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A Guide to Using

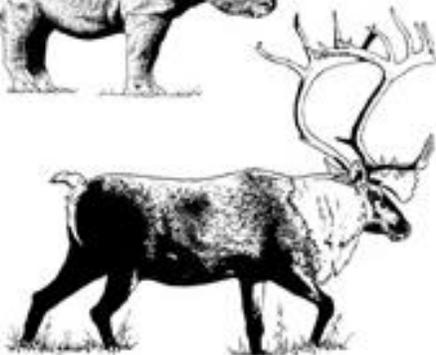
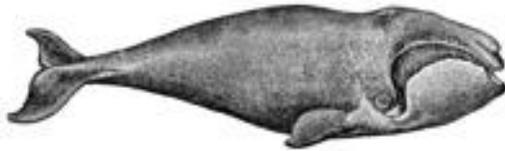
# RISKMAN

Stochastic and Deterministic Population  
Modeling RISK MANAGEMENT Decision Tool  
for Harvested and Unharvested Populations

Version 1.9.003

September 30, 2006

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Martyn Obbard  
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**Version 1.9.003**

**User Manual**

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# System Overview

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## General Overview

This document describes the structure and operation of RISKMAN (RISK Management) - a computer simulation system intended as a decision support tool for managers of harvested and unharvested populations who must base their decisions on uncertain information. RISKMAN employs a Monte Carlo approach similar to that used in population viability models to estimate the uncertainty of population trajectories based on estimates of population numbers and demographic parameters.

RISKMAN has two distinct uses:

- \* as a management tool, the system can be used by wildlife managers to design management strategies and regulations for specific populations of wildlife; and
- \* as a research tool, the system can be used to investigate the behaviour of populations under various management regimes and to investigate and understand the effects of uncertainty on population persistence.

### ***Background and General Description***

The development of RISKMAN is a collaborative effort, funded jointly by the Ontario Ministry of Natural Resources (OMNR) and the Nunavut Department of Sustainable Development. RISKMAN has its roots in a series of polar bear workshops intended to develop quantitative tools to determine the impact of harvest on polar bear populations, and the OMNR's interest in establishing a firm basis for managing black bears. RISKMAN has an annual, biannual and three-year life cycle options to allow accurate modelling of all bear species. RISKMAN is capable of simulating the population dynamics of most harvested wildlife species.

At the core of RISKMAN is a simple life-table model (Cole 1954, Caughley 1997), comprised mostly of "bookkeeping" functions associated with births, deaths, and ageing of animals in the simulated population.

RISKMAN allows users to select the model that correctly describes the life history biology of their target species (e.g., annual for furbearers and ungulates; two-year for black bears, or three-year for polar bears, grizzly bears and elephants). The user can define the number of age classes, and set the survival and recruitment rates for appropriate age strata, or for each age individually. Harvest scenarios can be

simulated by defining the number of annual hunting seasons (none, single or two), the quotas (or fraction of the population) of animals to be harvested, and relative selectivity/vulnerability of age/sex classes to hunting and non-hunting (human-induced) mortality.

RISKMAN has both a deterministic and a stochastic mode. The stochastic option is an individual based model using the variance of input parameters to provide Monte Carlo estimates of the uncertainty in simulation results. The rationale for the model structure and approach to variance is provided in a companion technical paper (Taylor and Cluff, 2002). RISKMAN also has the capability to include density effects. The user can specify a relationship of any of the vital rates (survival, proportion with litters, and litter size) to the density of in population sex or age strata.

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## Hardware and Software

RISKMAN has been developed to run in a Microsoft Windows 2000 or XP environment on a standard PC. It does not require any additional hardware or software beyond that associated with normal operation of Windows.

Some of the data can be exported into a “CSV” format, which is compatible with all major spreadsheet format (e.g. Microsoft Excel).

RISKMAN's interface uses standard conventions and keystrokes for Microsoft Windows-based software.

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## Installation Instructions

If you have an earlier version of RISKMAN installed on your computer, you should remove it using the **Start** button “**Settings / Control Panel / Add-Remove Programs**” utility.

Make sure to save any project files created with the previous version of the system. You will be able to continue to use them with the new version.

To install RISKMAN:

1. Close any open programs.
2. Insert the RISKMAN CD into your CD drive or place the downloaded program in a temporary directory.
3. Double-click on the “RiskmanSetup.exe” program.

Follow the prompts as the program asks you for the installation location and other installation details.

# Concepts and Common Functions

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## Overview

This section describes some of the concepts needed to better understand RISKMAN, and functions and procedures that are common to many of the program's features. For simplicity they are described once here rather than repeatedly throughout the manual. For specific details about each menu and screen, see the User Interface section.

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## Life Table Matrices

In order to simulate population changes that result from management decisions, users will likely be modifying or entering new data, changing age and encumbrance (females with offspring) groupings, selecting various density dependence relationships, and testing the effect of stochasticity on the results of simulation runs. Most of these options can be accessed from the life table screens present in the **Parameters** Menu.

### Modifying Data in Matrices

For each life table screen under the **Parameters** Menu, the dimensions of the matrix are determined by:

- \* the parameters entered in the *Species Definition* screen under the **Options** Menu
- \* by the user-defined age class and encumbrance (females with or without offspring) categories (i.e., strata), and
- \* by the *Information Display Format* selected in the *Strata Definition* screen.

Additionally, the tables for recruitment and individual survival each contain four layers of data that can be accessed by clicking on tabs across the top of the table. The four tabs are: *Rates*, *Standard Error*, *Carrying Capacity*, and *Shape Factor (KS)*. The *Rates* tabs contain base parameter data; the *Standard Error* tab contains measure of variability for stochastic simulations; the *Carrying Capacity* and *Shape Factor* tabs contain values describing the density dependent relationship.

**To enter or modify values in the life table screens:**

1. Select the cell to be modified by highlighting it with a click of the mouse. (Click again if you wish to modify individual digits in the cell.)
2. Type in the new value or digit.
3. If you wish to enter the same value into two or more adjacent cells in a block, use the blocking feature to simplify the process.
4. To save your changes to a life table matrix and return to the **Main** Menu screen, click **OK**.

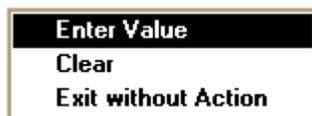
The *Standard Error* tab for both *Recruitment* and *Individual Survival* screens is available only when the model is set to run in *Stochastic* mode on the *Preferences* screen in the **Options** Menu. Standard error values can be modified using the system edit features.

Estimates of demographic parameters typically pool together the parameter uncertainty (due to sample size) and the environmental uncertainty (annual and individual differences). The *Preferences* screen in the **Options** Menu allows the user to partition the standard error into a parameter and environmental component. The parameter component is modelled by obtaining a random deviate (using the parameter portion of the total standard error) that serves as the mean for that particular run. A Monte Carlo simulation consists of many runs. The environmental component is modelled by using the run mean and the environmental portion of the total standard error for random variate for each iteration (year) of a given run. The recommended apportionment of the standard error is 75% parameter and 25% environmental uncertainty when the actual distribution has not been estimated. For further discussion and examples of the parameter and environmental uncertainty see the *Variance* section.

