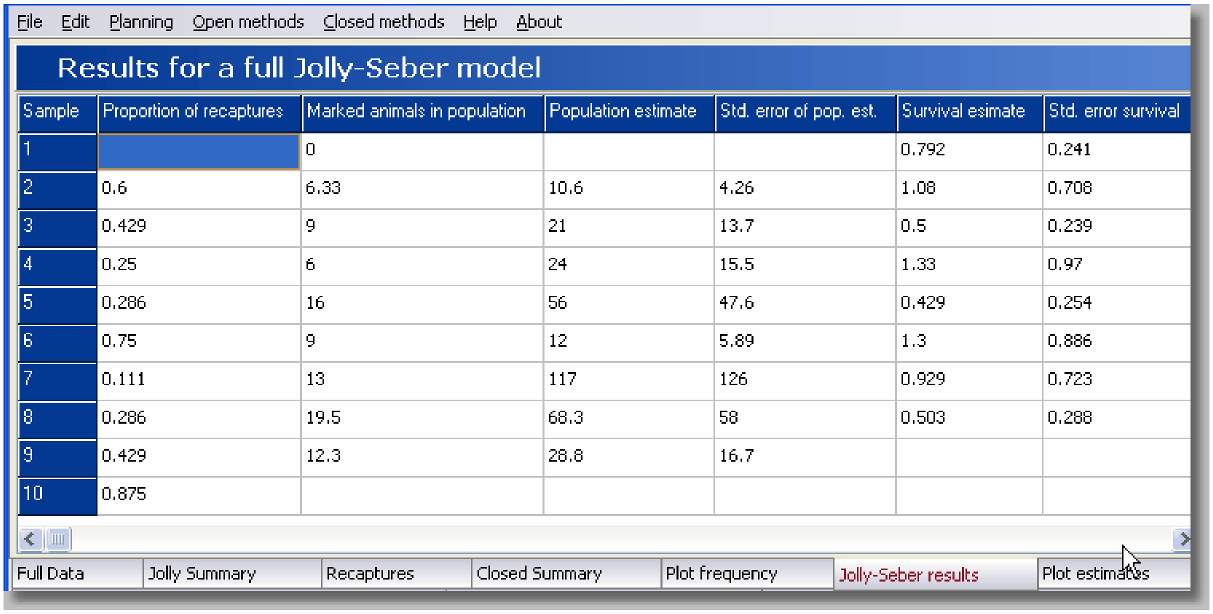
This tab shows the frequency distribution of recaptures in your data set. It plots how many animals have been caught one, two, three or more times over the experiment.

Many features of this plot can be changed by the user from Graph display options obtained from the toolbar above the chart.



3.8 Jolly Seber Results - tab

This form gives the results of a Jolly-Seber open population analysis.



Results for a full Jolly-Seber model

Sample	Proportion of recaptures	Marked animals in population	Population estimate	Std. error of pop. est.	Survival esimate	Std. error survival
1		0			0.792	0.241
2	0.6	6.33	10.6	4.26	1.08	0.708
3	0.429	9	21	13.7	0.5	0.239
4	0.25	6	24	15.5	1.33	0.97
5	0.286	16	56	47.6	0.429	0.254
6	0.75	9	12	5.89	1.3	0.886
7	0.111	13	117	126	0.929	0.723
8	0.286	19.5	68.3	58	0.503	0.288
9	0.429	12.3	28.8	16.7		
10	0.875					

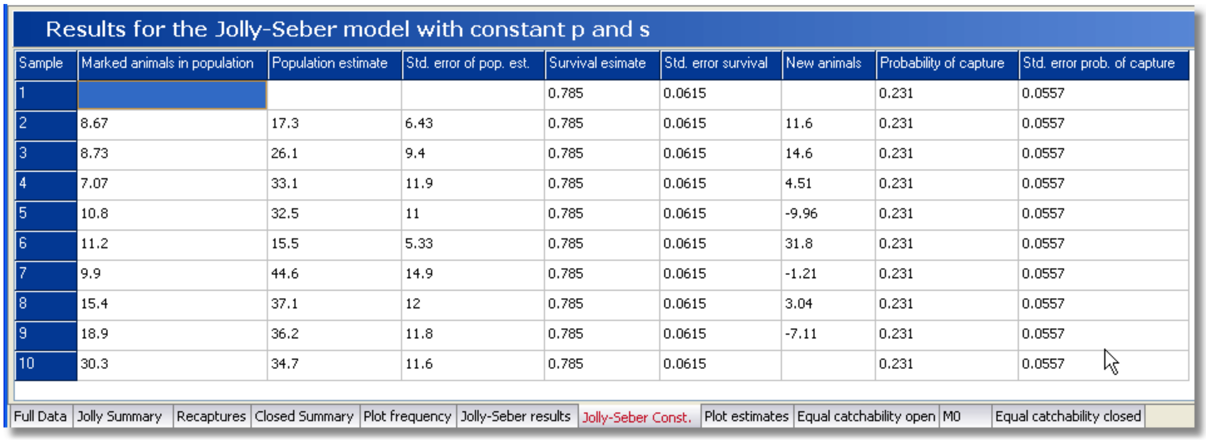
Column 1 gives the sample number.
Column 2 gives the estimated proportion of the population captured in each sample from sample 2.

Column 3 gives the estimated number of marked animals in the population.
Column 4 gives estimated size of the population.
Column 5 gives the standard error of the population estimate.
Column 6 gives estimates of the proportion of the population surviving between samples.
Column 7 gives the standard error of the survival estimates.
Column 8 gives the estimate of the new animals entering the population. A negative number occurs when there has been a net loss of animals.
Column 9 gives the estimated probability of capture for each sample.

See also:
Printing or exporting your results
Plotting population estimates
The recapture table

3.9 Jolly Seber Const. - tab

This form shows the resulting calculations for a Jolly-Seber model with constant survival and probability of capture.



Results for the Jolly-Seber model with constant p and s

Sample	Marked animals in population	Population estimate	Std. error of pop. est.	Survival esimate	Std. error survival	New animals	Probability of capture	Std. error prob. of capture
1				0.785	0.0615		0.231	0.0557
2	8.67	17.3	6.43	0.785	0.0615	11.6	0.231	0.0557
3	8.73	26.1	9.4	0.785	0.0615	14.6	0.231	0.0557
4	7.07	33.1	11.9	0.785	0.0615	4.51	0.231	0.0557
5	10.8	32.5	11	0.785	0.0615	-9.96	0.231	0.0557
6	11.2	15.5	5.33	0.785	0.0615	31.8	0.231	0.0557
7	9.9	44.6	14.9	0.785	0.0615	-1.21	0.231	0.0557
8	15.4	37.1	12	0.785	0.0615	3.04	0.231	0.0557
9	18.9	36.2	11.8	0.785	0.0615	-7.11	0.231	0.0557
10	30.3	34.7	11.6	0.785	0.0615		0.231	0.0557

The parameter estimates are arranged in columns, with the rows representing each of the sampling occasions:

Column 1 gives the sample number.
Column 2 gives the estimated number of marked animals in the population.
Column 3 gives estimated size of the population.
Column 4 gives the standard error of the population estimate.
Column 5 gives estimates of the proportion of the population surviving between samples. This will not change as a constant survival is assumed.
Column 6 gives the standard error of the survival estimates.
Column 7 gives the estimate of the new animals entering the population. A negative number occurs when there has been a net loss of animals.
Column 8 gives the estimated probability of capture for each sample. This will not change as a constant probability of capture is assumed.
Column 9 gives the standard error of the probability of capture estimate.

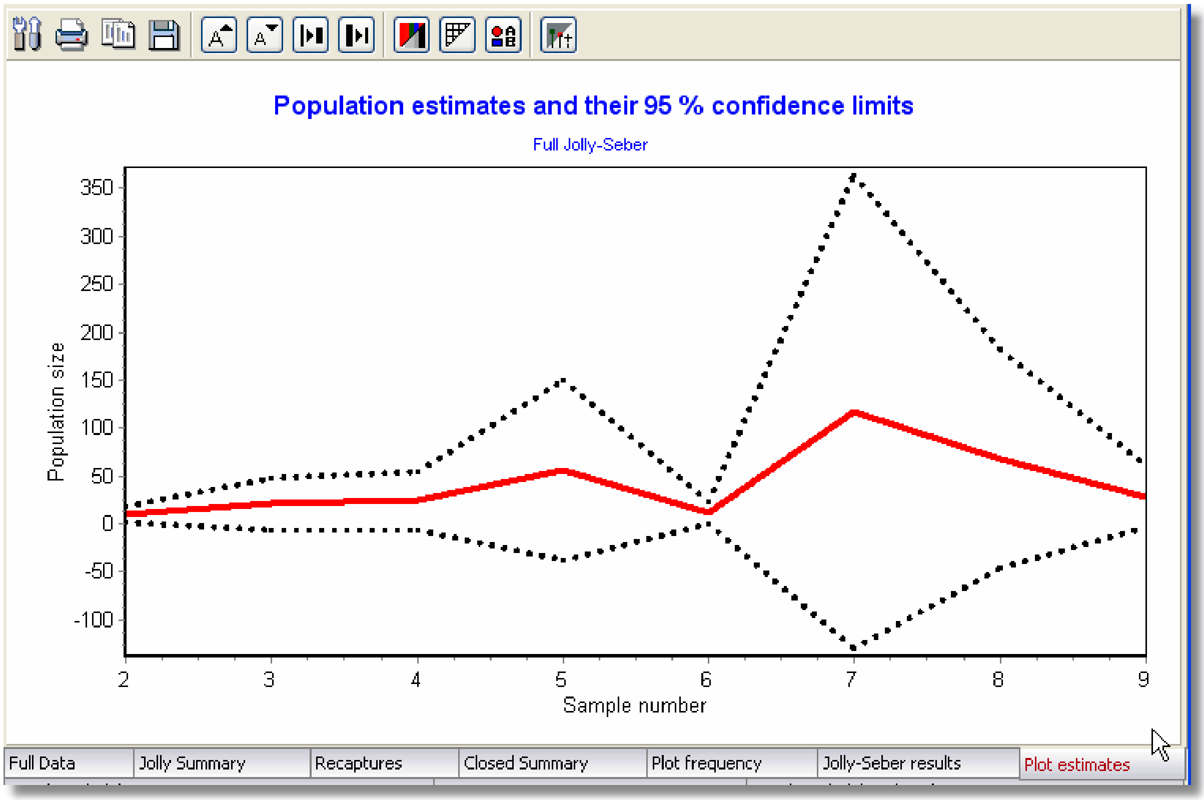
A plot of the population size through time (at the times when samples were taken) plus their 95% confidence limits is obtained by clicking on the Plot estimates tab.

See also:

Printing or exporting your results
Plotting population estimates

3.10 Plot Estimates - tab

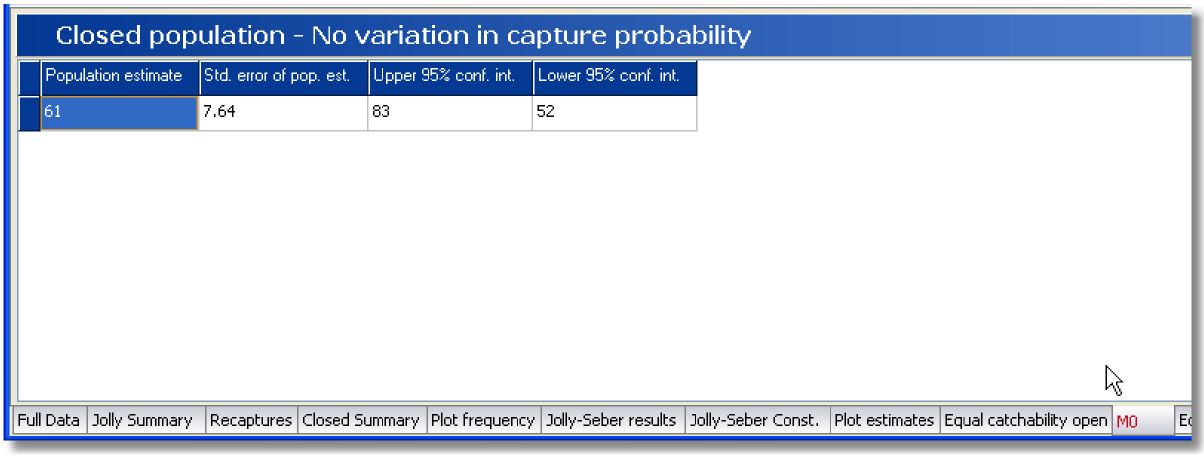
This tab form is visible after either a Full Jolly-Seber or a Constant p & s Jolly-Seber analysis has been undertaken.
It displays a plot of the estimated population size through time, and the upper and lower 95% confidence limits are shown as dotted lines. When possible, the lower confidence limit is constrained so that it can never be less than the actual number of animals captured. This constraint cannot be applied to a full Jolly Seber because deaths and emigration may reduce the size of the population below the actual total number caught.



Many features of this plot can be changed by the user - see Graph display options available from the toolbar.

3.11 MO - tab

This form presents population estimates calculated using a model that assumes no variation to capture probability through time or between individuals.



Closed population - No variation in capture probability

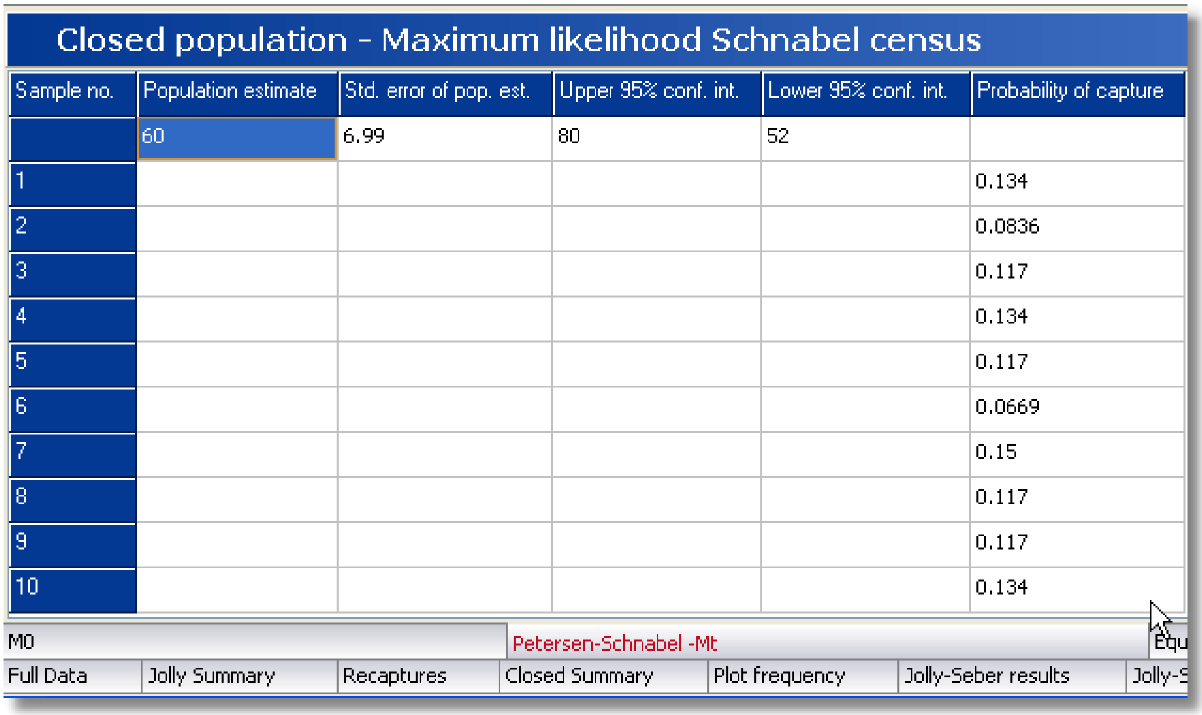
Population estimate	Std. error of pop. est.	Upper 95% conf. int.	Lower 95% conf. int.
61	7.64	83	52

Column 1 gives the population estimate,
Column 2 the standard error of the population estimate, and
Columns 3 and *4* the upper and lower 95% confidence intervals.

See also:
Printing or exporting your results

3.12 Petersen-Schnabel Mt - tab

This form presents population estimates calculated using the maximum likelihood calculations for a Schnabel census. If only two samples were taken, then it will give the results for a standard Lincoln index.



Closed population - Maximum likelihood Schnabel census

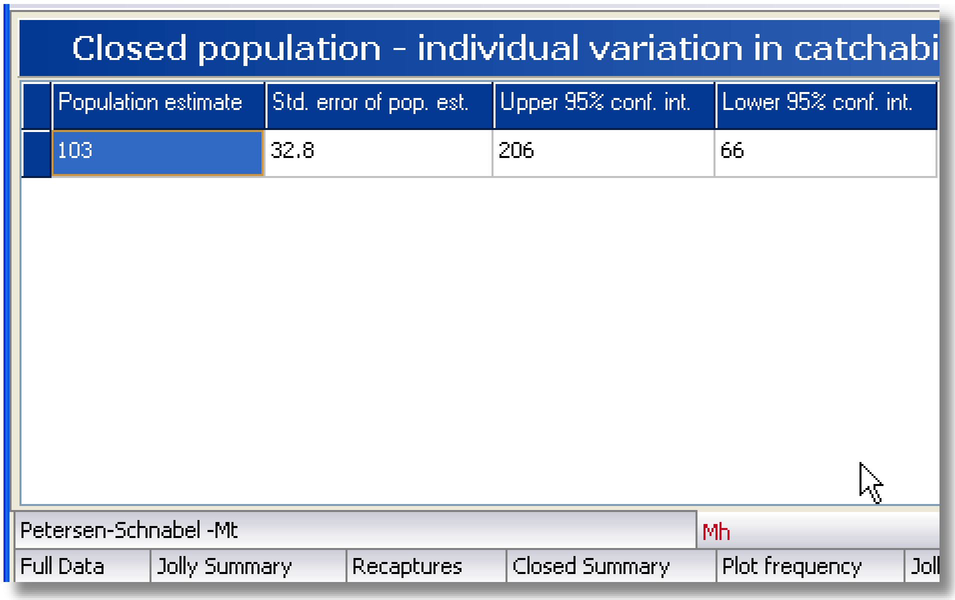
Sample no.	Population estimate	Std. error of pop. est.	Upper 95% conf. int.	Lower 95% conf. int.	Probability of capture
	60	6.99	80	52	
1					0.134
2					0.0836
3					0.117
4					0.134
5					0.117
6					0.0669
7					0.15
8					0.117
9					0.117
10					0.134

Column 2 gives the population estimate,
Column 3 the standard error of the population estimate,
Columns 4 and *5* the upper and lower 95% confidence intervals, and
Column 6 gives the estimated probability of capture for each of the sampling periods listed in Column 1.

See also:
Printing or exporting your results

3.13 Mh - tab

This form presents population estimates calculated using a model that assumes individual heterogeneity in capture probability.



Closed population - individual variation in catchabi

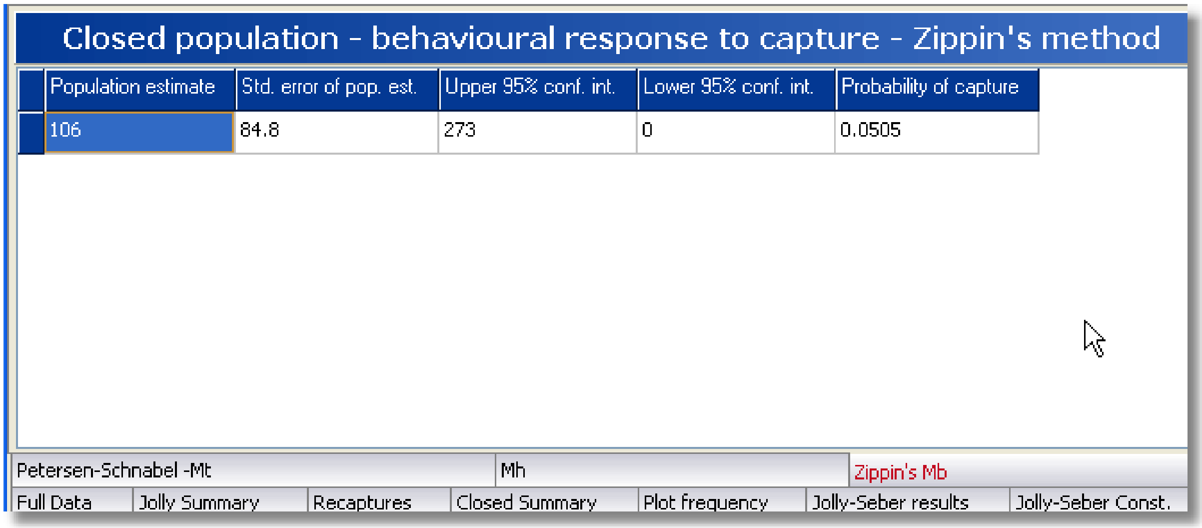
Population estimate	Std. error of pop. est.	Upper 95% conf. int.	Lower 95% conf. int.
103	32.8	206	66

Column 1 gives the population estimate,
Column 2 the standard error of the population estimate, and
Columns 3 and *4* the upper and lower 95% confidence intervals.

See also:
Printing or exporting your results

3.14 Zippin's Mb - tab

This form presents population estimates calculated using a model that assumes that the probability of capture changes after the animals have been captured once - what is often termed a behavioural response.



Closed population - behavioural response to capture - Zippin's method

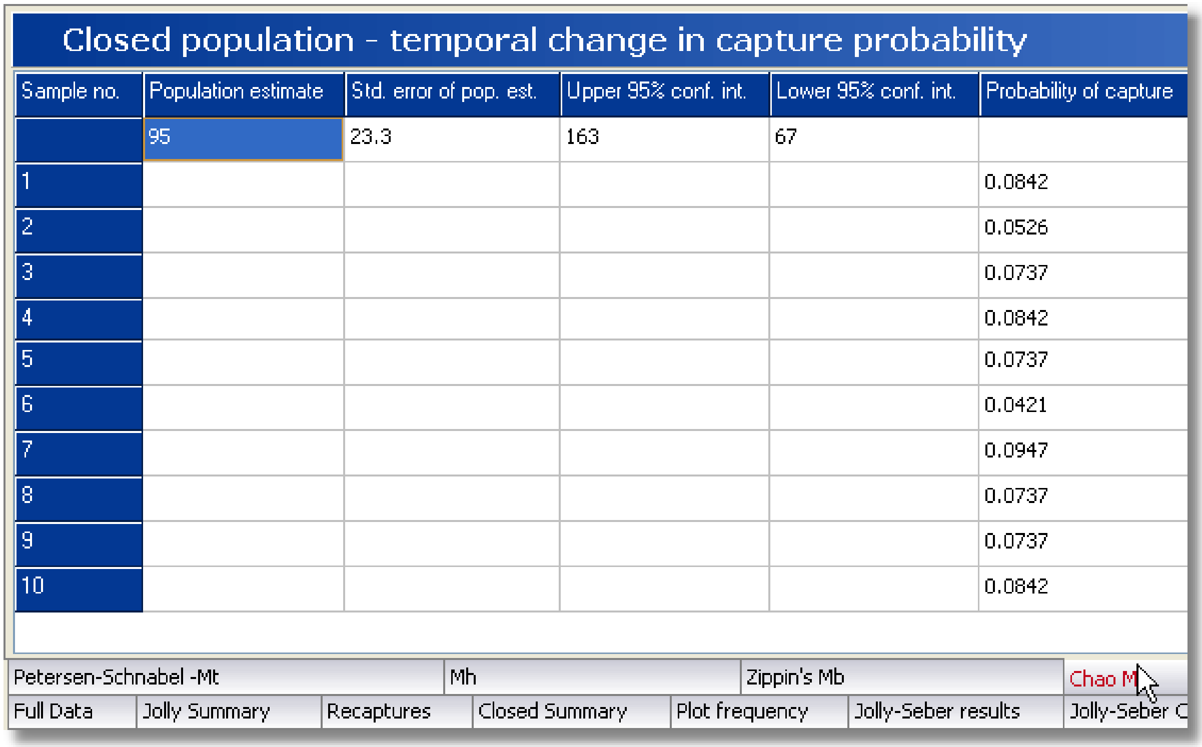
Population estimate	Std. error of pop. est.	Upper 95% conf. int.	Lower 95% conf. int.	Probability of capture
106	84.8	273	0	0.0505

Column 1 gives the population estimate,
Column 2 the standard error of the population estimate,
Columns 3 and *4* the upper and lower 95% confidence intervals, and
Column 5 the probability of capture.