The remaining two tabs, *Carrying Capacity*, and *Shape Factor (KS)*, are available only when *Density Dependence* is turned on (*Species Definition* screen in the **Options** Menu). These two parameters work together to define how the number of animals influences the behaviour of other population parameters such as the proportion of females with litters, mean litter size, survival, etc. For further discussion on density dependence see the *Density Dependence* section.

**Blocking Multiple Matrix Cells for Data Entry**

To select a block of cells, left-click on one of the corner cells of the block and right-click the opposite corner. The cells of the selected block will change colour and a pop-up menu will appear that shows the available actions.



*Enter Value* - inserts the number you wish to enter into each cell of the block  
*Clear* - resets all cells in the block to 0

*Exit Without Action* - select this option to leave the *Available Operations* screen without making any changes, or press the <Esc> key on your PC keyboard

To re-define an already selected block, right-click on the new corner cell. To unblock, simply left-click on any cell.

## Matrix Import and Export

The *Import* and *Export* command buttons are located on the right side of all **Parameters** Menu screens.

The export function converts the currently open matrix to comma and quote delimited ASCII format and saves it in a user defined file. ASCII format is suitable for importing into a spreadsheet or database application, or back into RISKMAN (using *Import*). The export feature allows users to save life table matrices independently of the project file, e.g., for exchanging between projects or between different screens.

The *Import* function imports a user selected comma and quote delimited ASCII file as a life matrix. The system will bring the selected file into the matrix that is currently open (e.g., into the *Recruitment by Age* life table matrix).

Two types of files can be imported and exported by the *Import* and *Export* functions. First is the format specific to the screen from which the data is being imported to or exported from. Most of the information present on the screen is saved in that format. The file extensions are unique to the screen. The second file type contains only the age structure on the screen. This format is common to all screens containing the full age matrix. Using this format, data can be copied from one screen to another. For example for harvest screens or “other” mortality screen.

Population structure data resulting from simulation runs can also be imported into a selected matrix from within RISKMAN using the **RISKMAN Export** function. For example, if you wish to use the stable age population structure of the species being modelled, first select the stable age distribution option on the *Initial Population* screen, then run the simulation. Following the run, select **RISKMAN Export** and **Stable Population Structure** from the **Options** Menu. Return to the *Initial Population* screen, click on the *Import* command button, select the file you have just exported and click on **OK**. The values of the stable age population structure will be inserted into the initial population matrix, overwriting the values that were there before.

## Strata Definition

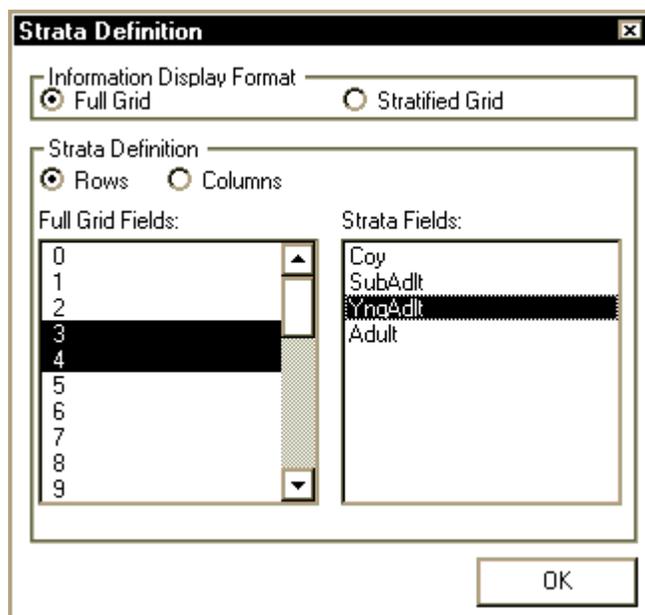
Strata are functional biological groupings of animals composed of age and encumbrance categories that have some life history parameter in common. For example, all 2- and 3-year old black bears might be defined as “juveniles” because they are all old enough to be independent of their mothers (i.e., greater than one year of age) but not old enough to produce young.

### Entering and Modifying Strata

The *Strata* command button allows users to define age class and encumbrance categories appropriate for their particular application. It is located on the right side of all screens listed under the **Parameters** Menu, except the *Initial Population* screen.

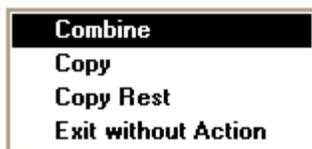
The system keeps strata definitions for each variable individually; users need to define strata for each life table data set they wish to stratify (e.g., recruitment, survival, hunting and other mortality, etc.).

Click on the *Strata* command button to activate the *Strata Definition* screen.



#### To define strata:

1. Select the type of strata you wish to define (Row/Column).
2. From the Full Grid Fields list, select the range of fields (click and drag) you wish to define.
3. Right-click on the highlighted block of fields to activate a pop-up menu listing the available actions.



*Combine* - groups the highlighted fields together into a single stratum and prompts the user for a stratum title.

*Copy* - copies a single selected category as a stratum.

*Copy Rest* - copies all as yet undefined full grid categories over to the *Strata Fields* list, creating one stratum for each category copied.

*Exit Without Action* - select this option to leave the *Available Operations* screen without making any changes, or press the <Esc> key on your PC keyboard.

*Note: In order to use strata all the row and columns must be included, even if each column (or row) has to become a stratum by itself.*

To review which *Full Grid Fields* have been included in a particular stratum, click on the stratum of interest in the *Strata Fields* list and the constituent fields will be highlighted.

The system also supports strata of non-contiguous rows or columns. To select those click on additional elements of the stratum while holding a <Ctrl> key. For example you may wish to combine females with juveniles and females with no cubs because the time of census for the population was fall, after the juveniles had all been weaned. Thus all these females would be without offspring, and the offspring would also be on their own.

All strata information is interdependent, for example if the strata in the harvest screen are changed, the user must click **Create S-V** on the **Hunt Data** screen to re-calculate the selectivity/vulnerability array.

#### **To edit existing strata definitions:**

1. Select the stratum to be modified.
2. Right-click on the selected stratum to activate a pop-up menu listing the available actions.



*Delete One* - removes the highlighted stratum definition; the constituent fields become unassigned.

*Sort* - sorts the strata listed in *Strata Fields* based on the order of the corresponding full grid categories.

*Rename* - allows you to give the highlighted stratum a new name.

*Delete All* - removes all strata definitions listed in *Strata Fields*.

*Exit Without Action* - select this option to leave the *Available Operations* screen without making any changes, or press the <Esc> key on your PC keyboard.

The system keeps strata definitions for each variable individually; users need to go through the steps described for each life table data set (e.g., recruitment, survival, hunting and other mortality, etc.) they wish to stratify.

The *Strata Definition* screen also allows users to select the format in which their data will be displayed. The *Information Display Format* section of the screen offers two options. Select *Full Grid* to display the data for each age class and each encumbrance class separately or *Stratified Grid* to display the user-defined strata (see the example). In both full and stratified grid display formats, the values in the cells of the life table matrices can be modified.

When a stratum is defined as including multiple full grid categories (e.g., the juveniles stratum might include all 2- and 3-year olds), the resulting stratum cell values in the corresponding row or column of the matrix become averages of the constituent values. When the user modifies a cell value the stratum the original values in the constituent cells will be changed to the newly entered value (i.e. they are not allocated proportionally).

If a value of a stratum is not modified, the system retains and uses the original values. The values used displayed in the stratified grid may be different from those used by the system in the simulations. To see the values used in the simulation switch to the *Full Grid* display

## Strata Definition Example

**Individual Survival**

Individual Survival Rates

	Survival Rates	Standard Error	Carrying Capacity	Shape Factor (KS)	
Age	Males	Fem n/c	Fem w/c	Fem w/y	Fem w/j
0	0.750	0.850			
1	0.990	1.000			
Juv	0.736	0.840			
SubAdlt	0.736	0.840			
Adlts	0.813	0.860	0.860	0.858	0.855

Import...  
Export...  
Strata...

Litter Survival Rate:      Std Error:

Age 0:         

Age 1:         

OK

As an example, the user may choose to combine all age classes into five categories. The *Strata Definition* screen allows the user to select the appropriate age classes for each group (e.g., 0 year old, 1 year olds, 2 and 3 year olds, 4 -year olds, and 5 to 24 years old) and create labels (e.g., cubs, yearlings, juveniles, sub-adults and adults) that appear as row names in the life table matrices. Similarly, a user may distinguish between females encumbered with cubs from those encumbered with yearlings. In this example, the resulting life table matrix contains five columns labelled males, unencumbered females (fem n/c), females with cubs (fem w/c) females with yearlings (fem w/y) and females with juveniles (fem w/j). The stratified grid there are also five rows: cubs (0), yearlings (1), juveniles (Juv), sub-adults and adults.

### To define the strata:

1. Activate the *Strata Definition* screen by clicking on the **Strata** command button on the right side of the *Individual Survival* screen.
2. Select *Rows* from the *Strata Definition* box near the top of the screen.
3. To define a stratum for cubs (i.e., 0 years of age), highlight the “0” in the *Full Grid Fields* list by left-clicking on it with the mouse.
4. Activate the *Available Operations* screen by right-clicking on the highlighted row.

5. Select either *Combine* or *Copy* to insert the single category into the *Strata Fields* list; the *Combine* option provides an immediate opportunity to name the stratum (e.g., cubs), whereas *Copy* gives the new stratum the same name as the original category (i.e., “0”).
6. Create a stratum for 1-year olds in the same way as for cubs.
7. To define a stratum for juveniles (i.e., 2- and 3- year olds), left-click on the “2” in the *Full Grid Fields* list and drag down to highlight the “3” as well; right-click on the highlighted rows to activate the *Available Operations* screen; select *Combine* and enter a title for the new stratum in the space provided.
8. Create a stratum for 4-year olds in the same way as for cubs and yearlings.
9. To define a stratum for adults (i.e., 5-year olds and older), follow the same procedure as for juveniles.
10. Review which *Full Grid Fields* have been included in a particular stratum by left-clicking on the stratum of interest in the *Strata Fields* list.
11. Repeat from Step 2 above to define strata for the columns of the *Individual Survival* matrix, starting by selecting the *Columns* option in the *Strata Definition* box near the top of the screen.
12. To display your newly defined strata in the *Individual Survival* matrix, select the *Stratified Grid* option from the *Information Display Format* area at the top of the *Strata Definition* screen and click **OK** to return to the *Individual Survival* screen.

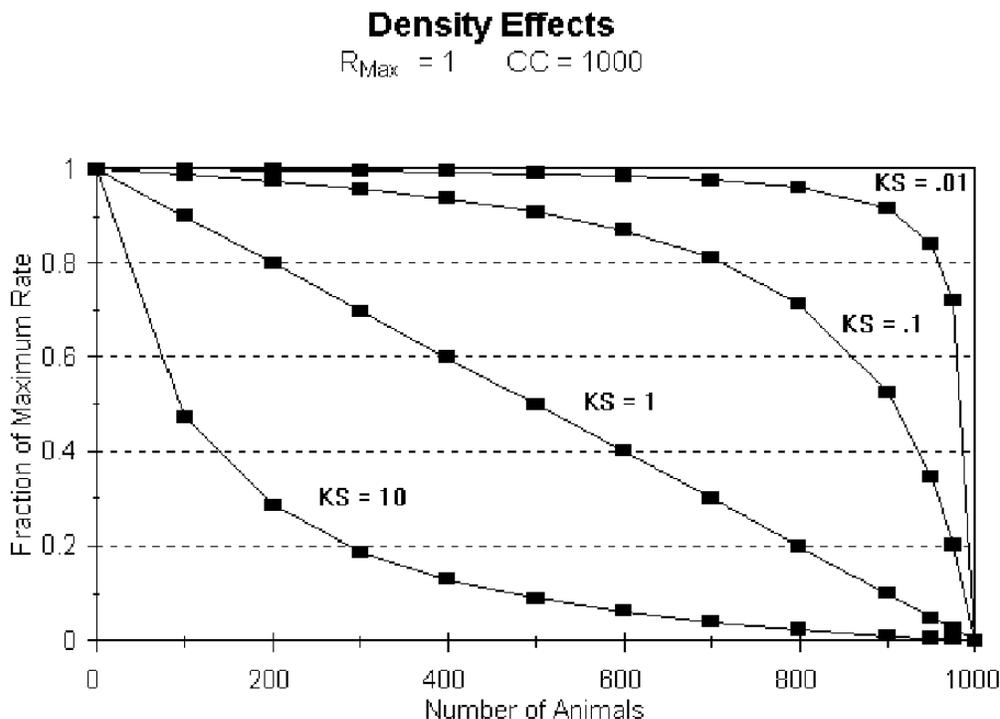
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## Density Dependence

The density dependence provides means of defining how population size can affect the vital rates within the RISKMAN simulations.

### Density Dependence Definition

RISKMAN defines density dependence in terms of proportion of population capacity (Carrying Capacity) and not in numbers per area. The Carrying Capacity value can represent the whole population or a user defined subset thereof.