See also:
Printing or exporting your results

3.15 Chao Mt - tab

This form presents population estimates calculated using a model that assumes that the probability of capture changes through time. Normally the Schnabel maximum likelihood method would be used, but this alternative approach developed by Chao is included for comparison.



Closed population - temporal change in capture probability

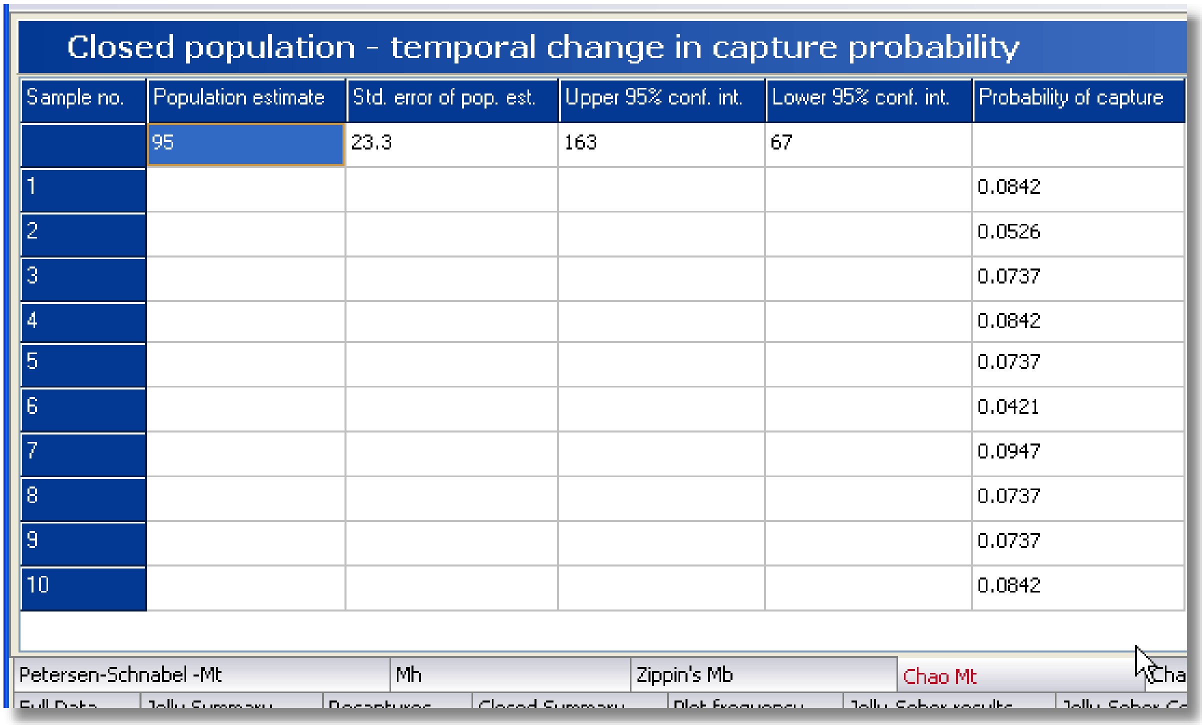
Sample no.	Population estimate	Std. error of pop. est.	Upper 95% conf. int.	Lower 95% conf. int.	Probability of capture
	95	23.3	163	67	
1					0.0842
2					0.0526
3					0.0737
4					0.0842
5					0.0737
6					0.0421
7					0.0947
8					0.0737
9					0.0737
10					0.0842

Column 2 gives the population estimate,
Column 3 the standard error of the population estimate,
Columns 4 and *5* the upper and lower 95% confidence intervals, and
Column 6 gives the estimated probability of capture for each of the sampling periods listed in Column 1.

See also:
Printing or exporting your results

3.16 Chao Mth - tab

This form presents population estimates calculated using a model that assumes that the probability of capture changes through time because of changes in capture probabilities, and there are also individual changes in behaviour that alter recapture probabilities. The method used was developed by Chao.



Closed population - temporal change in capture probability

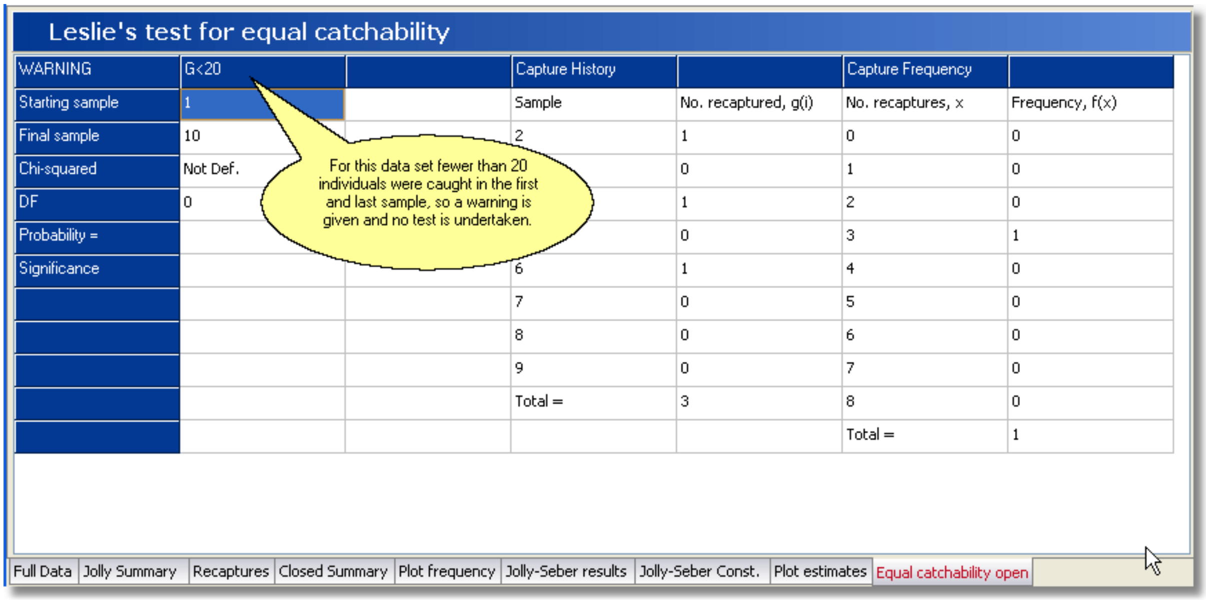
Sample no.	Population estimate	Std. error of pop. est.	Upper 95% conf. int.	Lower 95% conf. int.	Probability of capture
	95	23.3	163	67	
1					0.0842
2					0.0526
3					0.0737
4					0.0842
5					0.0737
6					0.0421
7					0.0947
8					0.0737
9					0.0737
10					0.0842

Column 2 gives the population estimate,
Column 3 the standard error of the population estimate,
Columns 4 and *5* the upper and lower 95% confidence intervals, and
Column 6 gives the estimated probability of capture for each of the sampling periods listed in Column 1.

See also:
Printing or exporting your results

3.17 Equal Catchability open - tab

This window shows the results of Leslie's test for equal catchability.



Leslie's test for equal catchability

WARNING	G<20		Capture History		Capture Frequency	
Starting sample	1		Sample	No. recaptured, g(i)	No. recaptures, x	Frequency, f(x)
Final sample	10		2	1	0	0
Chi-squared	Not Def.			0	1	0
DF	0			1	2	0
Probability =				0	3	1
Significance			6	1	4	0
			7	0	5	0
			8	0	6	0
			9	0	7	0
			Total =	3	8	0
					Total =	1

For this data set fewer than 20 individuals were caught in the first and last sample, so a warning is given and no test is undertaken.

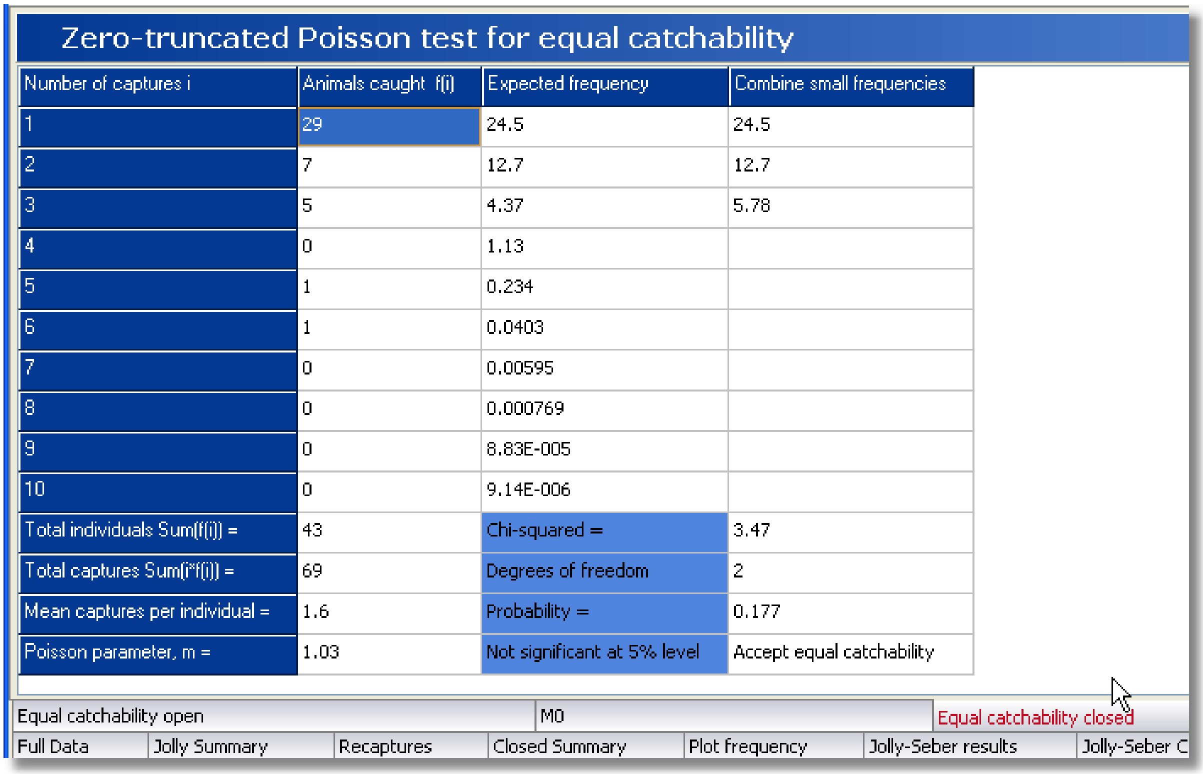
The results of the test are shown in the first two columns. The rest of the grid shows the intermediate calculations. The test is only reliable if >20 individuals were caught in the first and last samples, and a warning will be shown if this is not the case. If insufficient data are available then *Not Def.* will be placed in the Chi-squared cell.

The Capture history table records the number of individuals caught in the first samples that were caught in subsequent samples, and the Capture frequency table gives the number of individuals caught 1, 2 .. n times.

See also:
Printing or exporting your results

3.18 Equal catchability closed - tab

This window shows the results of a Zero-truncated Poisson test for equal catchability.



Zero-truncated Poisson test for equal catchability

Number of captures i	Animals caught f(i)	Expected frequency	Combine small frequencies
1	29	24.5	24.5
2	7	12.7	12.7
3	5	4.37	5.78
4	0	1.13	
5	1	0.234	
6	1	0.0403	
7	0	0.00595	
8	0	0.000769	
9	0	8.83E-005	
10	0	9.14E-006	
Total individuals Sum(f(i)) =	43	Chi-squared =	3.47
Total captures Sum(i*f(i)) =	69	Degrees of freedom	2
Mean captures per individual =	1.6	Probability =	0.177
Poisson parameter, m =	1.03	Not significant at 5% level	Accept equal catchability

The upper part of the window shows the observed and expected frequencies of capture.
The Combine small frequencies column is the same as the expected frequencies, with the low frequencies combined together to allow a Chi-squared goodness of fit test.
Below this table are placed the results of the Chi-squared test plus intermediate calculations used in the calculation of the Poisson parameter.

See also:
Printing or exporting your results

Part

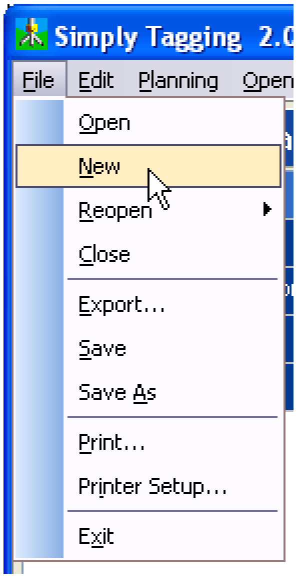
IV

4 Entering Data

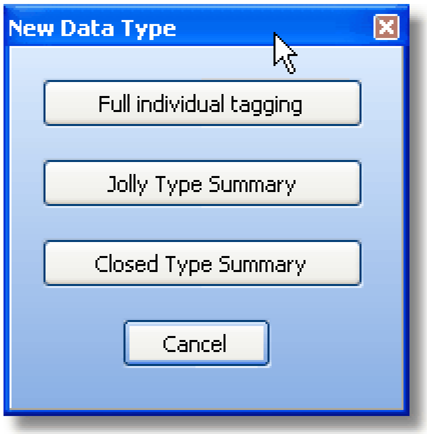
A data set can be created using any program capable of producing a CSV (comma-separated values) file. For example, you could prepare your dataset using Excel. To be used by *Simply Tagging* the file must be in the correct format. The easiest way to understand how to create a data set is to open one of the demonstration data sets.

DemoFull.csv is an example of a data set where individual capture histories have been entered. **Jolly_summary.csv** is mark-recapture summary data organised for the Jolly-Seber method, and **Closed_summary.csv** holds the summary data needed for the closed methods.

To create a new data set within *Simply Tagging* select **File: New** from the drop-down menus.



You will be presented with a window that offers 3 types of data for entry; Full individual tagging, Jolly-Seber summary and Closed summary.



Full individual tagging
If you have selected to enter the capture history of each individual, you will be presented with an empty grid which you will need to fill in for every individual.
Instructions for data entry

Editing data
Subsetting your data by size or sex

Jolly-Seber summary
If you have selected to enter your data as a Jolly-Seber summary table, then you will be asked to enter the number of samples taken and will then be presented with an empty grid which you will need to fill.
Instructions for data entry
Editing data

Closed summary
Instructions for data entry
Editing data
A simple example of data entry

4.1 Entering full individual tagging data

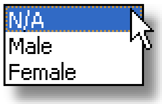
This type of data is only available when animals are individually tagged with a unique mark so that you have the full capture history of each animal. You can see examples of this type of data set either by opening the example file **DemoFull.csv** or by running the simulator.

Some methods for analysing closed populations require full capture history data. Given a full data set *Simply Tagging* will create other summary tables as required.

The data for each individual is arranged by columns.
Column 1, labelled 'Animal' is to hold a unique identification for the animal. This can be any combination of letters or numbers. It could, for example, be the tag number or the name given to the individual animal.

Column 2, labelled 'Wt' is designed to hold additional information such as weight, age or length that can be used to subdivide the data into size or age classes for separate analysis. This field need not be filled.

Column 3, labelled 'Sex' should hold Male, Female, or N/A for not applicable. It is used to subdivide the data by sex for separate analysis. This field can be ignored if sex is unimportant. To define the sex, click on a cell in the Sex column and a drop-down menu will appear.



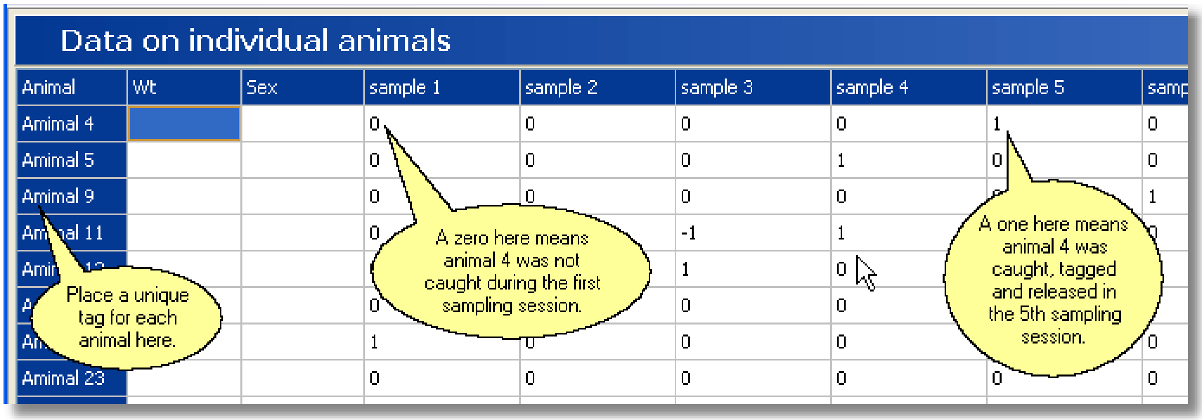
Columns 4 onwards are labelled Sample 1, Sample 2, Sample 3 etc., and are used to encode the capture history. For each sampling occasion enter:
1 if the animal was captured, tagged and released,
0 if the animal was not captured,
–1 if the animals was captured but not released (for example, if it was killed in the trap or during handling).

The Return key on your keyboard moves you sequentially through the grid, and when pressed with the cursor in the lower right hand column will add a new column (Sample).

To add a new row, press the Insert key on your keyboard. A row will be inserted below that currently selected.

Please note, if the text within a box is selected (it will usually appear blue), Insert will not work. Simply click on the cell again to select the entire cell, rather than the text inside it, and Insert will be activated.

Use the Delete key to remove a row.



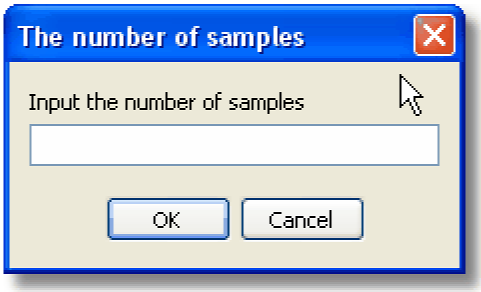
Data on individual animals

Animal	Wt	Sex	sample 1	sample 2	sample 3	sample 4	sample 5	samp
Amimal 4			0	0	0	0	1	0
Amimal 5			0	0	0	1	0	0
Amimal 9			0	0	0	0		1
Am al 11			0		-1	1		
Amir					1	0		
A			0		0	0		
An			1	0	0	0		0
Amimal 23			0	0	0	0	0	0

4.2 Entering data in a Jolly-Seber summary table

This data table can be created from either individual or batch tagging information. If you have individual tagging information then this can be entered as full individual tagging data and the program will create this table for you. You can see an example of this type of data set by opening the example file **Jolly-summary.csv**.

Having selected Jolly Type Summary, you are asked to enter the number of sampling occasions undertaken.



Enter an integer number and click on OK.

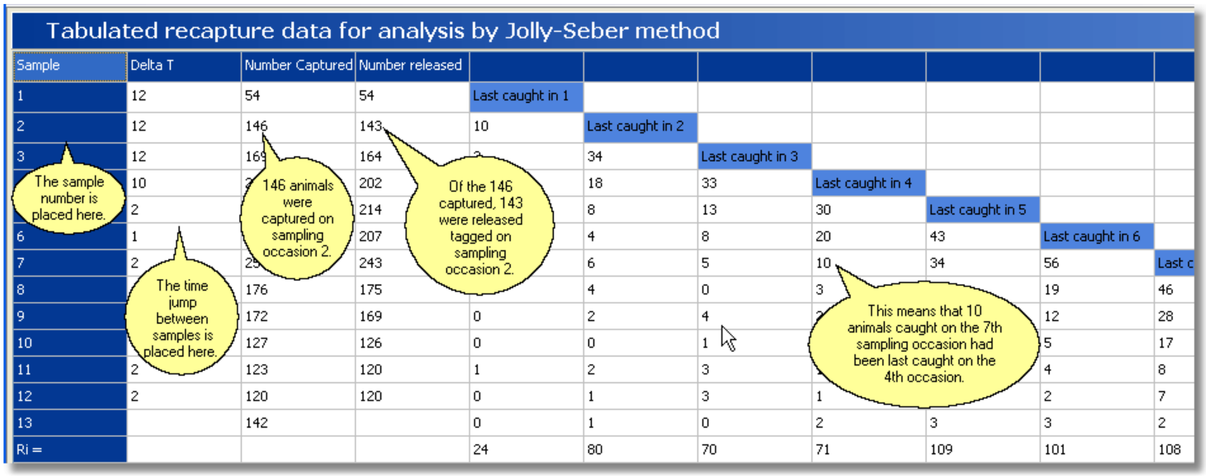
You will then be presented with an empty data grid.

Column 1 gives the number of the sampling occasion, i, and is filled automatically after you have entered the number of sampling occasions.

Column 2 holds the number of time steps between samples. These values do not need to be entered if you are undertaking a standard Jolly-Seber analysis. They become necessary if the constant probability of capture and survival version of the Jolly-Seber model is used. If no values are entered then a time step of 1 is assumed.

Column 3 holds the total number of animals caught on occasion i.

Column 4 holds the number released with tags – this will not be the same as the number in column 2 if animals were killed in the trap or during handling.
The rest of the table comprises the lower half of a square matrix in which are entered the number of animals captured at time i which were last previously captured in samples 1 to i-1.