The term Carrying Capacity (also sometimes referred to as K) is the population number that causes a density dependent reduction in the population growth rate to 0. However, density does not affect the population growth rate directly. Rather density affects birth and death rate, and those cause the change in population growth rate. Density may only affect the demographic rate of same sex and age strata. It may be that only the density of same sex and age strata is causing the density effect. RISKMAN provides a flexible empirical equation (inverted threshold-corrected Michaelis-Menton equation) to model the mechanism of density effect.

The rate value entered (e.g. survival rate) is considered to be the maximum rate value for a given iteration. The maximum rate is reduced based on the values of the X-Axis intercept (CC) which is the value where the rate goes to zero. The shape parameter (KS) determines whether the decline is linear (classical density effect) or non-linear. Many independent density effects can be specified simultaneously. If the sex and age distribution of the population are changing the impact of these demographic rate effects on overall population growth rate can be dynamic.

The values of the parameters used to model density effects can be determined by non-linear least squares regression. The density effects equation has been based on a threshold-corrected Michaelis-Menton curve. The equation is:

$$R = (R_{MAX}) \frac{\frac{CC}{N} - I}{\frac{CC}{N} - I + KS}$$

Where:

$R_{MAX}$  - maximum survival or recruitment rate

$CC$  - carrying capacity of the environment

$N$  - number of animals

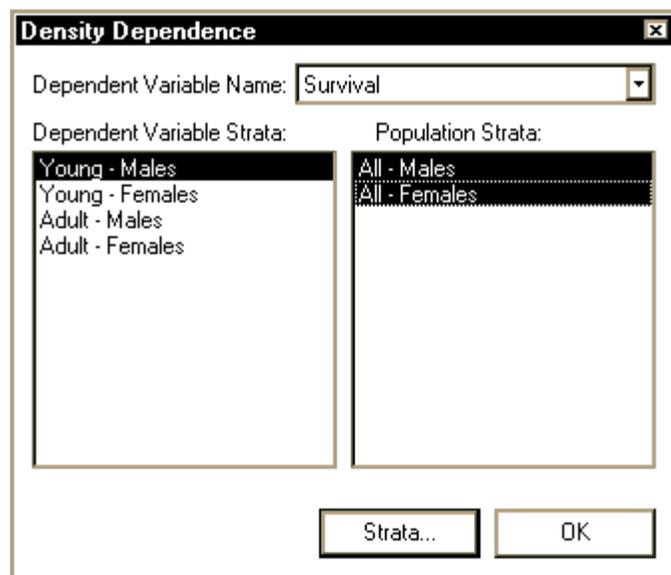
$KS$  - shape parameter controlling the degree of non-linearity due to density

Michaelis-Menton curve is only one of many empirical equations that could be used.

## Density Dependence Interface

The **Density** command button is common to both the *Recruitment* and *Individual Survival* screens of the **Parameters** Menu. This button will only be visible when the *Density Dependence* option is activated on the *Species Definition* screen in the **Options** Menu. Clicking on the **Density** button will activate a screen in which users can define the manner in which selected life history parameters respond to population density.

The *Density Dependence* screen features a drop-down list of *Dependent Variables* (survival, litter size, and proportion of females with litters), a list of *Dependent Variable Strata*, and a list of *Population Strata*.



*Dependent Variable Strata* are defined by the user through either the *Individual Survival* screen (for the *Survival* dependent variable) or the *Recruitment* screen (for the *Litter Size* and *Proportion of Females with Litters* dependent variables) via the **Strata** command button (see **Strata Definition** section for a step-by-step procedure to

define strata). *Population Strata* are defined using the **Strata** command button on the bottom of the *Density Dependence* screen, following the same procedures as described in the **Strata** section. These population strata are only used for defining density dependence.

To define relationships between pairs of dependent variable strata and population strata, start by selecting a dependent variable stratum with a click of the mouse. Identify one or more of the population strata (from the *Population Strata* list to the right) that will have a density effect on the selected dependent variable by highlighting each with the mouse. Continue to define density relationships for each of the dependent variable strata in the *Dependent Variable Strata* list. Click **OK** when done. If some of the age/encumbrance classes are not density dependent leave them without selecting the population strata.

Make sure to define the appropriate density dependence parameters (CC and KS) for each of the dependent variable strata. Pay particular attention if the dependent variables use different sets of population strata since the total of those population strata will constitute a different proportion of the carrying capacity and thus will be at a different point of the density dependence relationship.

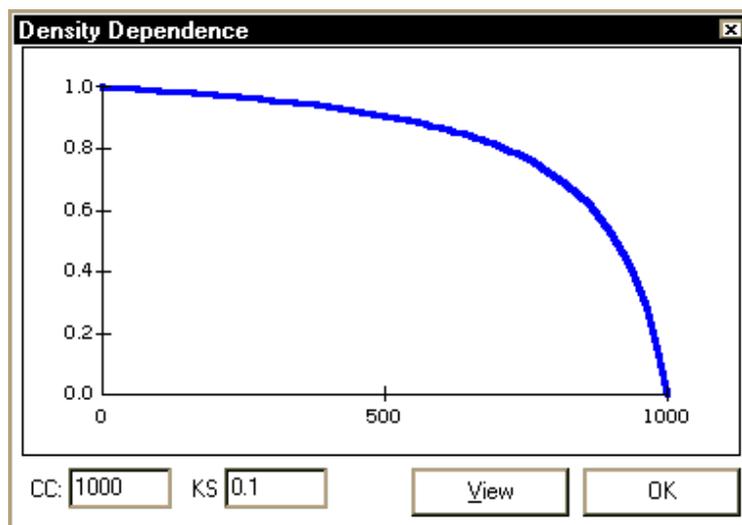
For example, to **define density dependence relationships** for the Survival dependent variable:

1. Enable density dependence on the *Species Definition* screen.
2. Establish the dependent variable strata with which you wish to work via the **Strata** command button on the right side of the *Individual Survival* screen.
3. Activate the *Density Dependence* screen by clicking on the **Density** command button on the right side of the *Individual Survival* screen; the *Dependent Variable Name* showing in the drop-down list will be *Survival* in this example; the strata you defined in Step 1 will be listed on the left side of the screen, under *Dependent Variable Strata*.
4. Define the *Population Strata* with which you wish to work by clicking on the **Strata** command button at the bottom of the *Density Dependence*; return to the *Density Dependence* screen.
5. Select a dependent variable stratum from the left-hand list with a click of the mouse; identify one or more entries from the *Population Strata* list that will have a density effect on the selected dependent variable stratum by highlighting each with a click of the mouse; you can de-select a population stratum by clicking on it again; continue until you have defined density relationships for each of the dependent variable strata in the *Dependent Variable Strata* list.
6. To review the density dependence relationships you have defined, left-click on each dependent variable stratum in turn (left list) and their related population strata will be highlighted.

## Density Dependence Plot

Another button present on the *Recruitment* and the *Individual Survival* screens is **DDPlot**. It leads to a screen where you can review the shape of the density dependence function used by the system.