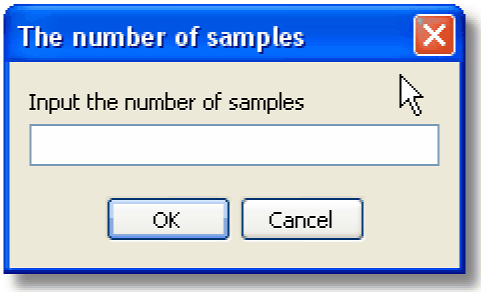
Tabulated recapture data for analysis by Jolly-Seber method

Sample	Delta T	Number Captured	Number released							
1	12	54	54	Last caught in 1						
2	12	146	143	10	Last caught in 2					
3	12	169	164	[illegible]	34	Last caught in 3				
[illegible]	10	[illegible]	202	[illegible]	18	33	Last caught in 4			
[illegible]	2	[illegible]	214	[illegible]	8	13	30	Last caught in 5		
6	1	[illegible]	207	[illegible]	4	8	20	43	Last caught in 6	
7	2	[illegible]	243	[illegible]	6	5	10	34	56	Last c
8	[illegible]	176	175	[illegible]	4	0	3	[illegible]	19	46
9	[illegible]	172	169	0	2	4	[illegible]	[illegible]	12	28
10	[illegible]	127	126	0	0	1	[illegible]	[illegible]	5	17
11	2	123	120	1	2	3	[illegible]	[illegible]	4	8
12	2	120	120	0	1	3	1	[illegible]	2	7
13		142		0	1	0	2	3	3	2
Ri =				24	80	70	71	109	101	108

4.3 Entering data in a closed summary table

This data table can be created from either individual tagging data or batch tagging information. If you have individual tagging information then this can be entered as full individual tagging data and the program will create this table for you. You can see an example of this type of data set by opening the example file **Closed_summary.csv**.

Having selected Closed Type Summary, you are asked to enter the number of sampling occasions undertaken.



Four data vectors each placed on a separate row are required.

Row 1 gives the sample number and is filled in automatically when you have specified the number of samples taken.

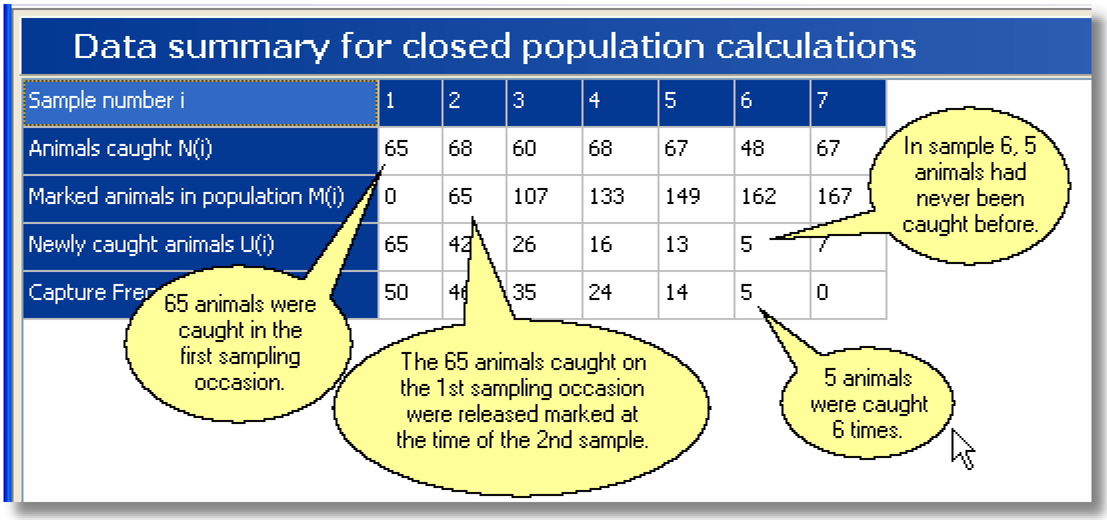
Row 2 holds the number of animals caught on each sampling occasion, N(i).

Row 3 holds the number of marked animals in the population, M(i). For sample i, this is the sum of the newly caught animals from sample 1 to sample i-1. If any animals were killed during capture and handling they must also be subtracted.

Row 4 holds the number of animals newly captured in the ith sample, U(i). These are the captured individuals that bear no previous mark.

Row 5 is the frequency distribution of the times of capture. Enter here a count of the number of individuals caught 1, 2, or more times during the study, F(i).

The figure below shows a typical example. Click within the boxes of dashed lines for an explanation of the rows.



Data summary for closed population calculations

Sample number i	1	2	3	4	5	6	7
Animals caught N(i)	65	68	60	68	67	48	67
Marked animals in population M(i)	0	65	107	133	149	162	167
Newly caught animals U(i)	65	42	26	16	13	5	7
Capture Freq	50	46	35	24	14	5	0

65 animals were caught in the first sampling occasion.

The 65 animals caught on the 1st sampling occasion were released marked at the time of the 2nd sample.

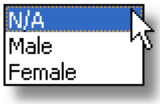
In sample 6, 5 animals had never been caught before.

5 animals were caught 6 times.

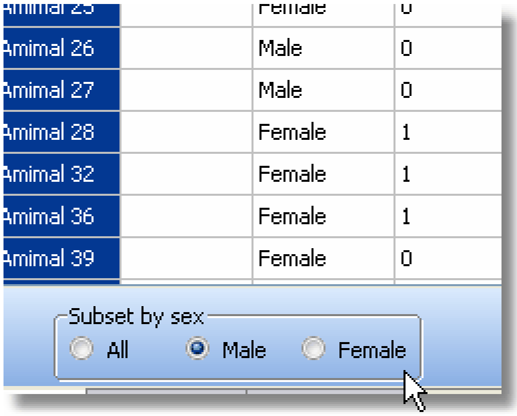
4.4 Subsetting by age, sex or size

If you have entered full individual tag data then you have the option to add information on the sex and some measure of size, weight or age which can be used to partition your data into separate groups for analysis. **You do not need to add any information to the size or sex columns, as these columns are only referenced when a subset is requested**.

Data in the size column must be entered as a single number eg 12.4, 2 or 0.7. This could be a weight, length, width or age. There are three options available for the Sex column; N/A, male or female. These can be entered by clicking 3 times on a cell and choosing one of the options from the drop-down menu that will appear.



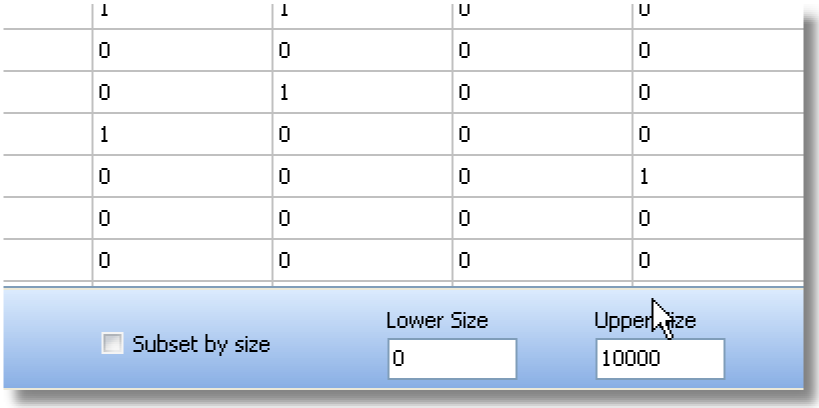
To subset the data by sex, choose one of the options on *Subset by sex* radio box below the data grid. All subsequent analyses will be carried out only on observations for the sex selected.



Amimal 26		Male	0
Amimal 27		Male	0
Amimal 28		Female	1
Amimal 32		Female	1
Amimal 36		Female	1
Amimal 39		Female	0

Subset by sex
○ All ● Male ○ Female

To subset by size (age) click on the *Subset by size* tick box and type upper and lower size limits in the boxes in the lower right hand area of the screen.



	0	0	0	0
	0	1	0	0
	1	0	0	0
	0	0	0	1
	0	0	0	0
	0	0	0	0

☐ Subset by size

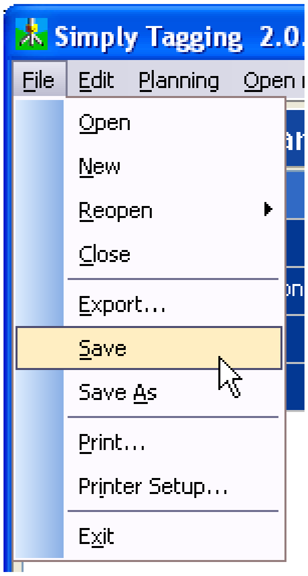
Lower Size: 0

Upper Size: 10000

4.5 Editing and saving data

The data grids can be edited by using the mouse to click into a cell to select it, and typing in a new value.

These changes will not alter the original data file stored on your hard drive file until **File: Save** is used.

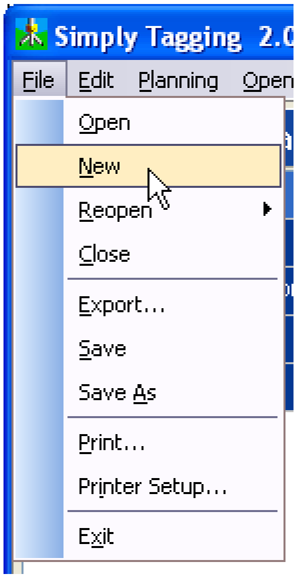


Data can be saved as a new data set using **File: Save As**. Any changes will not be displayed in the output forms until the method is re-run by selection from the drop-down menus.

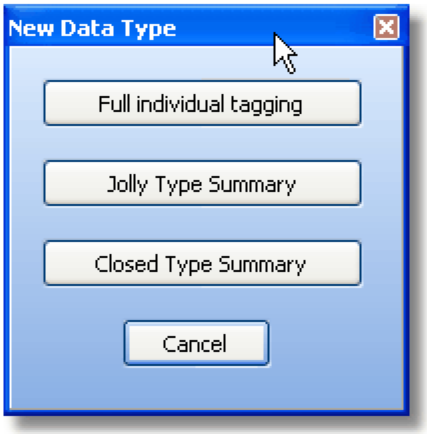
4.6 A simple example of data entry

A small 2-day experiment has been undertaken from which the population size will be estimated using a Petersen-Lincoln index.
On day 1, 56 individuals were caught and marked.
On day 2, 120 animals were caught, of which 25 bore marks from day 1.

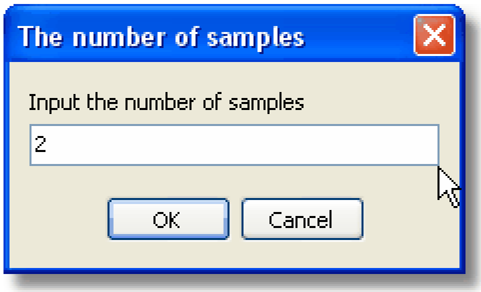
Choose **File: New** to create a new data file.



Next you will be asked to choose the type of data you wish to input. Click on the Closed Type Summary button.



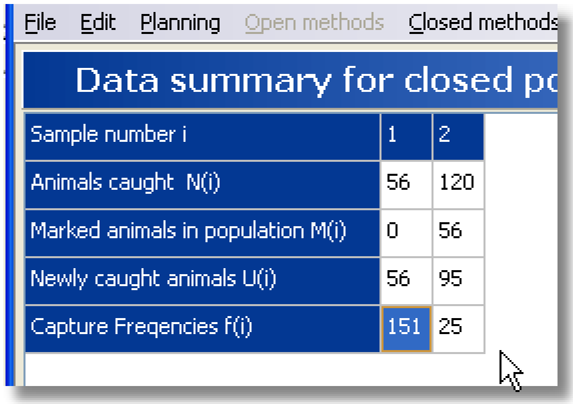
You will be asked to enter the number of samples; type in 2.



Input the number of samples

2

You will now be presented with an empty grid into which to type the observations. When completed the data grid should look like this:

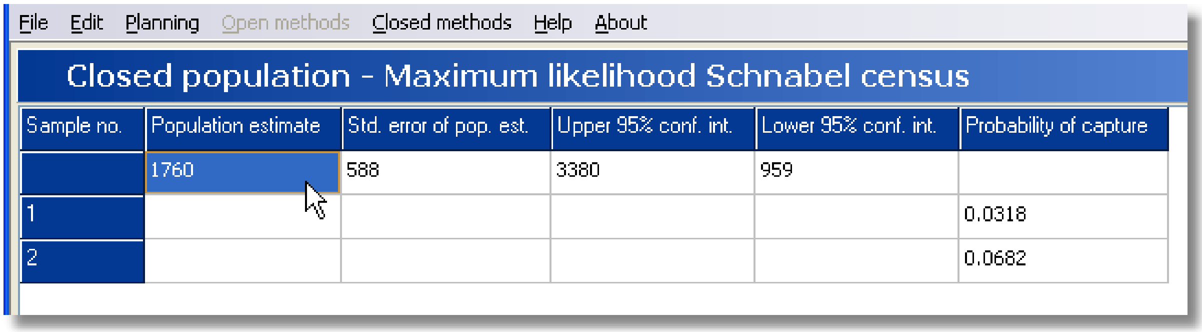


Sample number i	1	2
Animals caught N(i)	56	120
Marked animals in population M(i)	0	56
Newly caught animals U(i)	56	95
Capture Freqencies f(i)	151	25

U(2) = 95 because the new captures = 120-25

f(1) = 56+120-25=151

To undertake the calculations select **Closed methods: Temporal change in capture probability (Schnabel ML, Mt)** and the results will be displayed in the Mt tab. This will be the maximum likelihood estimate of population size, as per the Petersen-Lincoln index.



Sample no.	Population estimate	Std. error of pop. est.	Upper 95% conf. int.	Lower 95% conf. int.	Probability of capture
	1760	588	3380	959	
1					0.0318
2					0.0682

Part

V

5 Printing and saving results

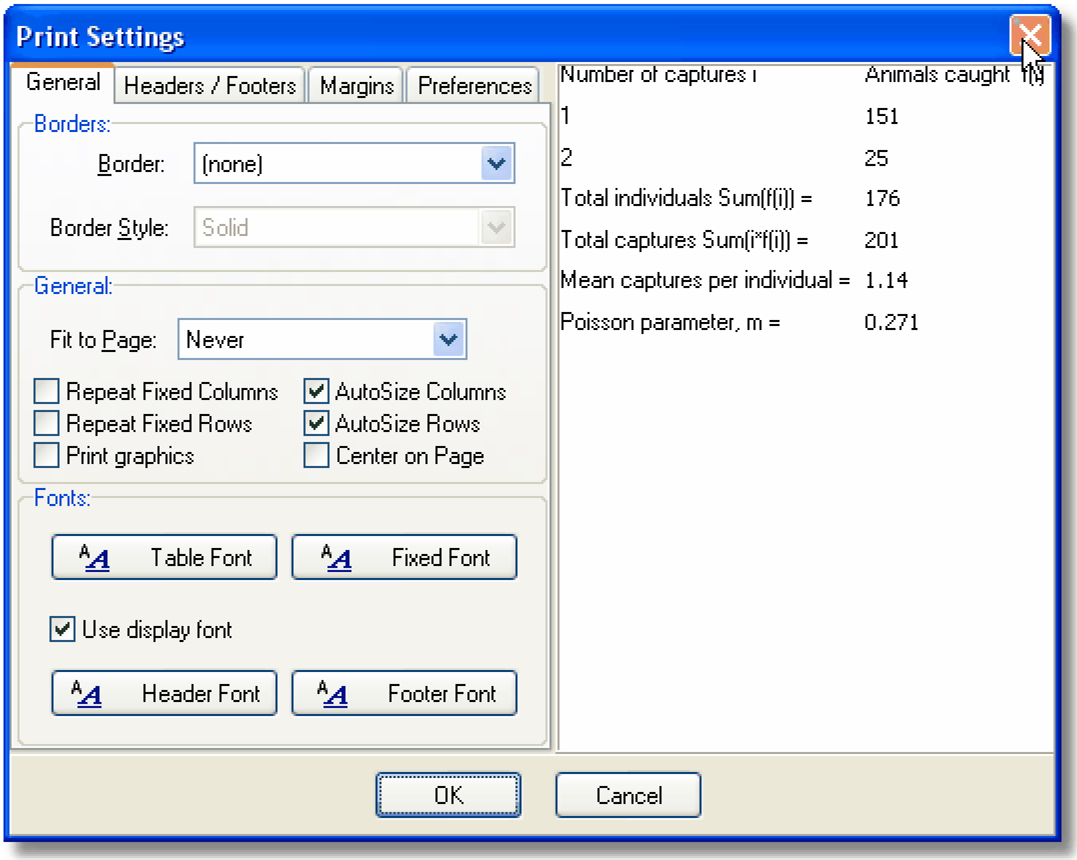
Output, both graphical and text, can be saved as a file, copied to the clipboard or printed. *Simply Tagging* also offers a wide variety of options for editing and designing your graphs, including pre-defined themes.

See topics below for further details.

Printing and exporting text and grid output
Printing charts
Exporting charts
Themes for charts

5.1 Printing and saving text and grid output

With an output grid showing, simply choose **File: Print** and a dialog box for printing options will be activated.

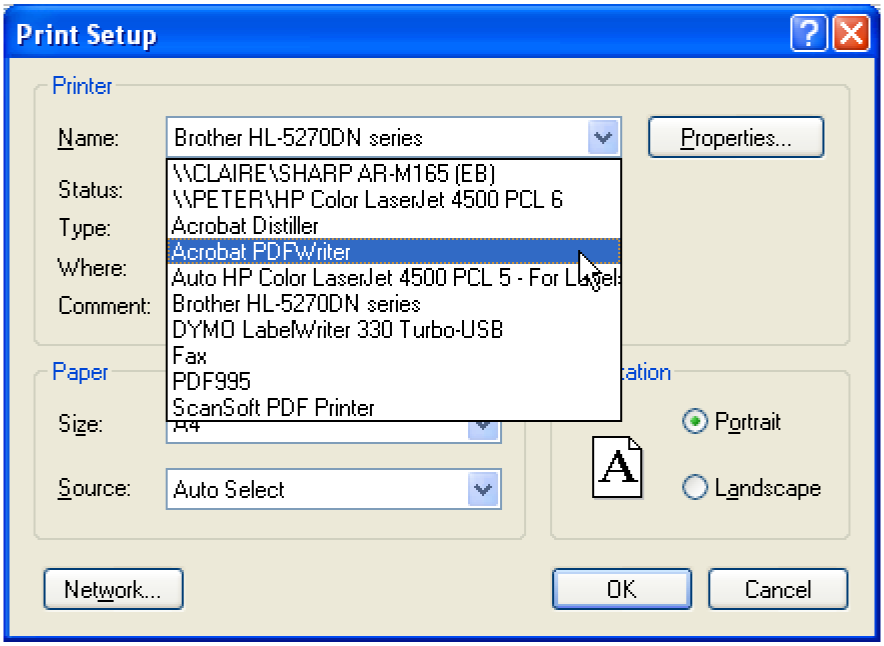


Border: (none)
Border Style: Solid
Fit to Page: Never
☐ Repeat Fixed Columns
☐ Repeat Fixed Rows
☐ Print graphics
☑ AutoSize Columns
☑ AutoSize Rows
☐ Center on Page
☑ Use display font

Number of captures i	Animals caught f(i)
1	151
2	25
Total individuals Sum(f(i)) =	176
Total captures Sum(i*f(i)) =	201
Mean captures per individual =	1.14
Poisson parameter, m =	0.271

Using the options presented, you can change almost all aspects of the printed grid.

To change the default printer, and the printer's settings, use the **File: Printer Setup** option:



Name: Brother HL-5270DN series

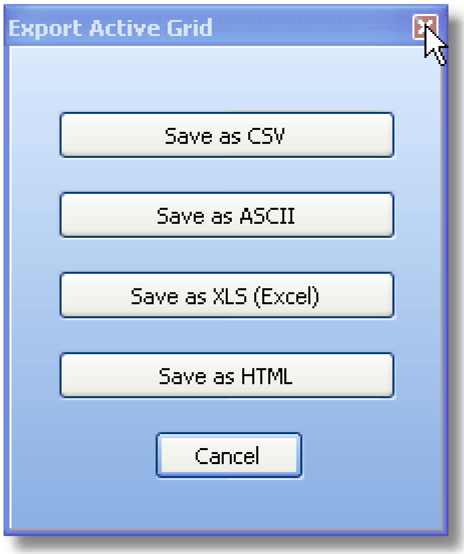
Size: A4

Source: Auto Select

● Portrait

○ Landscape

To save the results as a file choose **File: Export** and follow instructions in the dialog box. You will be able to save the text as a comma-delimited file (*.csv), ASCII text file (*.txt), Excel file (*.xls) or HTML.



5.2 Graph display options

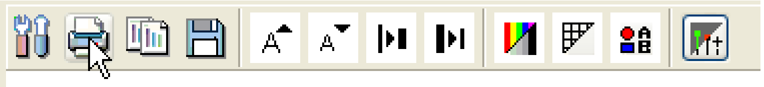
The Chart Toolbar allows you to print and save results, copy them to the clipboard, and edit charts. Almost every aspect of your graph can be edited.

The graph option buttons on the Chart Toolbar are described in order from left to right below. A hint will pop up if you hover over a button on the program.

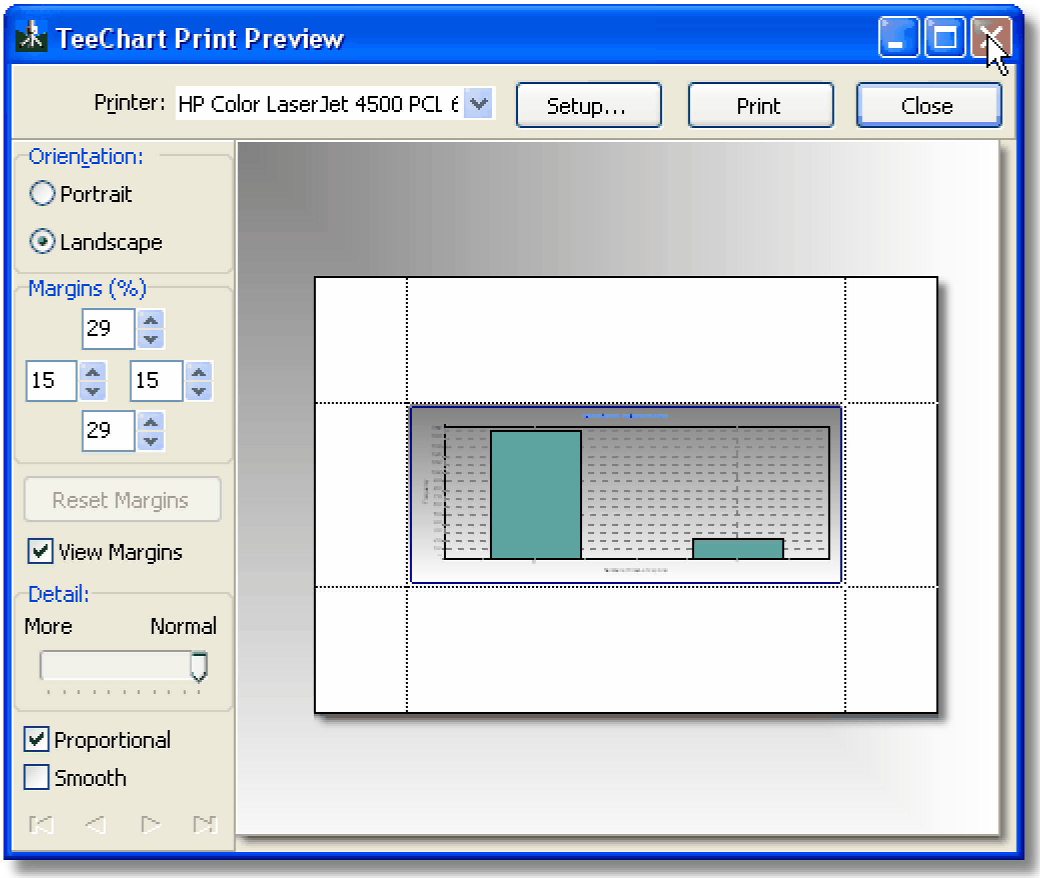
Edit - (Spanner/screwdriver icon) This button will offer a wide range of options to change the style of your graph. It is also used to export or copy your graph to file, and even to email it using the 'Send' button. For more information on chart editing use the TeeChart help system available from the Help button on the chart edit box.
Print - Use this button to print the graph
Copy - Use this option to copy the graph to the clipboard.
Save - Save the file in a variety of different formats.
Increase font - This will increase the font size of the chart titles.
Decrease font - This will decrease the font size of the chart titles.
Increase line thickness - This increases the thickness of plotted lines.
Decrease line thickness - This decreases the thickness of plotted lines.
Change between colour/grey scale - Change between a colour and greyscale plot.
Add grid - Add graph grid lines to the plot.
Add legend - Add legend to the plot. N.B. This legend can be used to select groups for plotting.
Select theme - Use to select a particular style of graph, for example black background. See Themes for charts.

5.3 Printing charts

The graphs can be printed using **File: Print**, or the **Print** button on the chart toolbar.



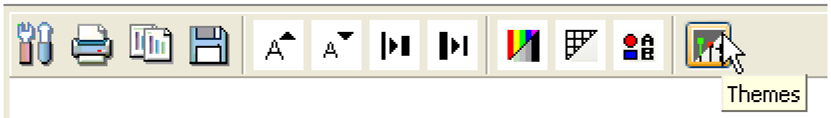
Using either option will call up the Print Preview dialog, showing the page layout, and allowing image size, margins, and paper orientation to be changed.



If you have the full version of Adobe Acrobat (**not** the free Acrobat Reader) installed on your computer, you will be able to convert the chart directly to a .pdf file by selecting the appropriate program from the list of available printers in the Print dialog box.

5.4 Themes for charts

Themes are general graph plotting styles that the user can select.
To choose a theme, click on the Themes button at the end of the graphics tool bar.



This will display the Themes dialog with a number of preset themes ready for selection.

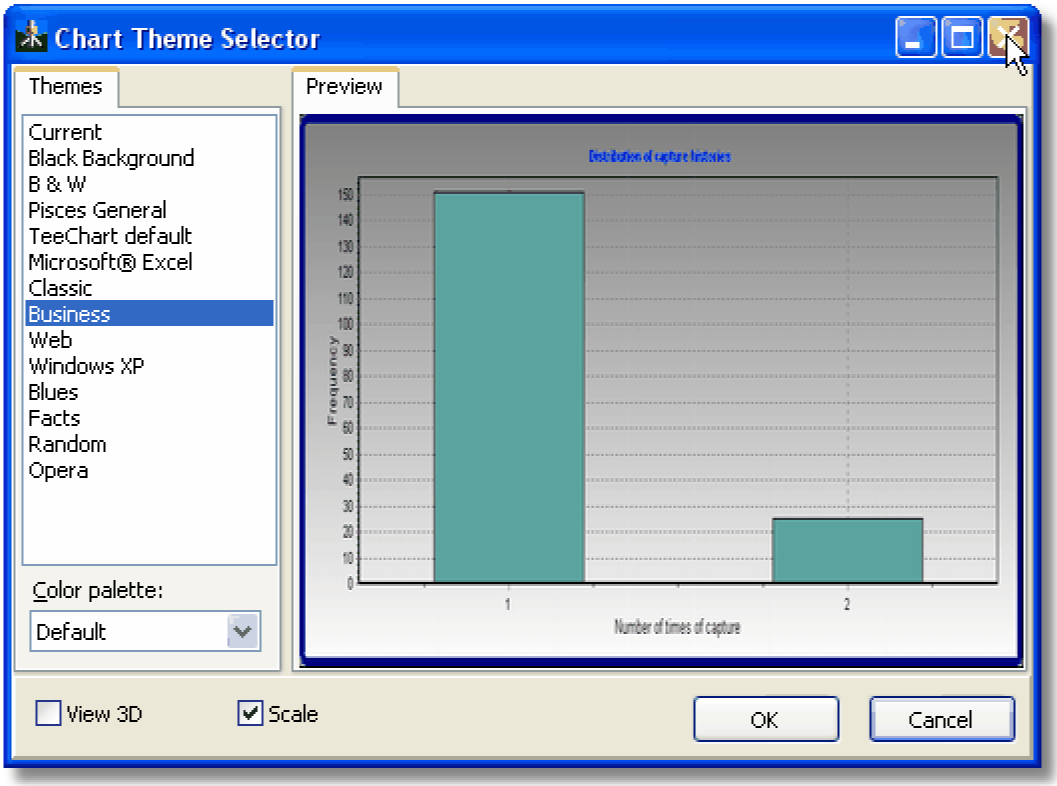


Chart Theme Selector

Themes

- Current
- Black Background
- B & W
- Pisces General
- TeeChart default
- Microsoft® Excel
- Classic
- Business
- Web
- Windows XP
- Blues
- Facts
- Random
- Opera

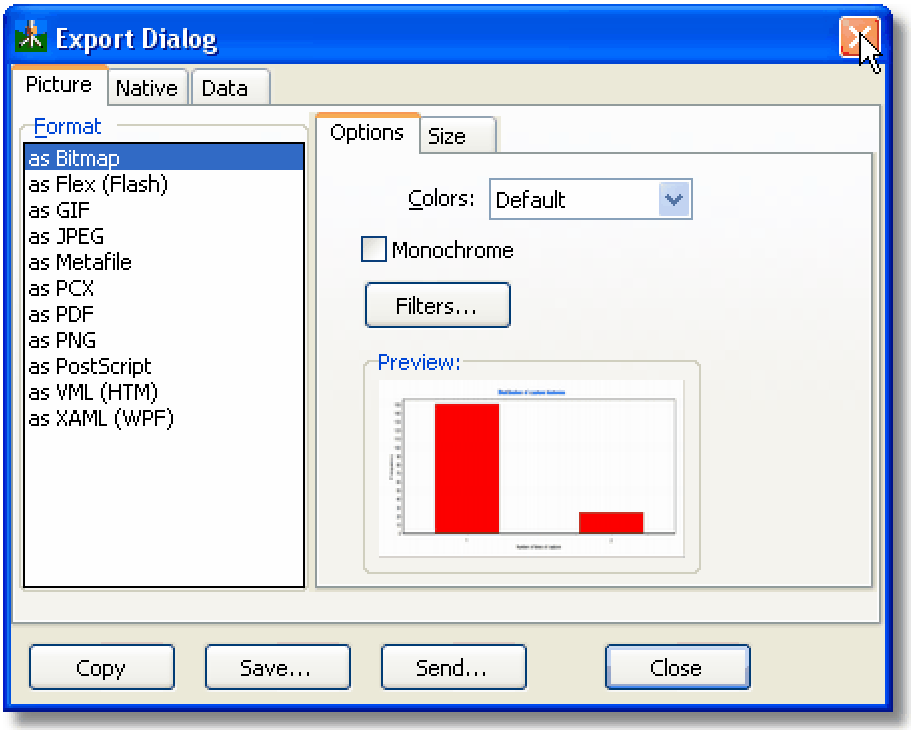
Color palette: Default

☐ View 3D ☑ Scale

Once a theme has been applied to a chart, it can be difficult to return to the plain default style used by the program, particularly if you have made modifications of your own to labels and legends, etc. It can be simpler to close the program and re-perform the analysis to regain the default style of chart.

5.5 Exporting charts

To export the image of a chart select **File: Export**. This will open the Export Dialog.



Colors: Default

☐ Monochrome

The chart can be saved in a number of different file formats: Bitmap (*.bmp), Flex, JPEG (*.jpg), Metafile (*.emf), PCX, PDF, PNG, GIF or Native (*.tee). Each file format has advantages and disadvantages.

- The advantage of Enhanced Metafile is that, if pasted into, for instance, a Word document, it can be resized by dragging, without losing resolution. However, when a page containing a Metafile is printed as a PDF document, the results can sometimes be disappointing.
- Bitmaps are a lossless method of saving; the stored file will not lose any of the original's detail. Because of this, bitmaps tend to be much larger than compressed files such as Enhanced Metafiles or JPEGs.
- JPEGs are files which can be compressed to take up less space - useful if you wish to send one by email, put it on a website, or paste it in to a document. If they are compressed too heavily, they can lose resolution and detail, and spoil colours.
- GIFs are also compressed files useful for web sites; they have a considerably smaller colour palette than JPEGs or BMPs; 256 colours, as opposed to many millions. This means that while a JPEG or BMP image can show a smooth gradation of colour (for instance in a graded background), saved as a GIF image, it will appear broken up into jagged zones of colour. GIF images are therefore better suited to images showing large discrete blocks of single colours.
- PDF is the Adobe Acrobat file format and is an excellent compressed format if you plan to produce a document in a pdf format.
- The Native (*.tee) format saves all the chart attributes, and the data series, rather than the image itself. This means that you can save the chart, and open it again at a later date to edit it, using the free TeeReader software supplied on the installation CD. Tee files tend to be very small indeed; often less than 1KB.

The Export dialog can also be used to export the data shown on the chart - click on the Data tab.

You can also copy a chart to the Windows clipboard using the Copy button on the graphics toolbar.

Part VI

6 Methods

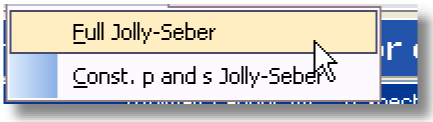
Simply Tagging has the following estimation methods for closed populations:
Model M0: Constant probability of capture
Model Mt: Maximum likelihood Schnabel census (Petersen-Lincoln index if samples = 2)
Model Mt: Chao method
Model Mh: Individual variation in probability of capture
Model Mb: Behavioural changes following capture
Model Mth: Temporal changes in catchability and individual heterogeneity

For open populations *Simply Tagging* offers both a full Jolly-Seber analysis and a reduced model in which probability of capture and survival are assumed to be constant over the period of the experiment.

Simply Tagging also offers a data simulation module.

6.1 Full Jolly-Seber

The following analysis is carried out if **Open methods: Full Jolly-Seber** is selected from the drop-down menu.



If full individual tagging data are input, then *Simply Tagging* calculates and tabulates the recapture data according to the date of initial capture (or mark) and the date on which the animal was last captured. The columns are then summed to give the total number of animals released and subsequently recaptured (Ri). Alternatively, if batch tagging has been undertaken then the user will enter this in the summary table. This recapture table can be viewed by clicking on the Jolly Summary tab.

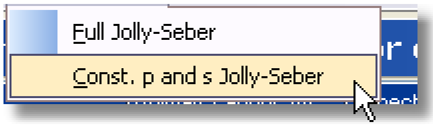
Once an analysis is initiated by selecting one of the options in the Open methods drop-down, another table is calculated giving the total number of animals recaptured on day *i* bearing marks of day *i-1* or earlier; this is done by adding each row in the Jolly Summary table from left to right and entering the accumulated totals. The number marked before time *i* which are not caught in the *i*th sample, but are caught subsequently (Z*i*), is found by adding all but the top entry in each column. This table is viewed by clicking on the Recaptures tab.

Then:
- The estimate of the total number of marked animals at risk in the population on the sampling day *i* is made.
- The proportion of marked animals in the population at the moment of capture on day *i* is found.
- The total population is estimated for each day.
- The probability that an animal alive at the moment of release of the *i*th sample will survive till the time of capture of the *i* + 1th sample is found. Survival rate estimates slightly over one may arise from sampling effects, but rates greatly above this indicate a major error! Frequently it will be found that the marks of one occasion have been lost or were not recognised. This survival rate may be converted to a loss rate (the effect of death and emigration):
- The number of new animals joining the population in the interval between the *i*th and *i + 1*th samples and alive at time *i + 1* is calculated.
- Standard errors (the square roots of the variances) are calculated.

The results of the above calculations are viewed by clicking on the Jolly-Seber results tab. The parameter estimates are arranged in columns with the rows representing each of the samples. A plot of the population size through time (at the times when samples were taken) is obtained by clicking on the Plot estimates tab.

6.2 Constant probability of capture and survival Jolly-Seber

Buckland (1980) discusses a solution to the frequently encountered problem of the Jolly-Seber model, which is that survival and birth rate estimates are found to be impossible (e.g. a negative birth rate). Jolly (1982) presents modifications, which by assuming constant survival and/or captures rates, gives a more parsimonious model, leading to more efficient estimators. Estimates assuming constant survival rates and probability of capture are calculated by selecting **Open methods: Const. p and s Jolly Seber** from the drop-down menu.



When this option is selected both the full Jolly-Seber and the constant survival and capture probability estimators are calculated.

6.3 Constant probability of capture (M0)

This is the simplest model in which every animal at all sampling occasions has the same probability of capture. For more than two sampling occasions the maximum likelihood estimator of population size is found using numerical methods as described by Otis *et al.* (1978)

This model can be viewed as a foundation against which to assess more general and complex models.

The results for an M0 model are displayed by clicking on the M0 tab which will appear once the model has been selected from the Closed methods drop-down menu.

6.4 Temporal change in capture probability (Mt)

This is the most commonly-used model, as experience has shown that the probability of capture varies between samples. Common causes of changes in capture probability are linked to changes in the weather. For example, fewer animals may be captured on cold or windy days or during rainy nights, compared with warm, sunny or dry periods, because of changes in animal activity. If equal sampling effort is used on each sampling occasion then this model may be appropriate if there are significant differences in the number of animals captured on each sampling occasion. Examine the sequence of newly-caught animals; if this shows large variation which you can relate to some environmental variable, then you probably have temporal variation. It is important to note that this model assumes that all animals in the population have an equal probability of capture at any one time. This is sometimes called a 'ball and urn model' since it assumes that the situation can be modelled as if we are sampling well-mixed beans in a plastic bag.

The program uses numerical methods to estimate the maximum likelihood estimator of population size and the probability of capture on each sampling occasion. This is a more mathematically rigorous approach than that originally devised by Schnabel (1938) and further developed by Darroch (1958). When only two samples have been collected, the maximum likelihood estimator is close to Petersen-Lincoln estimator, and this method will give the Chapman (1951) modification of the Petersen-Lincoln index.

The results for an Mt model are displayed by clicking on the Petersen-Schnabel tab, which will appear once the model has been selected from the Closed methods drop-down menu.

Simply Tagging also offers the Chao method for temporal variation in capture probability.

6.5 Individual variation in capture probability (Mh)

Capture probabilities often vary between individual animals; this may be related to sex, age, social dominance or individual differences in activity. If sex, age or size of individuals has been recorded, and sufficient observations are available, then *Simply Tagging* will allow you to subset the data into groups which can be assumed to show homogeneous behaviour, and model Mt, M0 or Mb applied. When this is impossible, *Simply Tagging* estimates population size using the method of Chao (1989).

The results for an Mh model are displayed by clicking on the Mh tab, which will appear once the model has been selected from the Closed methods drop-down menu.

6.6 Behavioural response (Mb)

The experience of being captured, tagged and released often changes an animal's subsequent behaviour so that it becomes either more or less likely to be captured again. Animals have memory, so that the experience of entering a trap may result in trap avoidance. Alternatively, if baited traps are used, an animal may be more willing to enter a trap in future. If recapture probability is considerably different from first capture probability, then a behavioural response can be suspected.

For model Mb, because of the change in behaviour following capture, only first capture data is used to estimate population size, which results in an estimation problem analogous to a removal trapping experiment. Zippin's removal trapping method is therefore used to estimate population number.

The results for an Mb model are displayed by clicking on the Mb tab, which will appear once the model has been selected from the Closed methods drop-down menu.

6.7 Chao temporal change in capture probabilities (Mt)

Chao (1989) presented a method for calculating population number when capture probabilities varied through time, which differed from the standard maximum likelihood estimator. However, this approach requires full individual data and therefore cannot always be used. *Simply Tagging* will not offer this option when only summary data are available. This will be the case when batch tagging was undertaken.

The results for a Chao Mt model are displayed by clicking on the Mt tab, which will appear once the model has been selected from the **Closed methods** drop-down menu.

6.8 Leslie's Test

This test is suitable for open populations that may have experienced both mortality and recruitment. However, it is only based on animals that were captured on the first sampling occasion that were also captured on the last sampling occasion. It therefore only uses part of the available data, and if few animals meet this criterion it cannot be applied. This test is automatically calculated whenever an open population estimation method is selected and full individual tagging data are available. The results can be viewed by clicking on the Equal Catchability Open tab. If fewer than 20 animals are available for analysis, the calculations are still undertaken, but a warning is given that the test is unreliable. A comparison is made of the actual and expected variances of a series of recaptures of individuals known to be alive throughout the sampling period; individual marks must have been used.

This test is best illustrated by a worked example taken from Leslie's appendix, based on the recaptures of shearwaters; with insects, of course, the recapture periods would be days or weeks rather than years.

32 individuals marked in 1946 were recovered for the last time in 1952, therefore they were available for recapture in the years 1947-51 inclusive, and the following two tables were prepared:

Year by year analysis

Year	No. of recaptures in each year (ni)
1947	7
1948	7
1949	6
1950	4
1951	7
	∑ni=31

All years analysis

No. of recaptures for each individual X	Frequency of X f(x)
0	15
1	7
2	7
3	2
4	1
5	0
	N = ∑f(x) = 32

The actual sum of squares:

= 69-30.03 = 38.97.

The expected variance :

= 31/32-199/322 = 0.9688-0.1943 = 0.7745

Then X2 = 38.97/0.7745 = 50.32.

X2 may be treated as equivalent to Chi-squared, and for degrees of freedom (N - 1) of between 20 and 30 the probability of a value as great or greater than this can be assessed from C2 tables. Leslie has suggested that the test should only be used when the number of individuals is 20 or more and the number of occasions on which recapture was possible is at least 3. This test will not distinguish whether the higher catchability of some individuals is due to catching effects or inherent individual differences.

6.9 Equal catchability

Simply Tagging offers two tests for equal catchability which are automatically run when either a closed or open estimation method is selected.

For open populations Leslie's Test (Leslie *et al*. 1953) is calculated using the first and the last samples in the series as the starting and finishing points.
For closed populations the Zero-Truncated Poisson Test is undertaken - this requires you to have 3 or more samples.

6.10 Zero-Truncated Poisson Test

This test requires more than three samples to be taken and is suitable for closed populations. It is automatically calculated whenever a closed population estimation method is selected, and the results can be viewed by clicking on the Equal Catchability Closed tab. It is zero-truncated because there is no information on the animals that avoided capture. The expected frequency distribution given equal catchability is determined using the mean number of captures for the tagged animals. This mean is then used to calculate the Poisson distribution parameter, m, by iteration.

The observed and expected distributions are then compared using a χ^2 test.

6.11 Both individual and temporal differences in capture probability (Mth)

It is possible to envisage situations in which both individual and temporal changes in capture probability are acting. For example, there could be individual differences in activity, and also changes brought about by the weather which affect all the animals. The estimator of Chao *et al.* (1992) is used. This method requires full individual data and therefore is unavailable within *Simply Tagging* if you have entered only summary data.

The results for an Mth model are displayed by clicking on the Mth tab, which will appear once the model has been selected from the Closed methods drop-down menu.

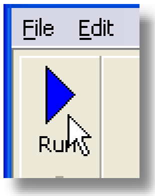
Part VII

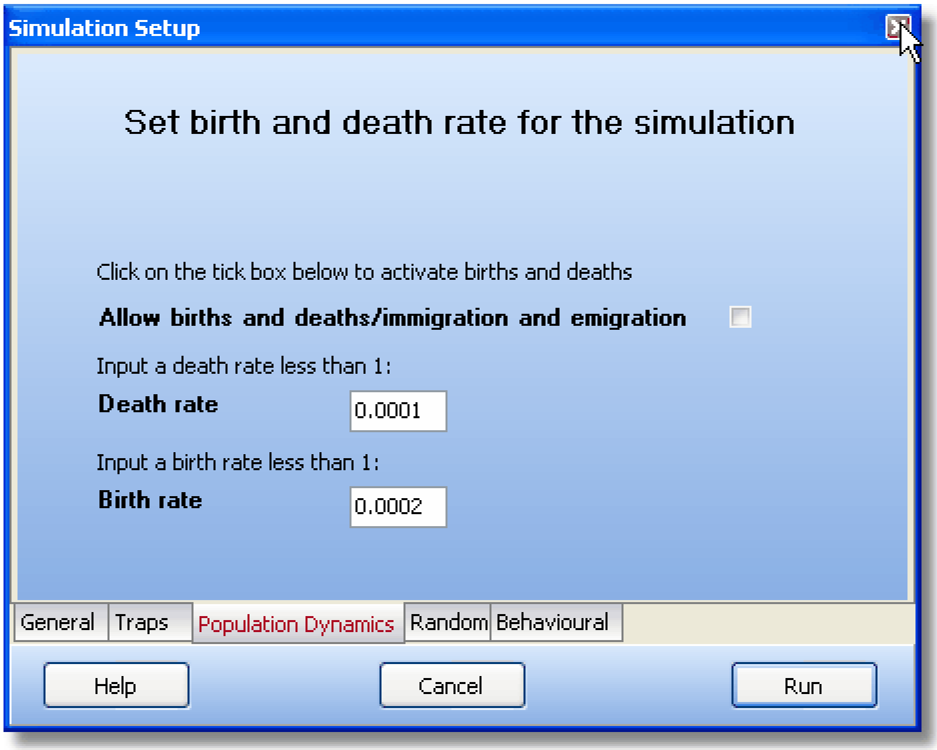
7 Simulating data

The simulator offers a visualisation of a mark-recapture experiment and produces data that can then be used to test the applicability of the various methods of analysis. You will begin to realise that a large proportion of the population must be marked for accurate population estimates to be obtained. The simulator works by setting in motion a known number of 'animals' and tagging those that enter traps. The motion of the animals, random or otherwise, can be selected.
Once the simulation is completed the data set produced can be viewed from the Full Data, Open Summary and Closed Summary tabs and is available to all of the methods.

To start the simulator select **Planning: Simulate** from the drop-down menus at the top of the program.

You will be presented in a blank area within which the simulation will be displayed. Click on the blue triangle Run button and the Simulation Setup window will be displayed.





Set birth and death rate for the simulation

Click on the tick box below to activate births and deaths

Allow births and deaths/immigration and emigration ☐

Input a death rate less than 1:

Death rate 0.0001

Input a birth rate less than 1:

Birth rate 0.0002

This window will allow you to select a variety of options for producing different types of simulation. The options available and their purpose are described below. At the bottom of the Simulation Setup window there are Help, Cancel and Run buttons. To undertake a simulation, click on the Run button.

Simulation options do not need to be set, as the program will use reasonably sensible default values.