The initial value used for the plot are the CC and KS values in the grid cell highlighted prior to entering the *Density Dependence Plot*, if those are available. You can explore different shapes by providing new values for CC and KS. Click the **View** button to update the curve to use the currently specified parameter values. Changing values on the plot screen does not affect the Recruitment or Individual Survival density dependence matrices.



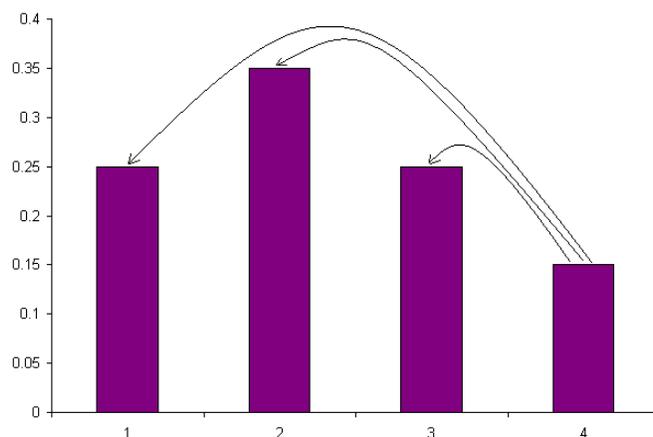
## Effect of Density Dependence on Litter Size

Litter size is treated a little differently from the other vital rates. Other vital rates are specified as simple rates (e.g. survival). The litter size is specified as a group of rates, one for each of the encumbrance classes. The density dependence affects the mean litter size, therefore, the system has to change the rates for individual encumbrance classes automatically.

The lowest encumbrance class is 1 (females with one offspring). To lower the values further you must designate the females as unencumbered by making the *Proportion of Females with Litters* also density dependent.

As the mean litter size decreases, the highest litter category is proportionally reallocated to the lower categories until the desired litter size is attained or the category is exhausted. If such removal of one category is insufficient the next lower category is also reallocated. The mean litter size cannot go below 1 (all encumbered females have only one offspring). Each age class can have an independent density

dependence relationship, therefore, distributions for various ages may be affected differently.



A similar algorithm employing the lowest encumbrance class is applied if the mean litter size increases.

## Variance

RISKMAN attempts to model all sources of uncertainty using the Monte Carlo method. The Monte Carlo method is a numerical rather than an analytical method of determining the variance of some parameter of interest. In this application, the Monte Carlo method entails repeating simulations many times using random deviates that are based on the mean and standard error of the simulation input parameters. The system attempts to use the correct underlying distributions for the random deviates, to allow the variance measures of the outcomes to be the actual estimates of the variance. Similarly, the proportion of the runs with outcomes not “exceeding criteria” in the stochastic mode to be equivalent to the probability of an outcome not “exceeding criteria”.

In stochastic mode, RISKMAN is an individual based model. Both survival and recruitment are modelled as Bernoulli trials. Similarly, assignment of individuals into distributions is done using the user defined matrices and random multinomial “allocation”. The binomial distribution represents the probability of  $x$  successes in  $n$  Bernoulli trials, similarly multinomial “allocation” results in a multinomial distribution (Kalbfleisch 1985).

## Parameter and Environmental Uncertainty

RISKMAN models three types of uncertainty: Demographic, Parameter, and Environmental.

Estimates of demographic parameters typically pool both the parameter uncertainty (sample size) and environmental uncertainty (annual and individual differences) (White 2000). The *Preferences* screen in the **Options** Menu allows the user to partition the standard error into a parameter and environmental component. The mechanism for partitioning the standard error requires first recovering the variance from the standard error estimates, then partitioning the variance and converting it back to the respective standard errors associated with parameter and environmental uncertainty. The total uncertainty (variance) is partitioned as parameter uncertainty ( $p$ ) and environmental uncertainty ( $1-p$ ).

$$Variance_{Parameter} = (Variance_{Total})p \quad Variance_{Environmental} = (Variance_{Total})(1-p)$$

Therefore, the partitioned standard error values are calculated as:

$$SE_{Parameter} = (SE_{Total})\sqrt{p} \quad SE_{Environmental} = (SE_{Total})\sqrt{(1-p)}$$

The parameter component of the uncertainty is modelled by obtaining a random deviate at the beginning of an iteration using the  $SE_{Parameter}$  that serves as the parameter mean for that particular run. The environmental component is modelled by using the run mean and  $SE_{Environmental}$  to obtain a random deviate for each year of the given iteration. Thompson et al. (1998) notes that parameter uncertainty has a larger effect on the simulation than environmental uncertainty, so increasing the portion that is assigned to parameter uncertainty will cause more runs to reach levels “exceeding criteria”. When it is not possible to obtain an estimate for proportions to partition the total uncertainty estimate, a division of 75% parameter and 25% environmental uncertainty is a reasonable although subjective compromise. Alternatively, a range of partition values can be used to examine the sensitivity of outcomes to how the variance is partitioned.

For normal parameters (e.g., population size), random normal deviates are obtained using the Polar Method (Law and Kelton, 1991). For binomial parameters, random deviates are obtained by determining a sample size “ $n$ ” based on the mean and the standard error values as follows:

$$n = \frac{p(1-p)}{Variance_p}$$

Then “ $n$ ” Bernoulli trials are conducted to determine the random deviate value. This method is used for both parameter and environmental uncertainty even though we recognized that environmental variation might be expected to be symmetrically distributed about an inter-annual mean. We choose the Bernoulli trials for binomial parameters because the behaviour of random deviates from a transformed-scale (e.g., arcsin or logit), and truncated symmetrical distributions, causes the resulting binomial random deviates to be biased. We choose to use the Bernoulli method for environmental random deviates because that method gave the best results.

## Co-variance

Generally environmental conditions that would favour recruitment would also favour survival. RISKMAN models a limited version of co-variance, to allow demographic parameters to co-vary. The model has a co-variance toggle that sets co-variance for environmental variance equal to 1.0. This is accomplished by using the same random deviate for all demographic parameters (individual natural survival, whole litter natural survival, proportion of females with litters, and mean litter size). In this way the effect of co-variance can be bounded by examining outcomes where it is 0.0 (demographic parameters are independent) or 1.0 (relevant demographic parameters are perfectly correlated for environmental uncertainty). For runs with co-variance toggle enabled, a truncated-for-symmetry normal distribution is used to obtain “environmental” random deviates for the relevant binomial parameters.

When deviates are truncated-for-symmetry the range of their variability is limited in such a way as to allow a symmetric range around the mean of the distribution. For example, if a survival rate is set at 0.95 the truncated-for-symmetry normally distributed values will range from 0.90 to 1.00. When random values fall outside the range they are set to the respective boundary values.

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## The “Mean” Look at Growth Rates

One of the graph panels in RISKMAN shows Growth Rates and a running Geometric Mean Growth Rate. The following discussion examines the correctness of use of the geometric mean versus arithmetic or harmonic mean.

### Mean Growth Rate Definition

The Growth Rate at time  $t$  is defined as  $GR_t = n_t/n_{t-1}$ . Where  $n_t$  is the population at time  $t$ . Growth Rate represents a year-to-year ratio of population sizes.

The arithmetic, geometric and harmonic means for the first  $n$  years of a simulation are defined as follows:

$$\text{Arithmetic Mean Growth Rate: } AMGR_n = \frac{1}{n} \sum_{t=1}^n GR_t$$

$$\text{Geometric Mean Growth Rate: } GMGR_n = \sqrt[n]{\prod_{t=1}^n GR_t}$$

$$\text{Harmonic Mean Growth Rate: } HMGR_n = \frac{n}{\sum_{t=1}^n \frac{1}{GR_t}}$$

Arithmetic Mean gives equal weight to all points considered, thus it is appropriate for symmetrically distributed data (e.g. number of individuals harvested). Growth Rates are not symmetric. A 20% increase in a value is not “cancelled” by a 20% decrease ( $1.2 * 0.8 = 0.96$ ). For skewed data a geometric or a harmonic mean is more appropriate.

To calculate an arithmetic mean as above we get:  $\frac{1.2+0.8}{2} = 1$

a geometric mean is  $\sqrt{1.2*0.8} = 0.9798$

a harmonic mean is  $\frac{2}{\frac{1}{1.2} + \frac{1}{0.8}} = 0.96$

Since the cumulative effect of Growth Rates is multiplicative the most appropriate way to summarize them across years within a single iteration is by use of a geometric mean. For example, with the values calculated above the cumulative effect using the arithmetic mean is  $1 * 1 = 1$ , which would imply that the population is constant and it is not. The cumulative effect using geometric mean is  $0.9798 * 0.9798 = 0.9600$ , equal to the product of the original values. For the harmonic mean the cumulative effect is  $0.96 * 0.96 = 0.9216$ , a value which is too low.

Unless the values are constant the arithmetic mean is greater than geometric mean, which in turn is greater than the harmonic mean.

## Implementation in RISKMAN

RISKMAN implements only a Geometric Mean Growth Rate in a form slightly modified from the definition. The following is a derivation for equation as it is implemented in RISKMAN:

$$\ln(GMGR) = \frac{1}{n} \sum_{t=1}^n \ln(GR_t)$$

$$\ln(GMGR) = \frac{1}{n} \sum_{t=1}^n \ln\left(\frac{x_t}{x_{t-1}}\right)$$

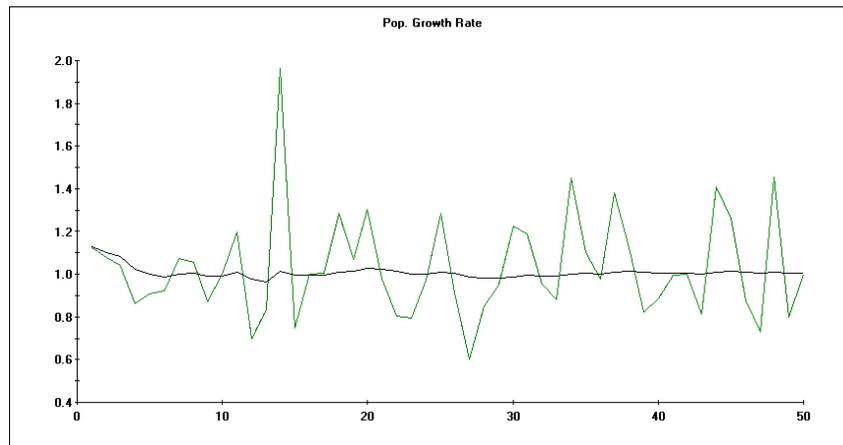
$$\ln(GMGR) = \frac{1}{n} \sum_{t=1}^n (\ln(x_t) - \ln(x_{t-1}))$$

$$\ln(GMGR) = \frac{1}{n} (\ln(x_n) - \ln(x_0))$$

therefore,

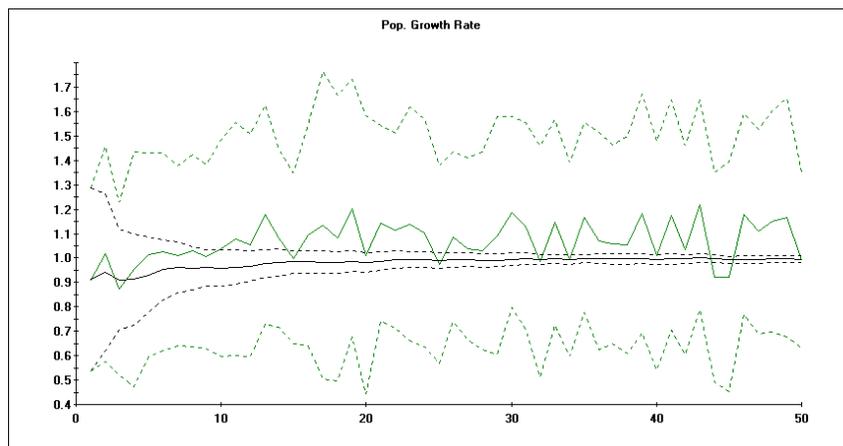
$$GMGR = \exp\left(\frac{1}{n} (\ln(x_n) - \ln(x_0))\right)$$

As is currently implemented in RISKMAN on a single stochastic run the system shows:



The more varied line represents individual inter-annual **Growth Rates** and the less varied line represents the **Geometric Mean Growth Rates** for all years up to that point in the simulation.

Therefore, for multiple runs the system shows:



The more varied solid line represents the average (i.e. the arithmetic mean) of individual growth rates across the iterations, the dotted varied lines are the 1 (or 2) SD lines on either side (depending on user setting). The less varied solid line represents the average of the Geometric Mean Growth Rates across the iterations with the “tapering off” dotted line showing the measure of dispersion. The “tapering off” in the distribution of the Geometric Mean Growth Rates exists because the “mean of means” has tighter distribution than sampled values do and the Geometric Mean Growth Rate has more points and thus is more “stable” the later it is in the simulation.

Geometric Mean is only calculated based on runs not “exceeding criteria”.

# User Interface

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## Overview

When RISKMAN is first installed it opens with a project “Default.prj”. You can select any of the pre-installed projects by selecting the **Open** option in the **File** Menu and searching in the “Projects” sub-directory.

During the normal course of operation the name of the last project used is stored in the file “Riskman.ini” in the program directory and the last project is opened upon start of the program.

Each time RISKMAN is launched, the **Main** Menu appears on the screen accompanied by a series of graphs. The title bar at the top of the screen identifies the program and displays the name of the project file that has been loaded. Users can access all of the functions of RISKMAN through the **Main** Menu. Each of the submenus and associated screens, fields and command buttons are described below.