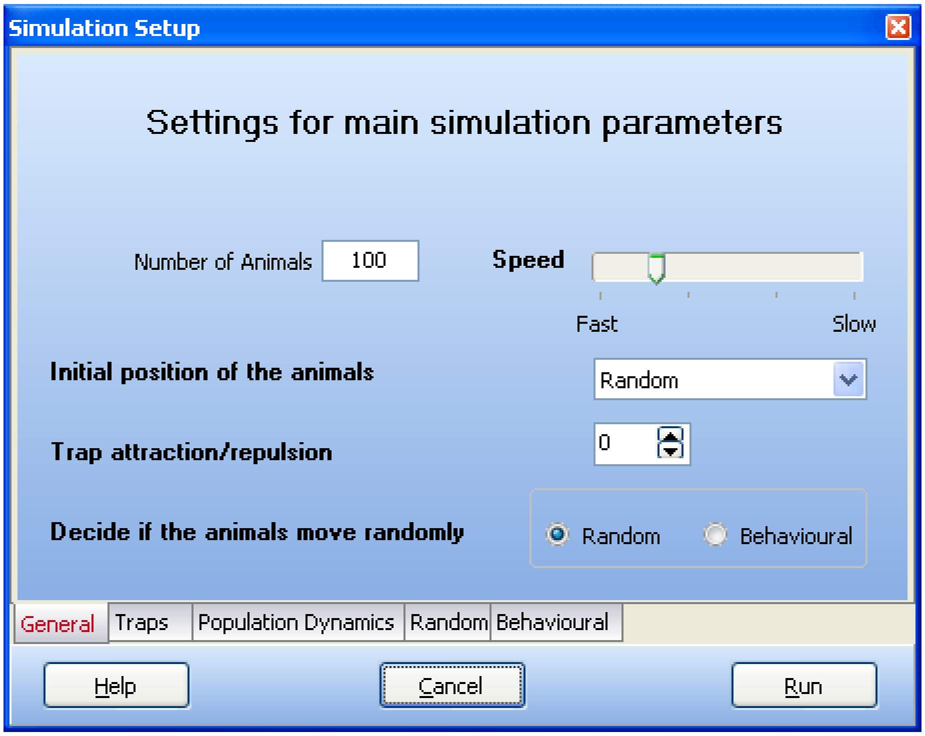
When a simulation is run you will be able to watch the data set being created. The traps appear as grey or black squares. They are only actively trapping when they change to black. The time when they are grey is used to give the 'animals' time to mix and disperse. The 'animals' are presented by small 'butterfly' icons. At the end of the simulation, or at any other time if you can catch them with the mouse, a click on one of the animals will present a colour coded history of its capture history along the left hand edge of the screen.

At the bottom of the screen are some summary statistics that will keep you informed of progress. Tagging No. gives the number of sampling occasions undertaken. No. Alive is the number of 'animals' currently alive in the simulation, No. Born gives the number of new arrivals which could either arise by birth or immigration, and No. Died gives the number lost either by death or emigration.

Setting simulation parameters

7.1 Setting simulation parameters

Simply Tagging offers a wide range of simulation options that will allow the effect of number of problems frequently encountered in mark-recapture experiments to be explored. The various options are arranged in a tabbed notebook on the Simulation Setup window.



Simulation Setup

Settings for main simulation parameters

Number of Animals: 100

Speed

Initial position of the animals: Random

Trap attraction/repulsion: 0

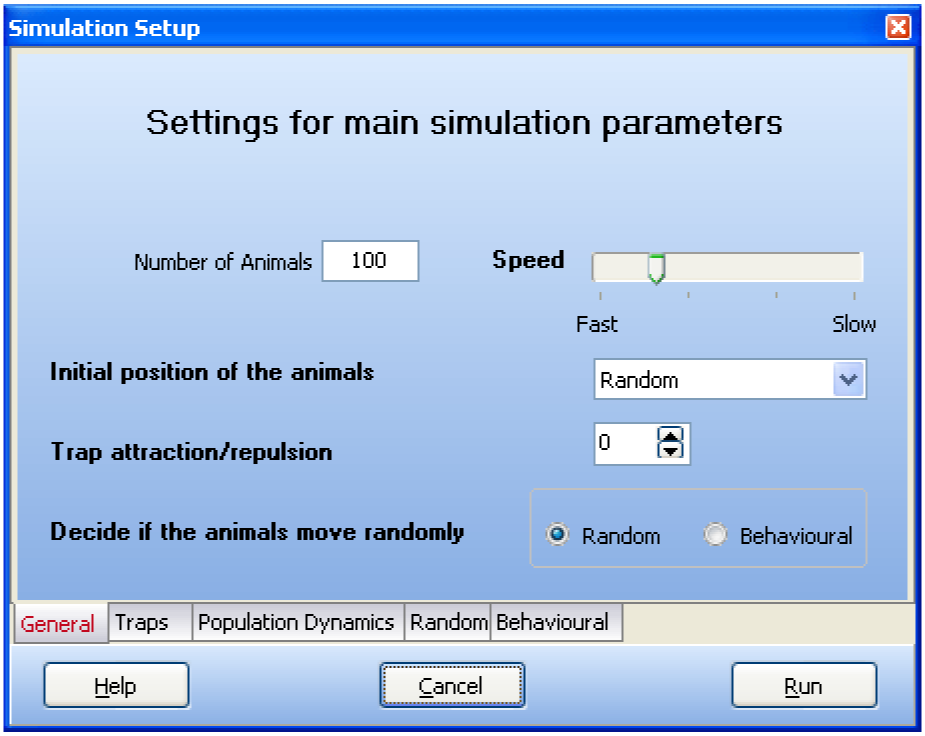
Decide if the animals move randomly: ● Random ○ Behavioural

The options available from each tab are described below.
General
Traps
Population dynamics

Random
Behavioural

7.2 Simulation parameters dialog - general

These parameters set some general conditions for your simulation.


Simulation Setup

Settings for main simulation parameters

Number of Animals 100

Speed

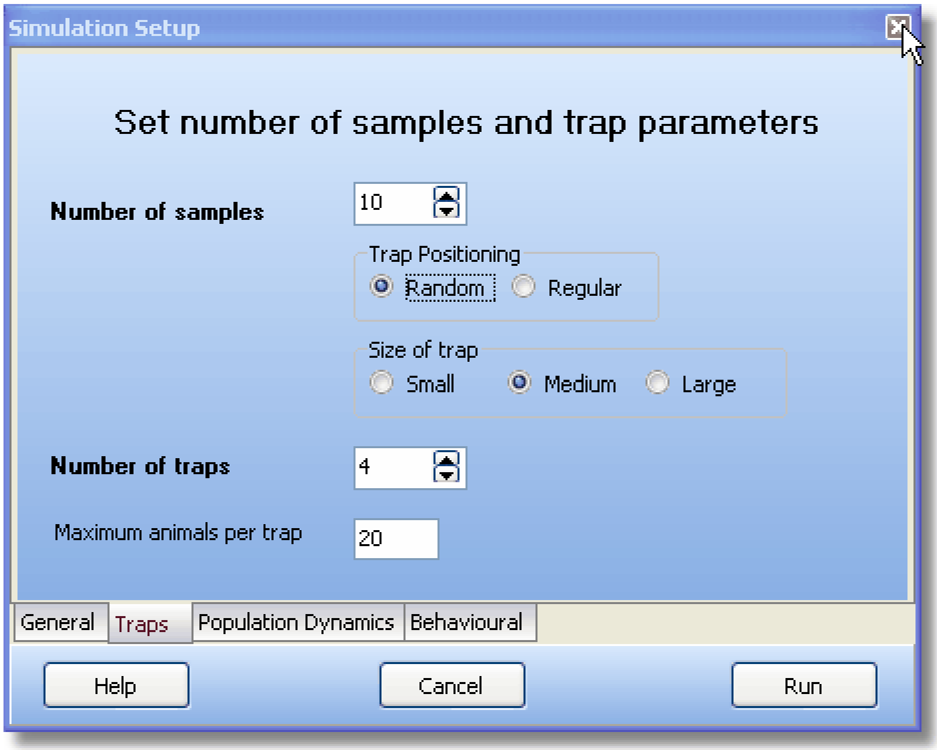
Initial position of the animals Random

Trap attraction/repulsion 0

Decide if the animals move randomly ● Random ○ Behavioural

Number of Animals: This gives the starting number of animals for the simulation. The maximum number is about 3000.
Speed: Move the slider to change the speed of movement of the animals. A higher speed will increase mixing.
Initial position of the animals: The initial position of the animals can be selected, using the drop-down menu, as random (the default), regular, clumped, and all at one point.
Trap attraction/repulsion: The animals can be made to be attracted or repelled by the traps. A zero value indicates no trap effect. The larger the positive value the higher the attraction of the traps to the animals, and the larger the negative value, the higher the trap avoidance. Attraction and repulsion to the traps increases with the number of times an individual is caught. Thus it is possible to run a simulation where a small number of individuals become trap-happy, as can occur with small mammals.
Decide if the animals move randomly: Click on Random for random movement. Click on Behavioural if you want the 'animals' to interact. If this option is selected, a Behavioural tab will appear, offering a further series of options that are described below. When Behavioural is selected, the movement of the animals will become non-random.

7.3 Simulation parameters dialog - traps



Simulation Setup

Set number of samples and trap parameters

Number of samples 10

Trap Positioning
● Random ○ Regular

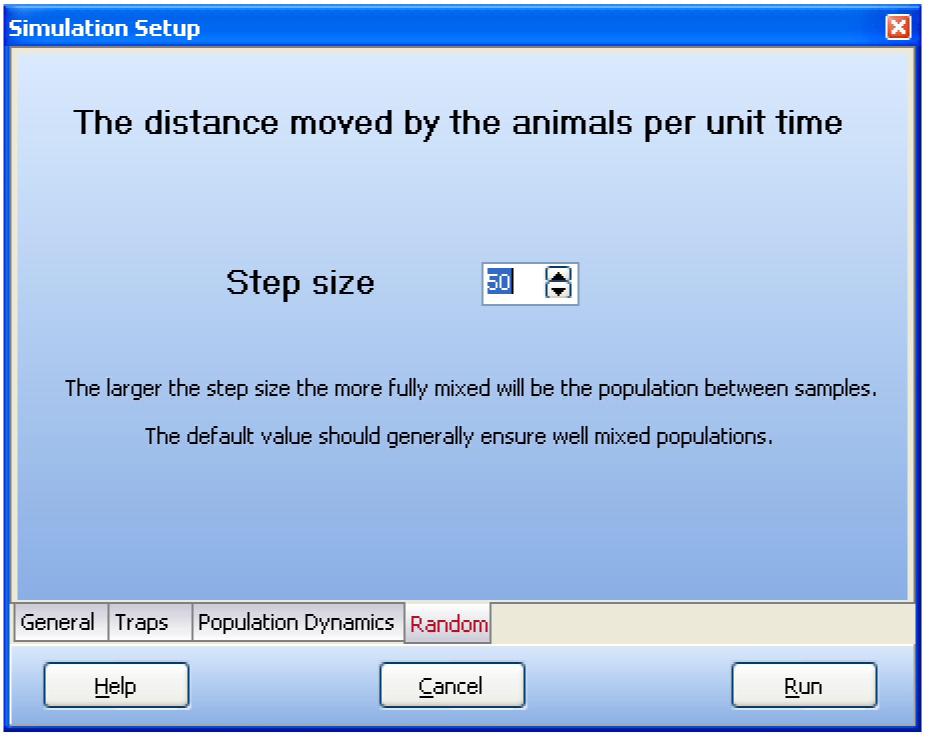
Size of trap
○ Small ● Medium ○ Large

Number of traps 4

Maximum animals per trap 20

Number of samples: This determines the number of trapping occasions that will be simulated. The number can range from 2 to 10.
Trap positioning: Traps can be either regularly or randomly positioned within the sampling area. A regular arrangement will usually maximise the number captured.
Trap size: Three trap sizes can be selected. The larger the trap the more likely the probability of capture. Therefore use large traps when it is desired to simulate an experiment when a large proportion of the population is captured.
Number of traps: From 1 to 25 traps can be used. A large number will result in a higher proportion of the population being tagged.
Capacity: This is the number of individuals a trap can hold. Some small mammal traps, for example, can only catch a single individual per sampling occasion.

7.4 Simulation parameters dialog - random


Simulation Setup

The distance moved by the animals per unit time

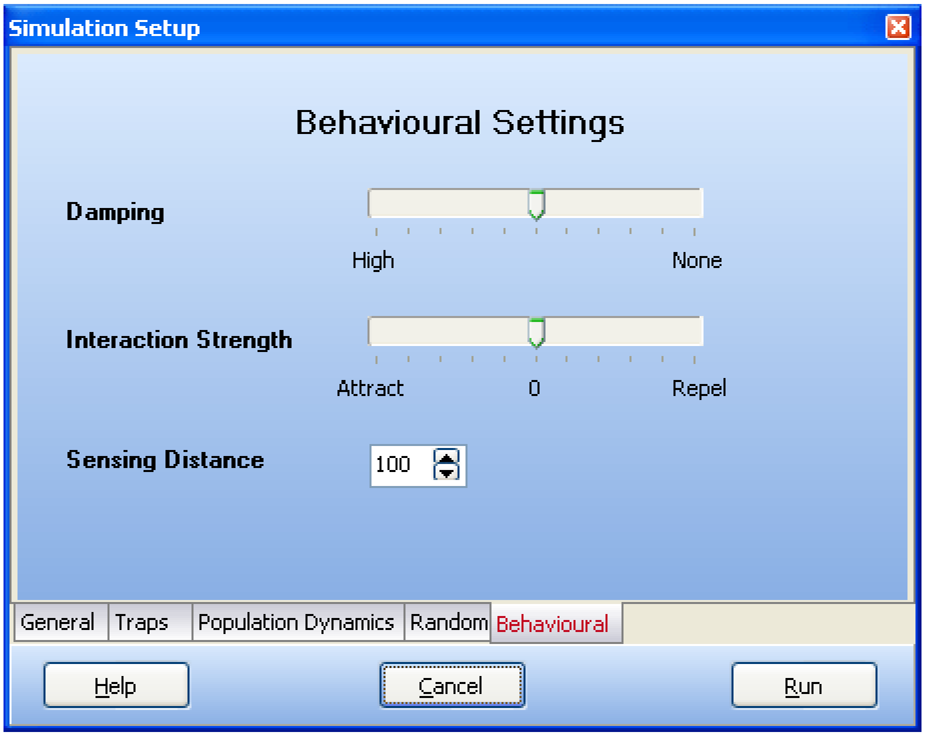
Step size 50

The larger the step size the more fully mixed will be the population between samples.

The default value should generally ensure well mixed populations.

If the animals' movement is set to Random, you can specify the step size - the distance moved by the animals per unit time. This in turn affects the degree to which the population is mixed.

7.5 Simulation parameters dialog - behavioural


Simulation Setup

Behavioural Settings

Damping

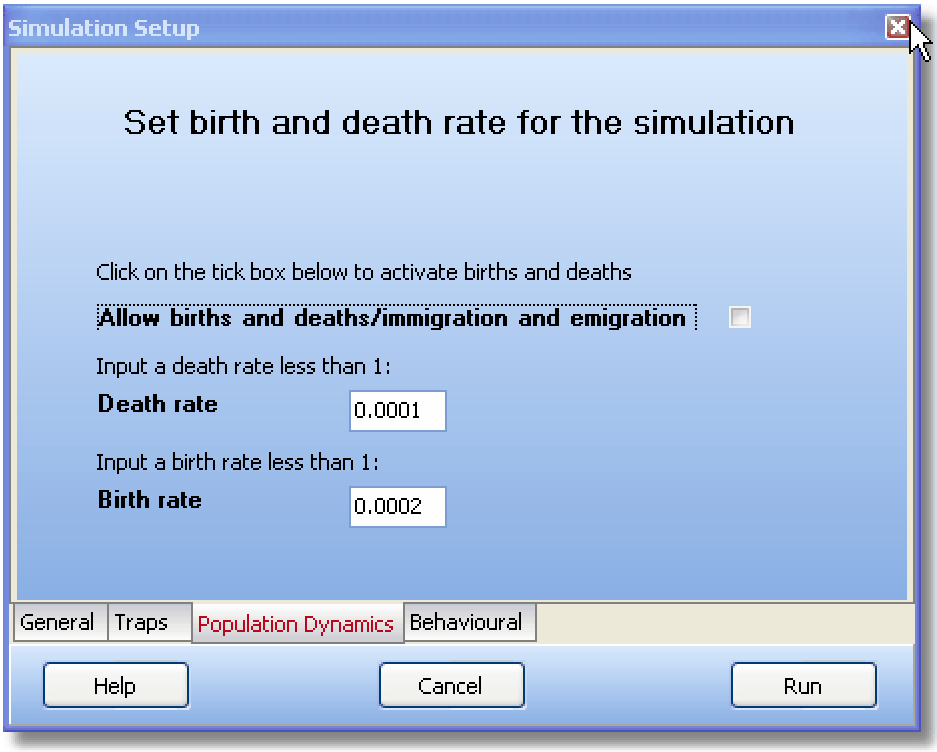
Interaction Strength

Sensing Distance 100

Damping: If animals are set to repel each other, this variable gives a measure of the speed at which they slow down as they move apart.
Interaction strength: This slider varies the strength of attraction or repulsion between individuals.
Sensing distance: This gives the maximum distance in pixels at which the animals will spot each other and interact.

7.6 Simulation parameters dialog - population dynamics

These options will allow you to make the simulated population either open or closed.



Simulation Setup

Set birth and death rate for the simulation

Click on the tick box below to activate births and deaths

Allow births and deaths/immigration and emigration ☐

Input a death rate less than 1:

Death rate 0.0001

Input a birth rate less than 1:

Birth rate 0.0002

Births and deaths/Immigration and emigration: check the tickbox if you want the population to change during the simulation.
Death rate: Enter a value for the proportion of the population that will die or emigrate between sampling periods.
Birth rate: Enter a value for the proportion of the population that will be born or immigrate between sampling periods.

Setting very high birth and death rates, or rates that differ significantly, can lead to rapid extinction of the entire population, or massive proliferation of the number of individuals. The latter can cause the performance of your computer to slow down while the simulation is in progress.

Part VIII

8 Programs for ecologists by PISCES Conservation Ltd

Software which allows you to quickly discover patterns and perform your analysis.

All our programs feature
- Designed to make difficult statistics easy.
- Easily import and export data.
- Proven high quality graphs.

More details of our programs, free downloads, FAQ and Technical Support information and much more can be found on our website at: www.pisces-conservation.com

Programs

CAP - Community Analysis Package

A fully-featured analytical package ideal for a very wide range of analytical techniques. CAP guides you through the complexities of multivariate statistics, with its 'Instant Assist' feature and a very extensive Help system that contains all the background to the methods that you could need. Includes a helpful worked example too! Buy bundled with ECOM for a substantial discount!

ECOM

The sister program to CAP, it complements CAP in providing analytical techniques to detect, visualise and order relationships from both species data and environmental variables. Used where you have environmental data as well as species data. Principal methods: Canonical Correspondence Analysis (CCA), Redundancy Analysis (RDA), Multiple Regression (MR) and Forward and Backward Stepwise Regression. (Discounts are available for buying CAP & ECOM as a bundle).

Species Diversity and Richness IV
A program to calculate and compare species diversity, estimate total species richness and study patterns of abundance.

Axis
For handling circular statistics. Essential in behavioural studies, biogeography and geology.

Fuzzy Grouping
Fuzzy Grouping offers two main methods of data analysis, firstly, fuzzy c-means and secondly, fuzzy ordination, for dealing with imprecise data and likelihood of group membership.

Population Estimation by Removal Sampling
A program to calculate the statistics from removal trapping experiments.

Growth II
To analyse growth curves from length and/or weight data - a major update to the program previously known as Simply Growth.

Simply Probit

A program for estimating lethal or environmental concentrations using toxicity data.

Simply Tagging
For estimating population size of both closed and open populations with mark-recapture methods. Includes data simulation options to model experiments for open and closed populations.

Density from Distance
Offering a range of analytical techniques commonly used by ecologists to estimate animal and plant density from measurements of the distance between objects or from a selected line or point to the objects.

Dynamica
Dynamica allows you to explore how animal populations and communities change through time.
The program uses a long-term data set from the Severn Estuary, England. Since 1980 fish and crustacean samples have been collected from Hinkley Point 'B' power station. Data are presented on every fish and most large crustaceans known from the estuary, producing an exceptional data set for those interested in population dynamics.

Hedgerow Assistant
The reliable way to survey hedgerows under the 1997 Hedgerows Regulations.

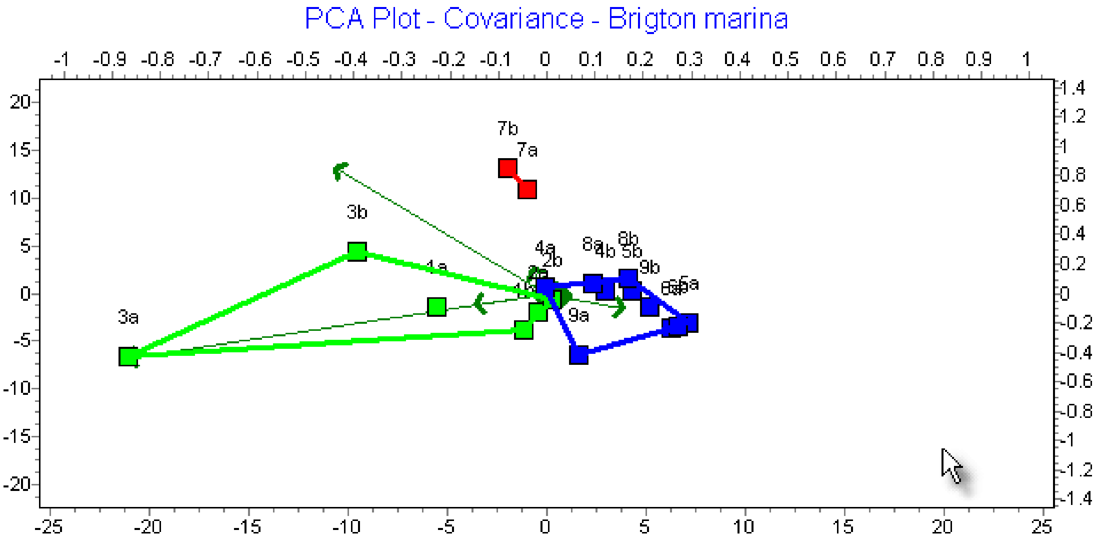
8.1 CAP

Community Analysis Package

For more information and a free demo visit our website here.

CAP is a fast, easy to use, multivariate analysis package for Windows PCs. It has superb graphical output that gives you complete control over how you want your graphics to look. The program offers you a simple way to discover the power of multivariate statistics. Now in version 3, it is a proven performer that is both easy to use and affordable.

CAP allows you to identify your groups that are then displayed on the output, and even surround them with a perimeter, as can be seen below.