The **File** Menu allows users to manage project files and create brief descriptions of their contents. The **Parameters** Menu provides users with the opportunity to enter data and modify biological parameters that will form the basis for model runs. Results can be viewed, printed, exported and organized into customized reports from the **Output** Menu. The **Options** Menu allows users to select and clear graphs, identify project defaults, mode of operation (i.e., the level of complexity required – deterministic, stochastic) and the wildlife species to be modelled. Finally, the on-line help system is available by selecting from among the options in the **Help** Menu.

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## File Menu

The **File** Menu contains the project file management and description options.

File	
<b>O</b> pen Project...	Ctrl+O
<b>S</b> ave Project	Ctrl+S
<b>S</b> ave Project <b>A</b> s...	
<hr/>	
<b>D</b> escription...	Ctrl+D
<hr/>	
<b>E</b> xit	

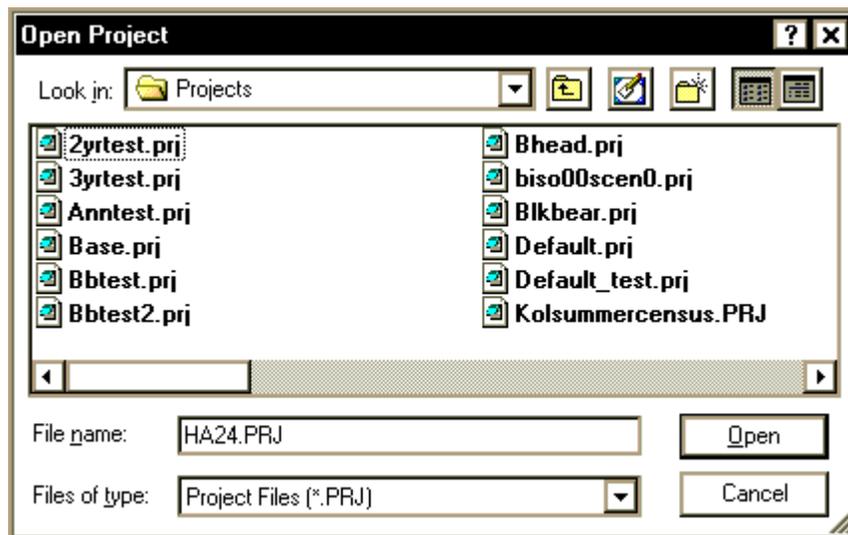
These file management options function as they do in any standard Windows application; additional windows appear to facilitate file management operations.

The file menu may also contain the names of up to four files most recently used by the program.

## Open Project

Selecting the **Open Project** option from the **File** Menu activates the *Open Project* screen. Prior to displaying the *Open Projects* dialog you will be asked to save any changes to the currently open project.

The dialog box will initially open in the directory where the current project is saved.

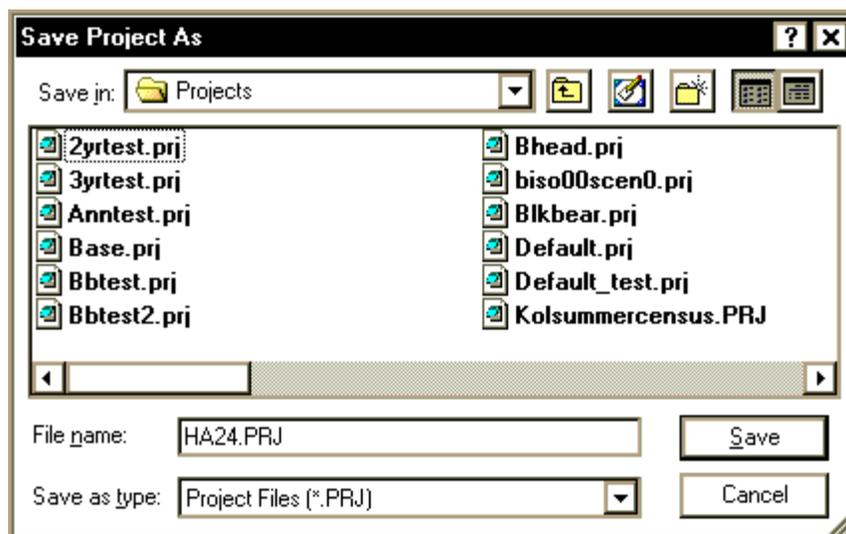


Choose a project file from the list of existing projects displayed on this screen or type the full project name into the *File Name* field. Click **OK** to open the chosen file or **Cancel** to return to the **Main** Menu.

Projects created with previous versions of the system can be read into RISKMAN, however, some of the parameters introduced in the system since the creation of the project file may not be initialized as needed.

## Save Project and Save Project As

To save a currently open project with its current name, choose the **Save Project** option from the **File** Menu. Any changes made to the data, parameters, options or preferences will be saved under the current file name, overwriting the contents of the original file with that name.



If you wish to create a new project first locate and open an existing one that most closely resembles the new scenario you wish to simulate, then save it under a new name using the **Save Project As** option. The file can be saved in the default projects directory or another user-selected directory. This option is useful when there are many populations being considered, or when the user wishes to organize imported files, exported files, or output files with the relevant projects.

Projects saved with your current version of the system may not be compatible with the previous versions of the system as new enhancements occasionally require new parameters to be saved in the project files. If an incompatible version of the project file is encountered (i.e. created with a later version of RISKMAN), the system issues a warning and does not load the file.

Click on **OK** to save the currently open file or **Cancel** to return to the **Main** Menu.

## Project Description

The **Description** option activates a screen that allows users to enter descriptive text to provide useful supplementary information about the current project file.

The screenshot shows a dialog box titled "Project Description". It contains three input fields: "Title" with the text "Test Project", "Owner" with the text "Phil McLoughlin Barrenland Grizzly Bear Vital Rates", and "Description" with the text "Best estimates from radio telemetry, extrapolations of density, and recorded human kill.". To the right of the fields are two buttons: "OK" and "Cancel".

Enter a full title for the project in the *Title* field, identify the creator of the project file in the *Owner* field and enter a brief textual description of the project file in the *Description* field.

## Exit

The *Exit* option in the **File** Menu will exit RISKMAN.

---

## Parameters Menu

The **Parameters** Menu provides users with the opportunity to enter data and modify the biological parameters that will form the basis of model runs.

The screenshot shows a menu titled "Parameters". The menu items are: "Recruitment...", "Individual Survival...", "Hunting Mortality...", "Other Mortality...", and "Initial Population...".

## Recruitment

Selecting the **Recruitment** option activates the *Recruitment* screen. The main component of this screen is the *Recruitment by Age* table and its four layers of data on the *Rates*, *Standard Error*, *Carrying Capacity*, and *Shape Factor (KS)* tabs.