Example PCA output from CAP

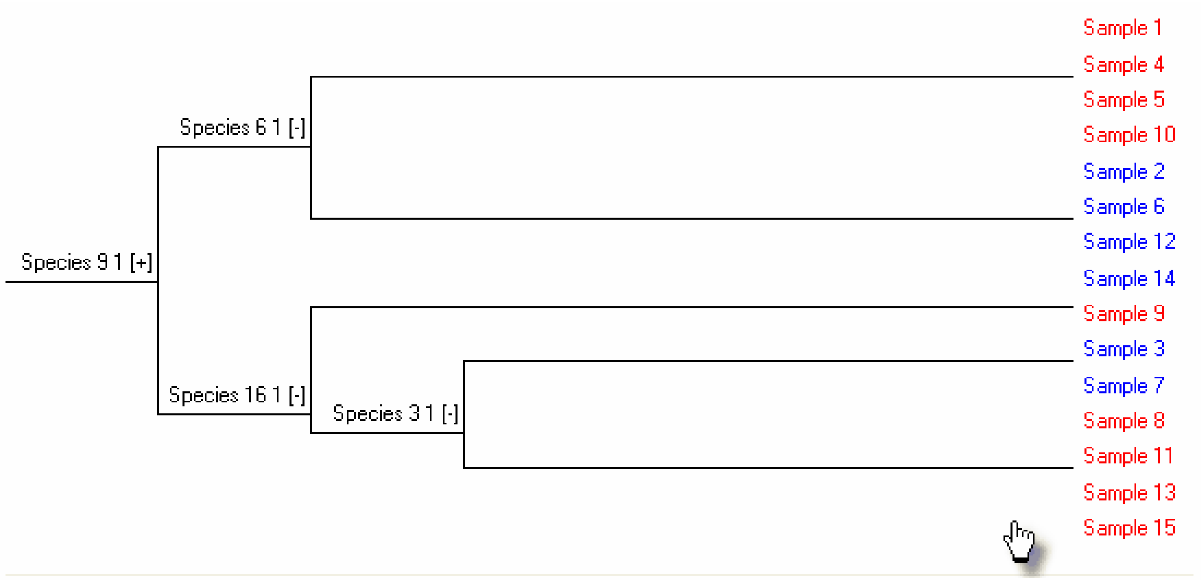
It offers all the analytical techniques commonly used by community ecologists, and researchers in other fields such as palaeontology, archaeology and the social sciences. It is particularly useful for ecological teaching because it allows students to quickly enter data, try different transformations, and explore a wide range of methods within a familiar Windows setting.

Its principal methods are:

- Two-way INdicator Species Analysis (TWINSPAN)
- Principal Components Analysis (PCA)
- Non-metric Multidimensional Scaling (NMDS)
- Detrended Correspondence Analysis (DECORANA)
- Analysis of Similarity (ANOSIM) and Similarity Percentages (SIMPER)
- Agglomerative clustering
- Species Filtering
- Reciprocal Averaging
- 26 Similarity and distance measures
- Divisive cluster analysis
- Association analysis

CAP also feature 'Instant Assist' an (optional) always-on help panel to guide you through your analysis, to tell you what's appropriate and what the pitfalls of any technique are likely to be.

CAP is an indispensable part of every ecologist's analytical toolbox.



An example Twinspan dendrogram from CAP

8.2 ECOM

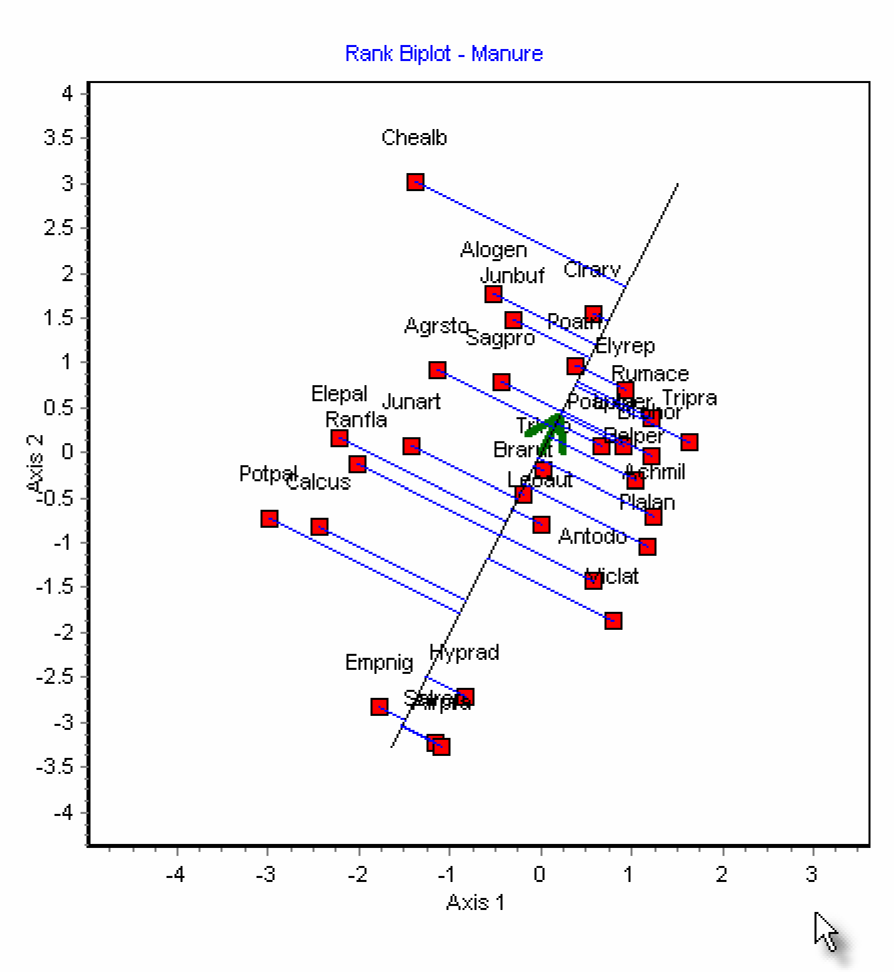
Ecological Community Analysis

For more information and a free demo visit our website **here**.

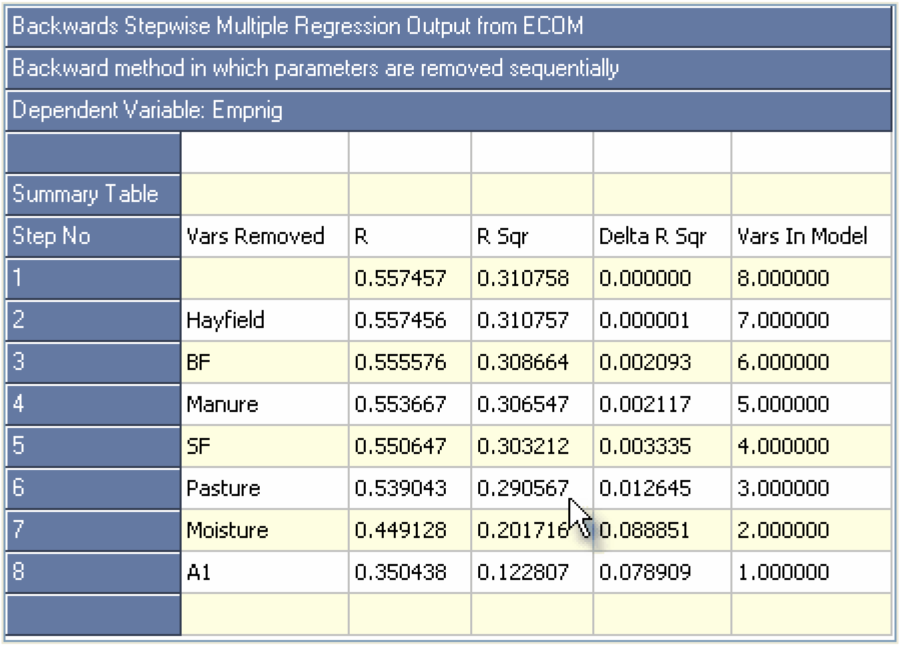
ECOM offers you a range of analytical techniques to discover, visualise and order relationships in multivariate data where the researcher has information on both the species present and the most influential environmental variables. For example, if you have sampled the animals from a series of habitats, and you have data on the environment for each sample, then this program is for you. These methods are used relevant to several fields such as palaeontology, archaeology and the social sciences.

The principal methods are:
- Canonical Correspondence Analysis (CCA),
- Redundancy Analysis (RDA)
- Multiple Regression (MR).
- Stepwise Regression (SR)

A particular feature of **ECOM** is the graphical output that enables you to quickly visualise the complex relationships within your data set. For example, CCA output includes plots of sample and species ordinations, environmental correlation vectors and biplots of species arranged along individual environmental axes. All aspects of the graphs can be altered, and printed or exported in a wide variety of formats.



The program works on two separate input data sets holding the biological and physical data for the samples (sites). The environmental data may be either continuous variables such as pH, temperature or current speed; or binary variables such as soil or treatment type, which are scored as either a 0 or 1.



Backwards Stepwise Multiple Regression Output from ECOM

Backward method in which parameters are removed sequentially

Dependent Variable: Empnig

Summary Table

Step No	Vars Removed	R	R Sqr	Delta R Sqr	Vars In Model
1		0.557457	0.310758	0.000000	8.000000
2	Hayfield	0.557456	0.310757	0.000001	7.000000
3	BF	0.555576	0.308664	0.002093	6.000000
4	Manure	0.553667	0.306547	0.002117	5.000000
5	SF	0.550647	0.303212	0.003335	4.000000
6	Pasture	0.539043	0.290567	0.012645	3.000000
7	Moisture	0.449128	0.201716	0.088851	2.000000
8	A1	0.350438	0.122807	0.078909	1.000000

ECOM complements CAP (Community Analysis Package) and Species Diversity and Richness IV (SDR) which offer a range of techniques that only require biological data to undertake the analysis.

8.3 Species Diversity and Richness IV

Species Diversity and Richness

For more information and a free demo visit our website **here**.

Calculate and compare species diversity, estimate species richness and study patterns of abundance in one easy to use program.

The methods on offer range from the familiar, such as the calculation of various diversity indices and the fitting of common distributions to more recently-developed techniques such as total species complement estimators. Taken together they provide a powerful suite of methods to explore compare and analyse community structure.

Number of random selections of sample order 2

Sample	H	Variance H
Canopy	2.641	0.0003865
Understory	2.983	0.0002548
All Sample Index	3.275	

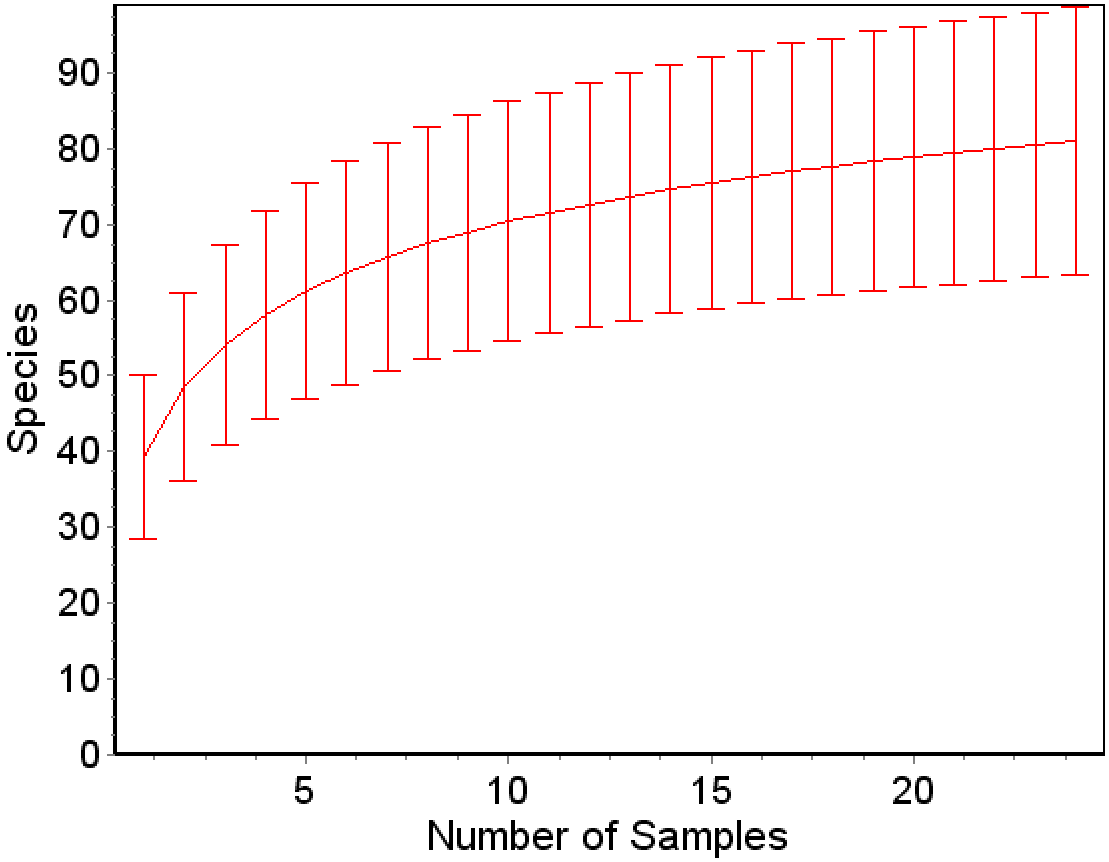
No. Samples: 2 No. Species: 74 Runs = 2

Species diversity and richness is a Windows program designed for both the professional ecologist and students.

Species diversity and richness version 4 offers considerable improvements over version 3. Existing users will immediately note the redesigned menu system and improved graphics, data input and printing. Probably the greatest recent improvements have been the extended range of methods and statistical tests on offer. The program offers all the analytical tools that a general ecologist needs for analysing and comparing the diversity of communities.

Methods available within *Species diversity and richness* include

- 11 Alpha diversity indices including Shannon's, Simpson's, Fisher's and Q statistic.
- 14 Evenness measures
- Bootstrapping of confidence intervals.
- Randomization tests to compare diversity between sites.
- Jackknife errors of total diversity/evenness
- 2 diversity ordering methods.
- 14 methods to estimate total species richness
- Rank order, K Dominance and species accumulation curves.
- 8 beta diversity measures
- SHE analysis
- Fitting of log series, log normal, geometric and broken stick abundance models
- Ability to generate simulated data
- Freshwater quality measures including BMWP, ASPT, LIFE & Irish quality rating, including the revised BMPS scoring system



Species diversity and Richness offers
An attractive user interface.
Extensive help system.
Easy data importation.
High quality graphical output.

and is ideal for

Community ecology research.
Undergraduate teaching.
Applied ecologists.
Ecologists with limited computer experience.

8.4 Axis

Axis

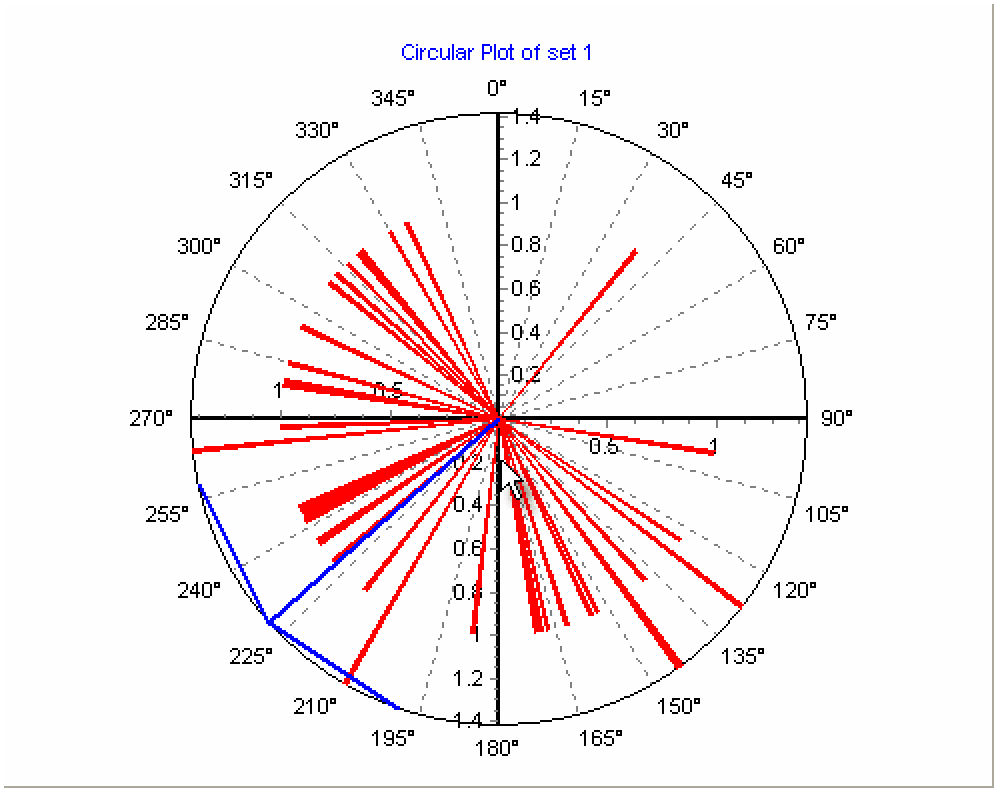
For more information and a free demo visit our website **here**.

Finally a program that allows you to discover the relationships within your circular data. It offers a range of graphical and analytical techniques commonly used by biologists, geologists and archaeologists for the analysis of circular data.

Axis implements the principal graphical methods and statistical tests described by Fisher (1993) in *Statistical Analysis of Circular Data*. Periodic data of many kinds can be represented and analysed using the methods available within Axis.

While compass bearings are the most obvious examples of circular data, other examples could be the time of events over a 24-hour period, and the occurrence of activity over the lunar cycle.

Available plots within Axis include linear, circular and angular histograms, and optional smoothing by Fast Fourier Transform. Tests include: correlation between samples, uniformity or randomness, and specified mean direction. Simulated data sets can be created conforming to various distributions.



Axis has extremely versatile graphing capabilities, and can export images in .emf, .jpg, .png or .bmp formats. Tabulated data can be exported as plain text, .csv, or .xls files which will load into Excel or other spreadsheets - or even in HTML format.

Data sets can be imported from standard spreadsheets such as Excel, or created within the program.

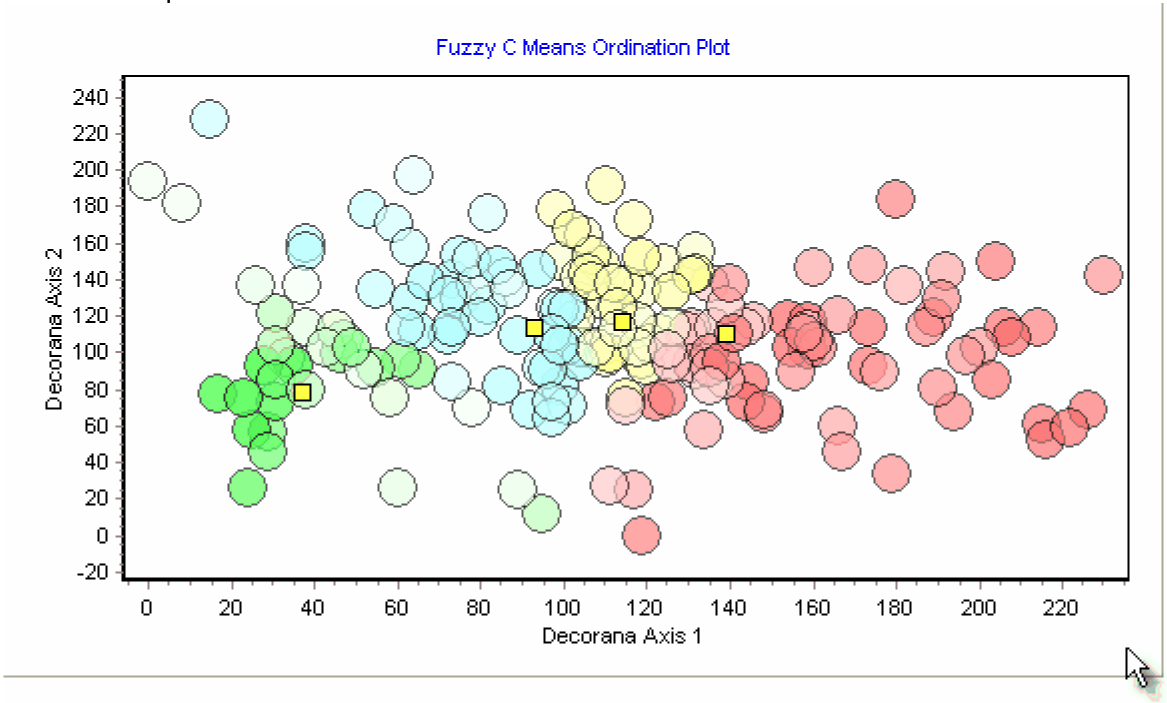
8.5 Fuzzy Grouping

Fuzzy Grouping

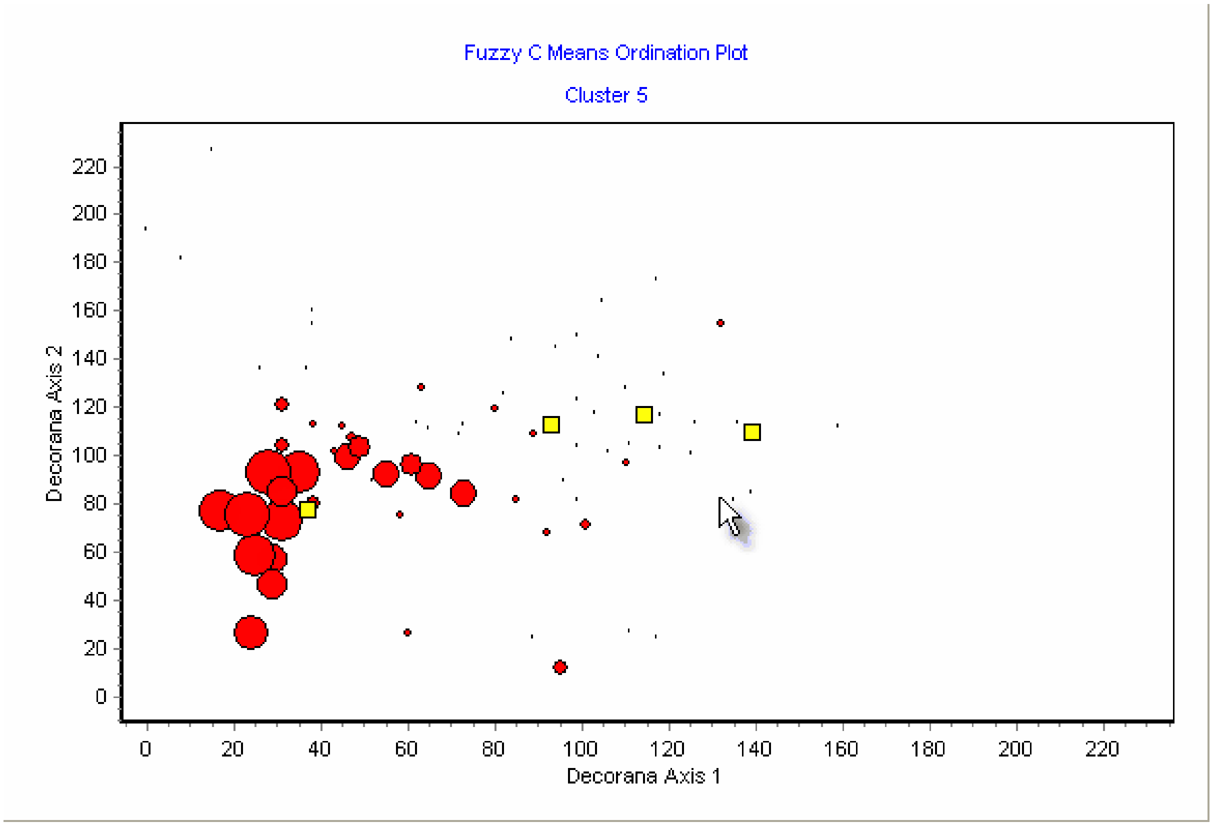
For more information and a free demo visit our website **here**.

Fuzzy clustering methods allow samples to belong to more than one group. This easy-to-use program for the PC allows the user to quickly carry out these techniques and is aimed to meet the needs of ecologists, palaeontology, archaeology and the social sciences. This has not been readily available before, and this has undoubtedly slowed the introduction of these techniques into these fields.

Lotfi Zadeh introduced the notion of a fuzzy set in 1965, as an approach for the handling of uncertain knowledge. Today these techniques are widely used over a range of scientifically disciplines, and seem to be particularly appropriate to ecological analysis where the boundaries between groups such as communities or taxonomic units may be far from sharp.



In ordinary cluster analysis a sample or site either belongs, or does not belong, to a particular group or set. We can score membership as a value of 1 and non-membership as 0. In fuzzy clustering a degree of membership can be assigned as a value between 0 and 1 so that a value of say 0.8 would indicate a high probability that the sample belonged to the particular group in question. Thus, for a data set comprising many samples that can be hypothesized as being divisible into c groups, each sample has a degree of membership of belonging to each of the c groups.



Fuzzy Grouping offers three main methods of data analysis, first, fuzzy c-means, second, fuzzy ordination and finally fuzzy linear discriminant analysis. The first technique is appropriate for data that you suspect can be divided into c-groups but for which you may have no *a priori* information on group membership. The second, fuzzy ordination is appropriate when you have information on possible group membership. The second will allow you to plot a selected number of fuzzy groups in a space in which their differences are displayed to best effect and a measure of the ability of the groups to explain the total variability presented.

To help users to understand how to use Fuzzy Grouping, the instructions are written from an ecological viewpoint.

Fuzzy complements CAP (Community Analysis Package) and ECOM (Ecological Community Analysis)

8.6 Simply Tagging

Simply Tagging

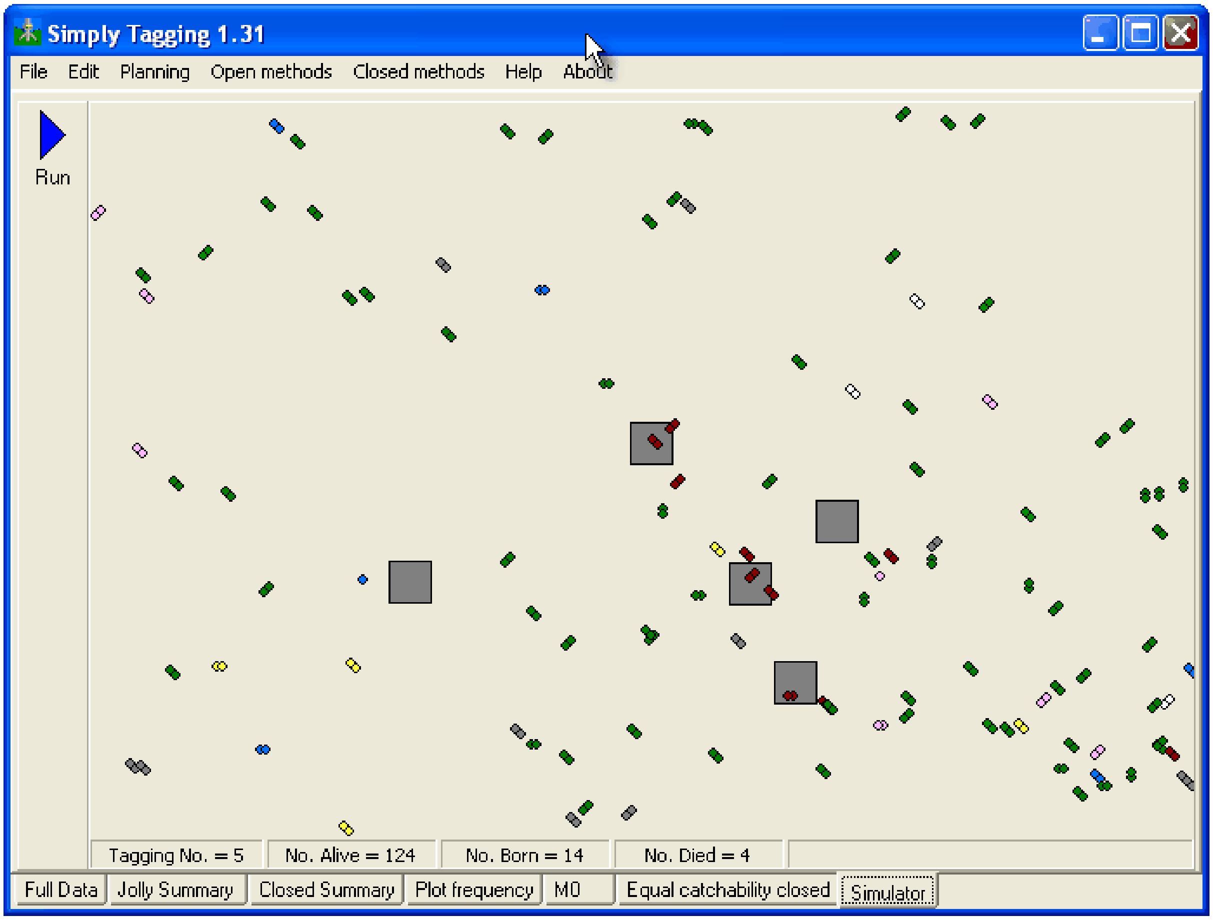
For more information and a free demo visit our website **here**.

Estimate the population size for both closed and open populations using mark-recapture methods. Simply Tagging is designed to be used by undergraduates and professionals and allows them to simulate data and explore the accuracy and reliability of mark-recapture methods.

Main features:
- Data can be entered as individual animal capture histories or as summary tables.
- Ability to subset data by sex or age.
- Wide range of methods available for closed populations including Schnabel census and methods which assume behavioural differences between individuals.
- Undertakes full Jolly-Seber or constant survival and probability of capture model.
- Plots of population estimates and frequency of capture.

As with all Pisces software, Simply Tagging has an attractive user interface, extensive help system and good quality graphical output.

Tagging also includes a data simulation option to model mark-recapture experiments for open and closed populations. The user can vary sampling intensity, population size, animal behaviour and birth/death rates.



Tagging No. = 5
No. Alive = 124
No. Born = 14
No. Died = 4

8.7 Population Estimation by Removal Sampling

Removal Sampling

For more information visit our website here.

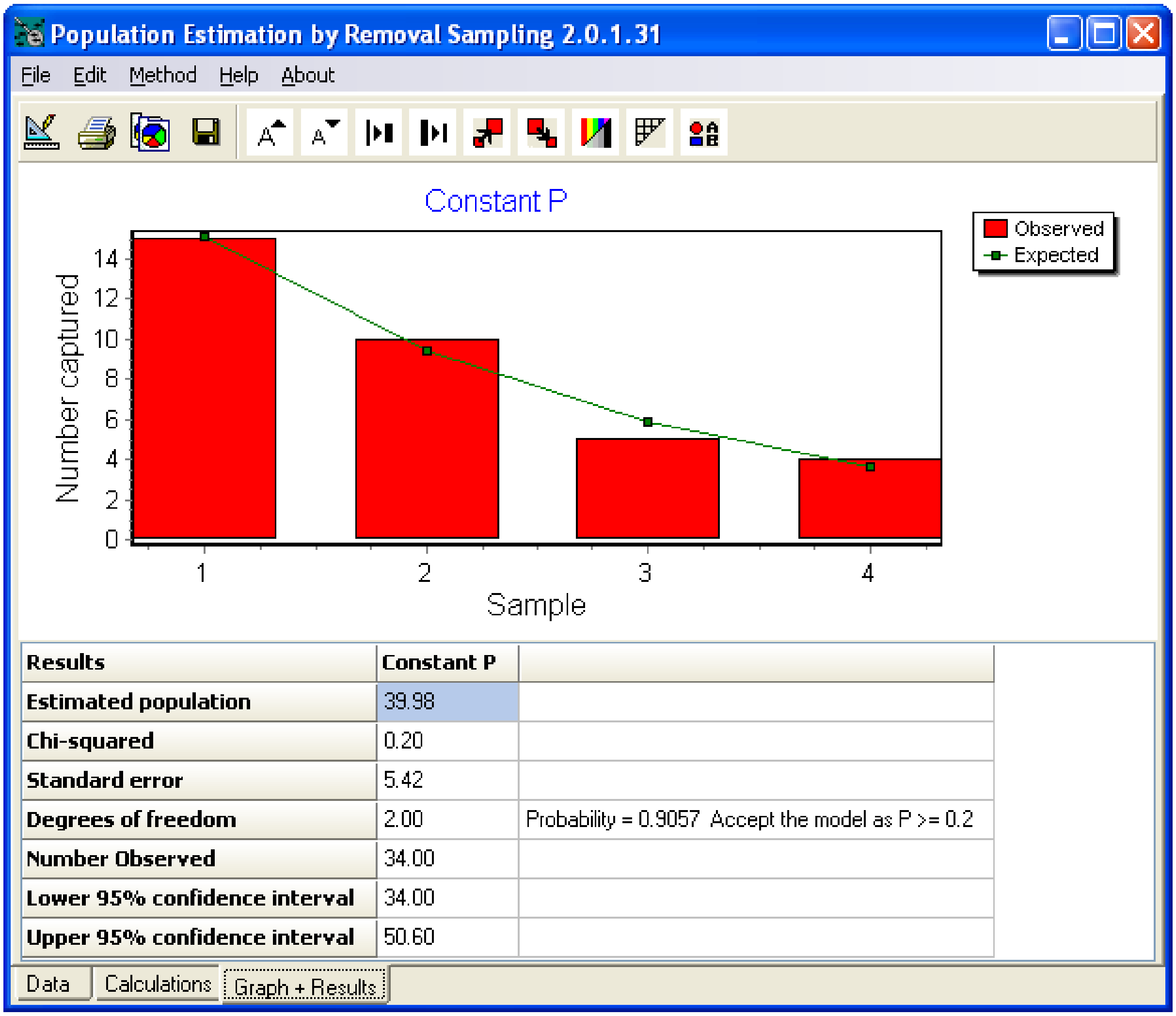
Removal Sampling allows you to calculate the statistics from removal trapping experiments. It contains three easy to use methods: constant & variable probability of capture (Zippin's maximum likelihood, ML) and a regression model.

Using the ML methods the program can calculate a population estimate, the upper & lower 95% confidence intervals & the probability of fit of the model.

The program allows instantaneous graphical comparison of the various methods & rapid sub-division of the data. Data from spreadsheets such as Excel can be imported as CSV files.

Removal Sampling is particularly useful for:

1. The estimation of fish densities using data collected by electric fishing:
2. Small mammal population estimation using traps.
3. Studies on insects that live in small, discrete populations that can be sampled using techniques such as sweep netting or pitfall traps.



Results	Constant P	
Estimated population	39.98	
Chi-squared	0.20	
Standard error	5.42	
Degrees of freedom	2.00	Probability = 0.9057 Accept the model as P >= 0.2
Number Observed	34.00	
Lower 95% confidence interval	34.00	
Upper 95% confidence interval	50.60	

8.8 Density from Distance

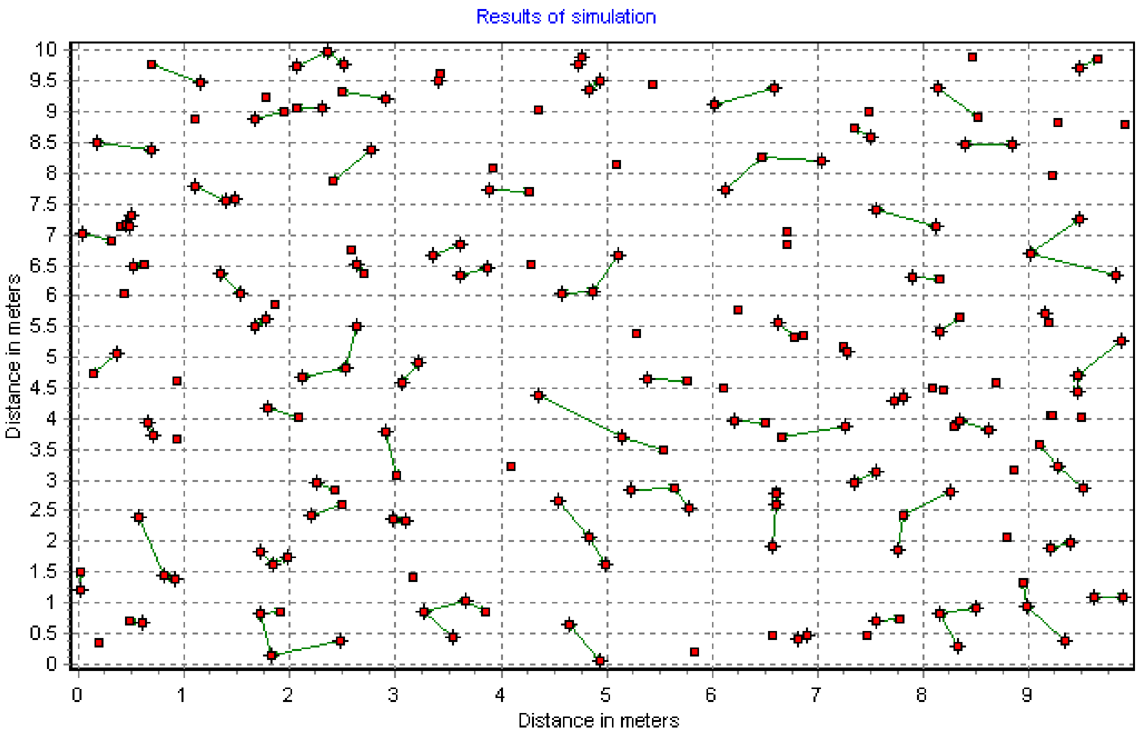
DfD - Density from Distance

For more information visit our website here.

A range of analytical techniques are available in Density from Distance for you to estimate animal and plant density from measurements of the distance between objects, or from a selected line or point to the objects.

DfD has been designed for ease of use on Windows PCs. While designed for research use, the program is particularly useful for ecological teaching because it allows students to quickly enter or simulate data and explore a range of methods within a familiar Windows setting. The program is particularly useful for botanists, and zoologists studying birds or large mammals.

An example of a simulation using Nearest Neighbour:



8.9 Growth II (Simply Growth)

Growth II

A major update of our Simply Growth program, Growth II is the easy way for you to analyse growth curves from length and/or weight data.

A full list of the New Features in Growth II

New Models
- Exponential
- 4 Parameter Gompertz
- 4 Parameter logistic
- 3 Parameter Weibull
- 4 Parameter Weibull
- Morgan-Mercer-Flodin (MMF)
- Janoschek
- 4 Parameter Richards
- 5 Parameter Richards
- Non Linear Seasonally adjusted von Bertalanffy
- Linear Seasonally adjusted von Bertalanffy

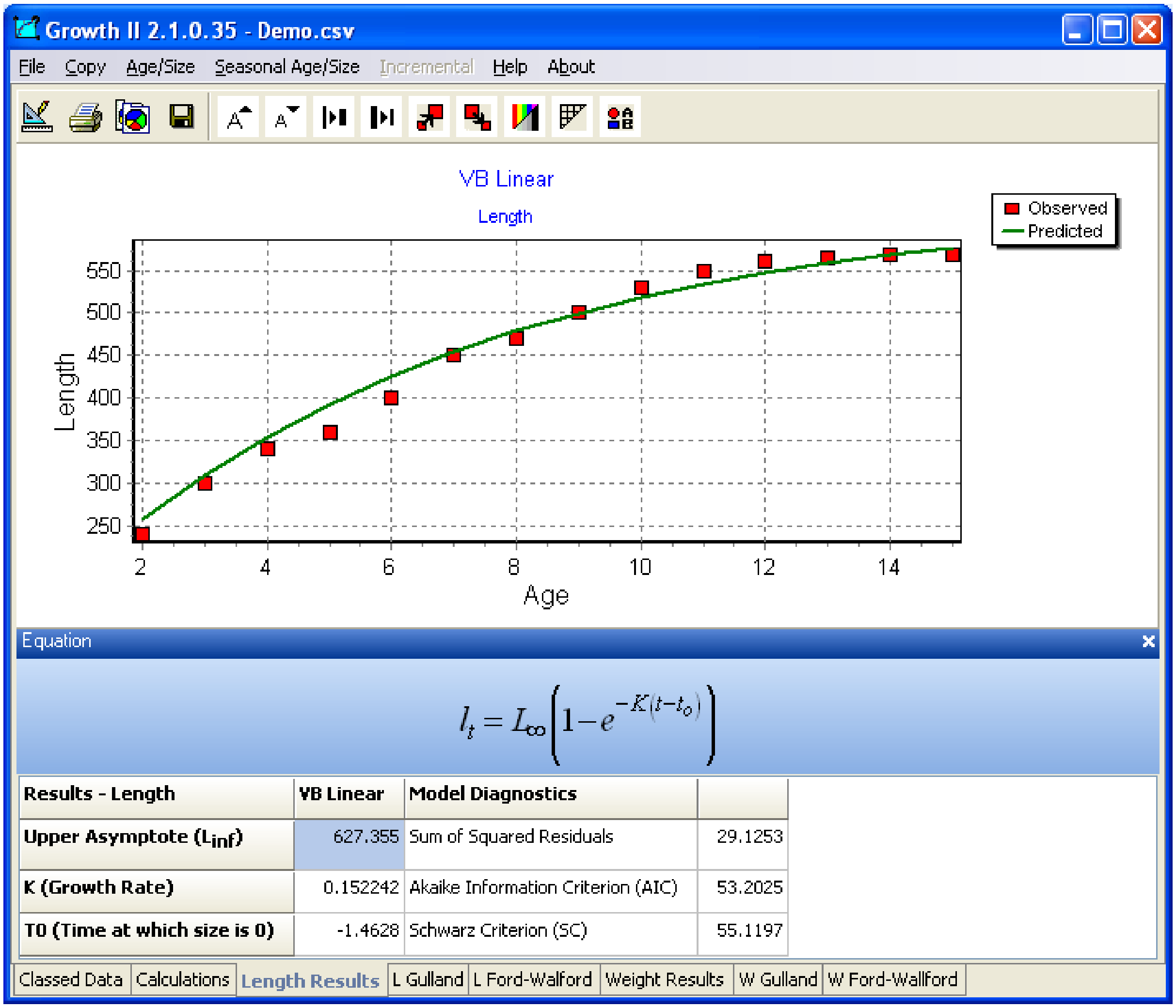
New Appropriate Model Statistics
- Akaike Information Criterion (AIC)
- Schwarz Criterion (SC)

Improved Models
- Non Linear Von Bertalanffy
- 3 Parameter Gompertz
- 3 Parameter Logistic

Improved Graphic
- Export Charts as BMP, WMF, EMF, JPEG, PCX, GIF and PDF
- Updated graphics
- New tools on each graph making publication quality charts easier
- Active clicking on graphs – takes you to the editor for each part of the graph
- Interactive results and Equation – click on a parameter and the corresponding part of the equation will be highlighted

Improved data entry and editing
- Redo/Undo on grids
- Paste in to grid
- Output to grids
- Opens Excel (*.xls) files

New Help
- Completely rewritten Help
- Explanations of the models
- Tutorials and worked examples



$$l_t = L_\infty\left(1-e^{-K(t-t_0)}\right)$$

Results - Length	**VB Linear**	**Model Diagnostics**	
Upper Asymptote (L_{inf})	627.355	Sum of Squared Residuals	29.1253
K (Growth Rate)	0.152242	Akaike Information Criterion (AIC)	53.2025
T0 (Time at which size is 0)	-1.4628	Schwarz Criterion (SC)	55.1197

For more information visit our website here.

8.10 Dynamica

Dynamica

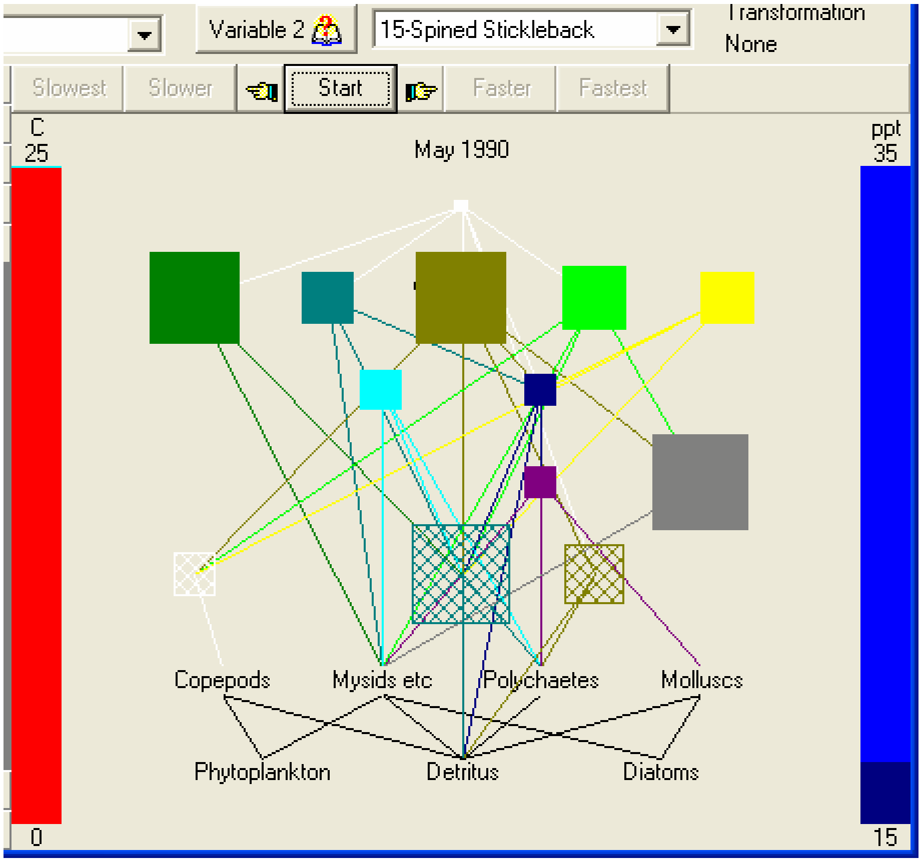
For more information visit our website here.

You can explore real data, and reach your own conclusions about how animal numbers are inter-related and change through time. Data is from the Hinkley Point 'B' power station, Severn Estuary, UK

Dynamica features:
- Monthly abundance estimates of fish and crustaceans from January 1981 to January 1995.
- Time series for more than 100 species are available for study.
- Contains environmental data such as temperature, salinity and tides.

- Food webs that change through time.
- Statistics allow you to explore the complex inter-relationships between species and environmental factors.
- Length data for the common species of fish.
- Scientific papers from this data
- Details about data collection and habitat are also given.

The strong theme running through Dynamica is the study of community-level dynamics. Books often portray communities and food webs as static entities. This program will show you just how dynamic food webs are. Perhaps the most popular community statistic is a diversity index; Dynamica will let you compare different indices and appreciate how they change through time.



Dynamica has been designed to be useful to anyone with an interest in natural time series. It presents a range of elementary techniques for time series analysis, including data transformations, autocorrelations, moving averages and Fourier analysis. The program presents a wide range of natural dynamic behaviours which make good examples for study.

More information is available on the Hinkley Point sampling on our website

8.11 Hedgerow Assistant

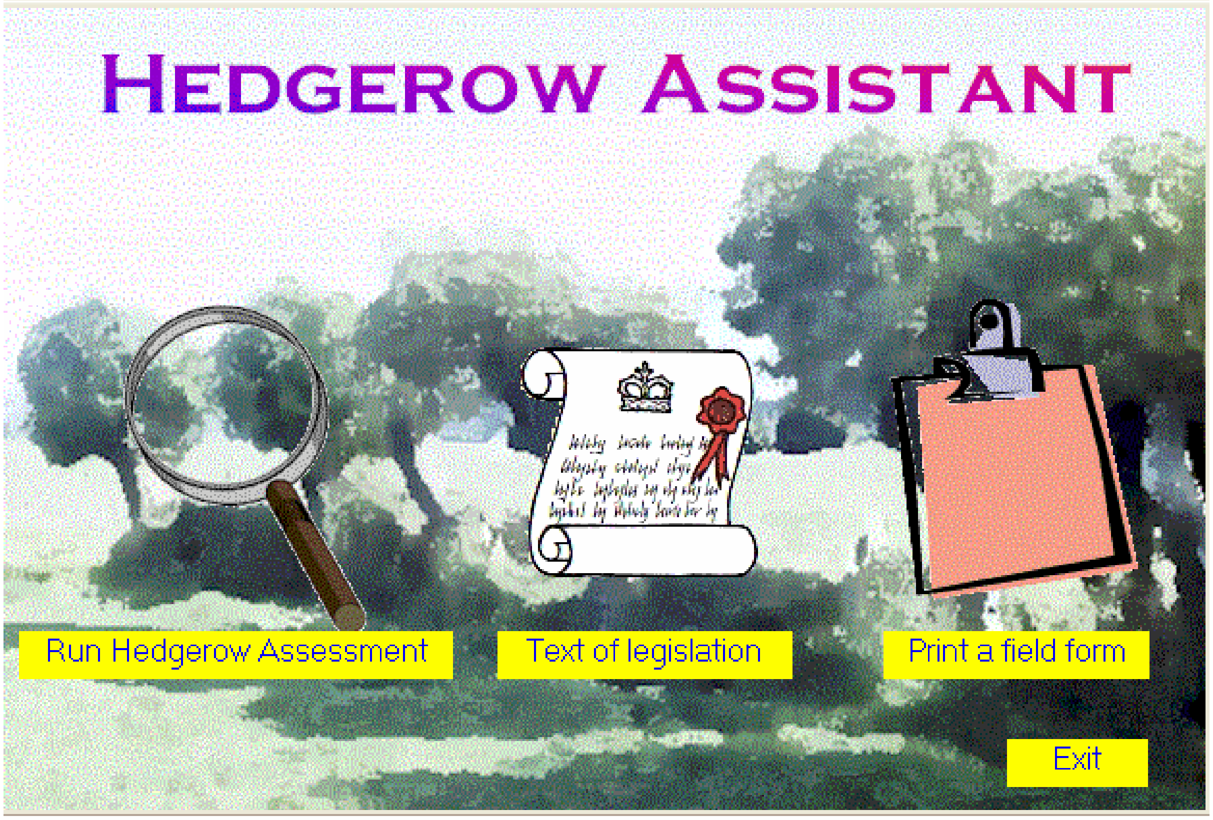
Hedgerow Assistant

For more information visit our website here.

Hedgerow Assistant provides the reliable way to survey hedgerows under the 1997 Hedgerows Regulations.

The 1997 Hedgerows Regulations provide standards by which hedgerows are evaluated and protected. The rules are complex and hard to interpret. Hedgerow Assistant guides you through the survey procedure, telling you which species to look for, which parts of the hedge to survey and which features to record. For environmental surveyors it saves time, work and money.

Features include:
- Step by step hedgerow evaluation.
- Lists of Red Data Book and Scheduled species.
- Full texts of relevant legislation.
- Advises on which parts of the hedge to survey.
- On-line help to interpret complex clauses.
- Prints field survey forms to guide data collection.



8.12 Simply Probit

Simply Probit

For more information visit our website here.

Estimate lethal or environmental concentrations using toxicity data.

The program offers two types of analysis:

- Lethal dose calculations: a probit analysis of the survival of organisms exposed to a range of concentrations. Conforms to ISO/DIS 146609.
- Growth analysis: studies the inhibition in the growth of organisms exposed to different levels of a compound. Conforms to ISO 10253 .

Part

IX

9 Lecture Resources

Lecture Resources

For more information visit our website here.

Our current titles include:
- Seashore Ecology
- The Ecology of Freshwaters
- The Galapagos Islands from an Ecological Perspective - Peter Henderson & Scott Henderson
- An Introduction to Multivariate Statistics
- An Introduction to Diversity and Richness Methods

9.1 Seashore Ecology

Seashore Ecology

For more information visit our website here.

This CD contains nine PowerPoint presentations showing the plants and animals of the seashore, and the techniques required to study and understand their ecology.

PowerPoint viewer software is included on the CD, so the lectures can be viewed on any PC.

Over 480 original photographs!

9.2 The Ecology of Freshwaters

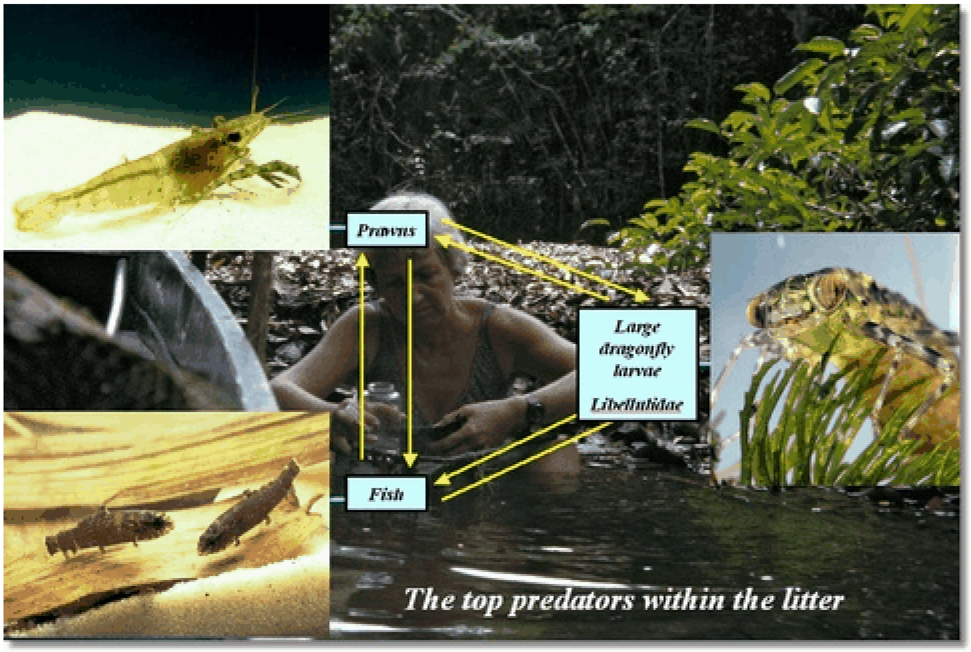
The Ecology of Freshwaters

For more information visit our website here.

This CD contains seven PowerPoint presentations showing the plants and animals of freshwaters around the world, and the techniques required to study and understand their ecology.

PowerPoint viewer software is included on the CD, so the lectures can be viewed on any PC.

Over 370 original photographs!



9.3 The Galapagos Islands

The Galapagos Islands from an Ecological Perspective

For more information visit our website here.

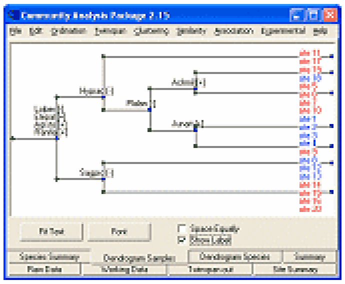
This CD contains a PowerPoint presentation on the plants and animals of the islands, and exploring their habitats and ecology. Over 50 original photographs by senior ecologists and researchers at the Charles Darwin Research Station.

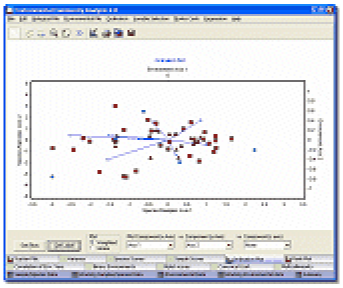
PowerPoint viewer software is included on the CD, so the lectures can be viewed on any PC.

9.4 An Introduction to Multivariate Statistics

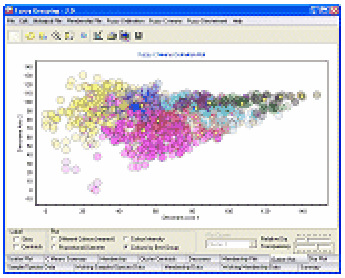
An Introduction to Multivariate Statistics

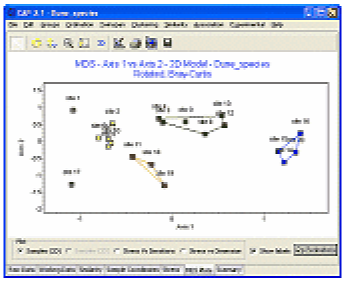
For more information visit our website here.





This CD contains two PowerPoint presentations exploring the principles of multivariate statistical analysis, with guidance and example hints from biology, archaeology and geology. Lecture contents are designed to be accessible to senior undergraduate students, MSc students and postgraduates. They will, however, be useful to anyone seeking a better understanding of techniques of multivariate analysis.



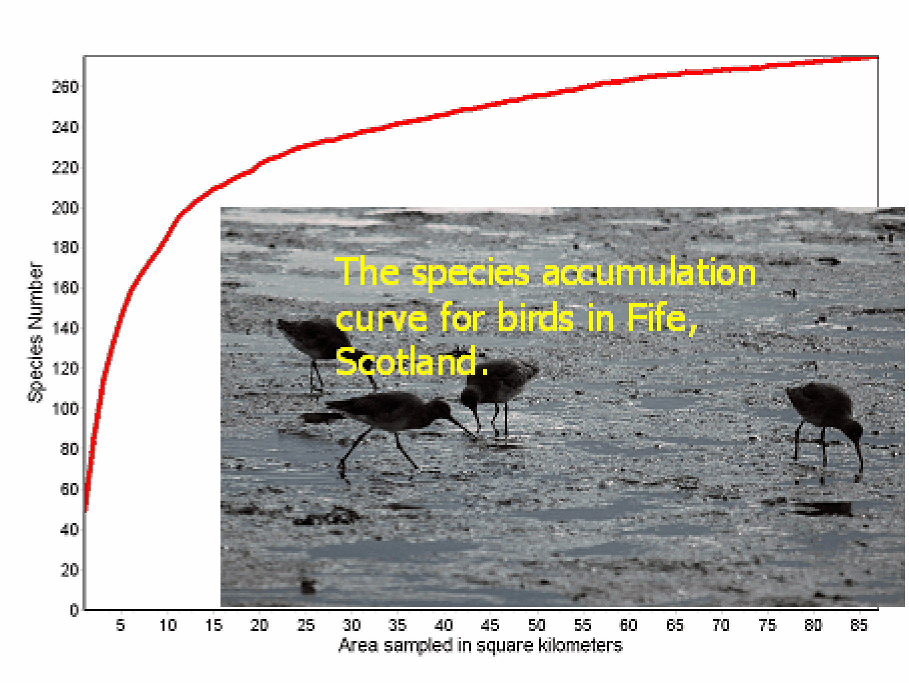


PowerPoint viewer software is included on the CD, so the lectures can be viewed on any PC.

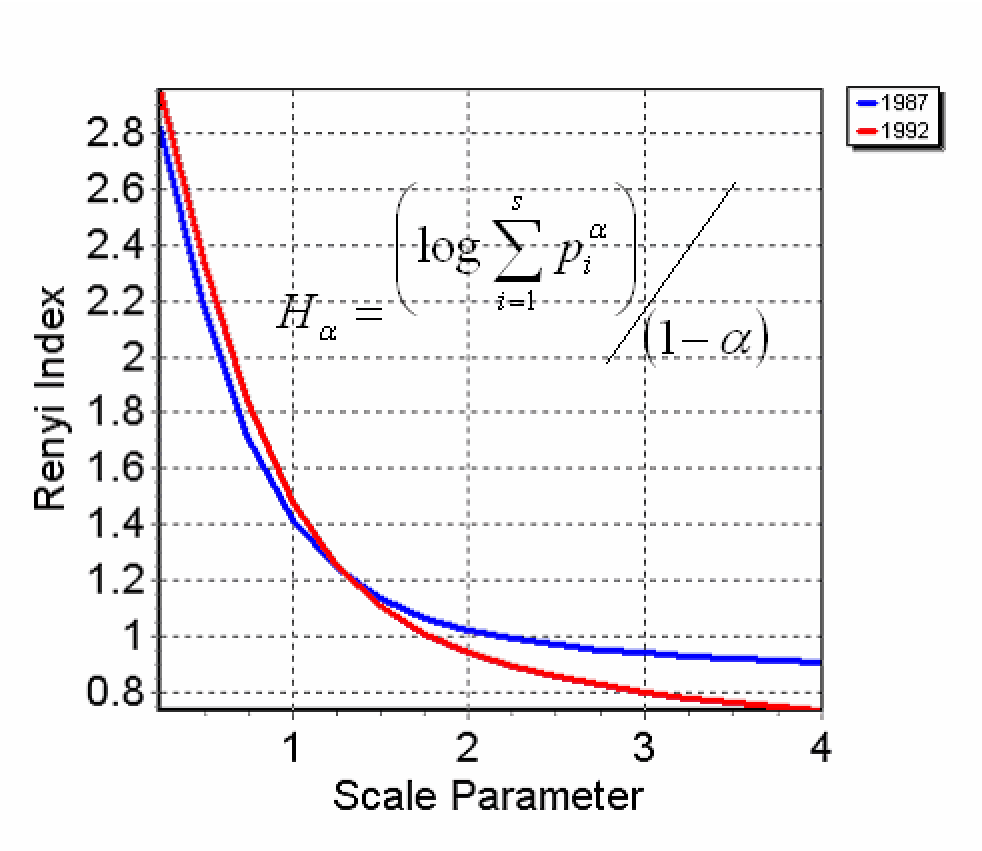
9.5 An Introduction to Species Diversity and Richness

An Introduction to Species Diversity and Richness

For more information visit our website here.



This CD contains two PowerPoint presentations exploring the principles of Species Diversity and Richness, with guidance and example hints. Lecture contents are designed to be accessible to senior undergraduate students, MSc students and postgraduates. They will, however, be useful to anyone seeking a better understanding of techniques of Species Diversity and Richness.



PowerPoint viewer software is included on the CD, so the lectures can be viewed on any PC.

Part

X

10 E-books

E-Books

Our library of e-books is growing continuously.

Pisces e-books are supplied on CD as Adobe Acrobat PDF files. The PDF format is well known, extremely versatile, and will run on both Windows and Mac operating systems. The Acrobat Reader software to use them is available as a free download from Adobe - and we also supply the 2 latest Windows versions on the e-book CDs.

Many e-books are simply 'photographic' copies of the originals. This means that the pages are scanned images of the book. This can give a poor-quality image, with a huge file size, and means that the text can not be selected, or searched. Pisces e-books are carefully scanned from the originals, repeatedly proof-read, saved as fully-searchable text, and paginated exactly as the original, so that all page and index references remain correct. We do not make corrections or alterations to the original, except:

- in the case of obvious typos, where the correction is added in [square brackets], and
- where the original contains an 'Errata' section.

Quotes from customers about Pisces e-books:

" ... very well done for the service you are providing for naturalists and the quality of your products".

" … Pisces are putting essential works back into the reach of many who needed them".

We now have e-books for those interested in the fields of entomology, botany, marine zoology and early exploration of the natural world.

For more information visit our website here.

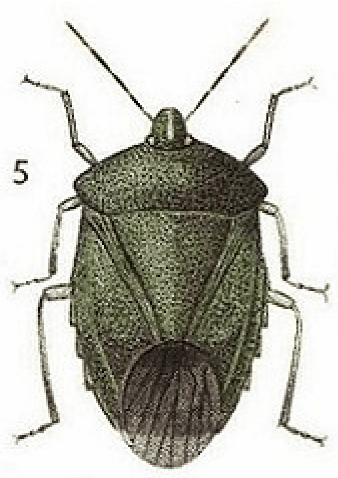
Our current titles include works on the following:

- Entomology
- Aquatic Biology
- Botany
- Classics of Science and Exploration
- Pisces Thesis Series

10.1 Entomology

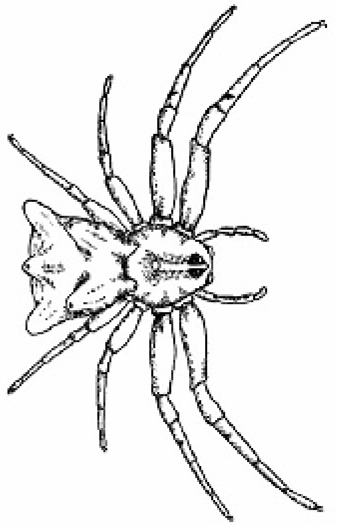
Entomology

For more information visit our website here.



Our current titles include (ebooks unless stated):

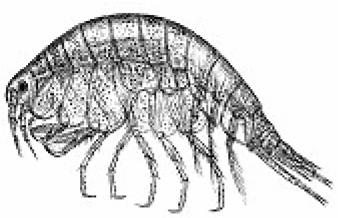
- Land and Water Bugs of the British Isles - Southwood & Leston
- Land and Water Bugs - 2005 print edition
- British Tortricoid Moths - Bradley, Tremewan & Smith
- British Water Beetles - Balfour-Browne
- Centipedes of the British Isles - Eason
- Larvae of the British Butterflies and Moths (Wm. Buckler):
  Vol. 1
  Vols. 2 & 3
  Vols. 4 to 6
  Vols. 7 & 8
  Vol. 9
- British Spiders (Vols 1-3) - Locket & Millidge
- Mantidae - Giglio-Tos
- The Comity of Spiders - W.S. Bristowe
- Collected Essays of J. Henri Fabre - Vol. 1
- The Genitalia of the Geometridae - Pierce
- The Genitalia of the Rhopalocera / Larger British Moths - Pierce
- The Genitalia of the Tortricidae - Pierce
- The Gentialia of the Pyrales, Deltoids and Plumes - Pierce



10.2 Aquatic Biology

Aquatic Biology

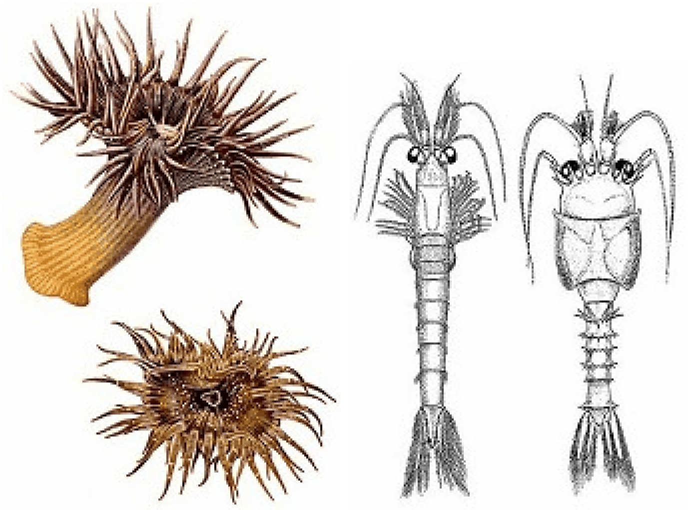
For more information visit our website here.



Our current titles include

- British Sea Anemones - Stephenson
- British Mysidacea - Tattersall & Tattersall
- British Naked-eyed Medusae - Forbes
- The Tunicata - N.J. Berrill
- Freshwater Ostracods - Henderson
- Amazonian Fishes & Their Habitats - Henderson
- Crustacea of Norway, Vol. I: Amphipoda - G.O. Sars
- Crustacea of Norway, Vol. II: Isopoda - G.O. Sars
- Crustacea of Norway, Vol. III: Cumacea - G.O. Sars
- Crustacea of Norway, Vol. IV: Copepoda (Calanoida) - G.O. Sars
- Crustacea of Norway, Vol. IX: Ostracoda - G.O. Sars
- British Fresh-water Copepods, Vols. I - III - Robert Gurney
- British Bivalve Seashells - Norman Tebble

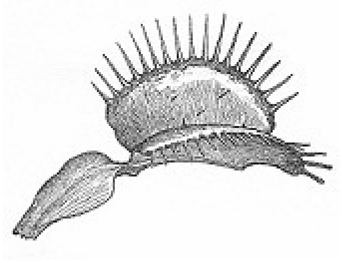
- Marine Plankton - A Practical Guide - Newell & Newell
- Marine Plankton - A Practical Guide - 2006 facsimile edition
- British Marine Amphipoda: Gammaridea - Roger J. Lincoln
- Biology of Intertidal Animals - Richard C. Newell



10.3 Botany

Botany

For more information visit our website here.



Our current titles include :

- Insectivorous Plants - Darwin
- Brambles of the British Isles - Edees & Newton
- The Naturalist on the River Amazons - Bates
- Notes of a Botanist on the Amazon and Andes - Spruce
- Travels on the Amazon and Rio Negro - Wallace
- The Malay Archipelago - Wallace
- A Botanist in the Amazon Valley - Ruggles Gates

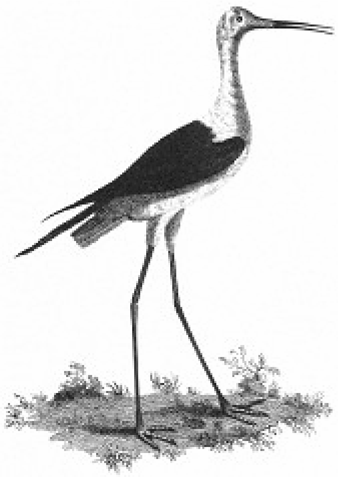
10.4 Classics of Science and Exploration

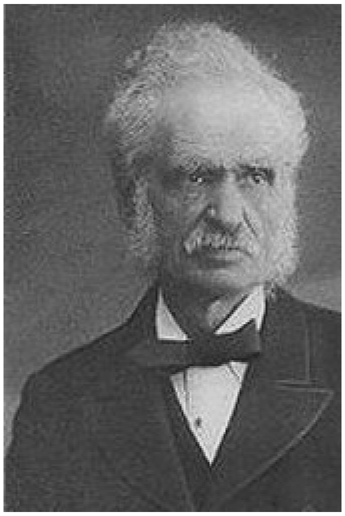
Classics of Science and Exploration

For more information visit our website here.

Our current titles include:

- On the Origin of Species, and The Descent of Man - Darwin
- The Naturalist on the River Amazons - Bates
- Notes of a Botanist on the Amazon and Andes - Spruce
- Travels on the Amazon and Rio Negro - Wallace
- The Malay Archipelago - Wallace
- A Botanist in the Amazon Valley - Ruggles Gates
- The Natural History of Selborne - White
- Amazonian Fishes & Their Habitats - Henderson





Contemporary Science

- The River - A Journey to the Source of HIV and AIDS - Edward Hooper

10.5 Pisces Thesis Series

Pisces Thesis Series

For more information visit our website here.

Our current titles include

- Satellite mapping of vegetation change - Canney
- Ground Ant Communities of Kakamega Forest - Espira
- Coral reef fish populations in Zanzibar, Tanzania - Tyler

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