Recruitment

Recruitment By Age

Rates Standard Error Carrying Capacity Shape Factor (KS)

Age	Prob. with 1	Prob. with 2	Prob. with 3	Mean Litter Size	Propn. wi
5	0.170	0.460	0.370	2.200	
6	0.170	0.460	0.370	2.200	
7	0.170	0.460	0.370	2.200	
8	0.170	0.460	0.370	2.200	
9	0.170	0.460	0.370	2.200	
10	0.170	0.460	0.370	2.200	
11	0.170	0.460	0.370	2.200	
12	0.170	0.460	0.370	2.200	
13	0.170	0.460	0.370	2.200	
14	0.170	0.460	0.370	2.200	
15	0.170	0.460	0.370	2.200	
16	0.170	0.460	0.370	2.200	
17	0.170	0.460	0.370	2.200	
18	0.170	0.460	0.370	2.200	
19	0.170	0.460	0.370	2.200	
20	0.170	0.460	0.370	2.200	
21	0.170	0.460	0.370	2.200	

Propn. Males at Birth:  Standard Error:  OK

The *Rates* tab displays the top layer of data and contains the values that define the rate of recruitment in the population.

For example, a species with a maximum age of reproduction set to 20 and minimum age of reproduction set to four will be represented by 17 rows of data in the recruitment screen. The number of columns is determined by the maximum litter size. The maximum litter size, the minimum and the maximum age of reproduction are entered in the *Species Definition* screen. For example, the maximum litter size set at 3 offspring, results in three *Probability of Litter Size* columns (abbreviated to *Prob. with X* in the table) plus two additional columns, *Mean Litter Size* and *Proportion of Females with Litters (Propn. with Litters)* on the far right of the table (use the horizontal scroll bar to access these as required).

Enter or modify values in the *Recruitment* screens according to available knowledge about the general biology of the species being modelled. Cells in the *Probability of Litter Size* columns can be modified. Note that the values entered for any given age class (i.e., row) must sum to 1.0. For example, a user may enter the following values for 6-year old female bears with litters: 0.170 (17%) have single cubs, 0.460 (46%) have twins, 0.370 (37%) have triplets. These three values add to 1.0 (100%). The *Mean Litter Size* is calculated as a weighted average of values in the *Probability of Litter Size* columns for each age class. The mean litter size values cannot be modified.

The *Proportion with Litters* column (far right) values are the user supplied fractions of the surviving available-to-mate females that produce litters. For species with annual reproduction cycles, all adult females are considered available each year. However, for species with extended maternal care (e.g., bears), females with dependent offspring do not mate and are not “available”. The values for *Proportion*

with *Litters* only apply to the reproducing females who are available to mate. For clarity, these values **are not** equivalent to mean natality rates corrected for litter size except for annual birth pulse species.

The *Recruitment* screen also offers the options to **Export**, **Import** and define **Strata** as well as to identify **Density** dependent relationships and view the Density Dependence plot (**DDPlot**).

At the bottom of the *Recruitment* screen is a field in which users can specify the *Proportion of Males at Birth*. In addition in *Stochastic* mode only, users must specify a value for the *Standard Error* associated with the proportion of males at birth. The *Standard Error* field will not display if *Deterministic* mode is selected in the *Preferences* screen (**Options** Menu).

## Individual Survival

The **Individual Survival** option in the **Parameters** Menu activates the *Individual Survival* screen.

Individual Survival Rates

Survival Rates	Standard Error	Carrying Capacity	Shape Factor (KS)		F
Age	Males	Females unenc.	Fem w/1 age0	Fem w/2 age0	
0	0.727	0.727			
1	0.683	0.683			
2	0.983	0.980			
3	0.983	0.980			
4	0.983	0.980			
5	0.983	0.980	0.980	0.980	
6	0.983	0.980	0.980	0.980	
7	0.983	0.980	0.980	0.980	
8	0.983	0.980	0.980	0.980	
9	0.983	0.980	0.980	0.980	
10	0.983	0.980	0.980	0.980	
11	0.983	0.980	0.980	0.980	
12	0.983	0.980	0.980	0.980	

Litter Survival Rate:      Std Error:

Age 0:       

Age 1:           

Buttons: Import..., Export..., Strata..., Density..., DD Plot..., OK

This screen provides users with the opportunity to enter/modify values that will define the probability of survival for all age and encumbrance categories. Like the *Recruitment* screen, the *Individual Survival* screen features four layers of data on the *Rates*, *Standard Error*, *Carrying Capacity*, and *Shape Factor (KS)* tabs. It also has five command buttons on the right hand side that allow users to **Export** and **Import** matrices, define **Strata**, identify **Density** dependence relationships, and view the density dependence plot (**DDPlot**).

At the bottom of the *Individual Survival* screen is a field in which users can specify *Litter Survival Rate*. The litter survival rate entered here is applied to whole litters and this is done before the system applies individual survival rates. The number of values requested depends on the maximum age of offspring unable to survive on their own. This feature would only be used when there is evidence that mortality occurs to the whole litter, as in the case of total milk failure, or environmental conditions too extreme for young. When the model is being run in *Stochastic* mode, users must also specify a value for the *Standard Error* associated with litter survival rate. The *Standard Error* field will not display if *Deterministic* mode is selected in the *Preferences* screen (**Options** Menu).

## Hunting Mortality

Selecting the **Hunting Mortality** option activates the *Hunting Mortality* screen. The *Hunting Mortality* screen is available only if the user has selected *Annual* or *Spring and Fall* for *Hunting Seasons* on the **Species Definition** screen.

**Hunting Mortality**

Spring **Fall**

Mortality Level

Phased in/out Quota      Duration: 0       Automatic     Manual    Set

Number of Animals:      Init Mean: 45      Final Mean: 0      Parm. SE: 49

Proportion of Initial Population:      0      0      0

Proportion of Censused Population:      0.23      0      0

Relative Selectivity/Vulnerability

Age	Males	Females unenc.	Fem w/1 age0	Fem w/2 age0	Fem w/3 age0
0	0.000	0.000			
1	0.000	0.000			
2	0.000	0.000			
3	0.000	0.000	0.000	0.000	0
4	0.000	0.000	0.000	0.000	0
5	0.000	0.000	0.000	0.000	0
6	0.000	0.000	0.000	0.000	0
7	0.000	0.000	0.000	0.000	0

Sample Size: 100     Unselective Harvest     Sex Selective Harvest    Prop Fem: 0.3

End runs with unfilled harv

Import...  
Export...  
Strata...  
Normalize  
Hunt Data..  
Batch...

OK

If hunting has been defined to contain two seasons there is a pair of tabs labelled "Spring" and "Fall" at the top of the *Hunting Mortality* screen. If there is only one hunting season defined there is no tab selection present. The hunting seasons can be chosen as the hunting option in the *Species Definition* screen (see the **Options** Menu). Click on the appropriate tab to modify the hunting parameters.

The "*Spring*" and "*Fall*" hunting seasons can represent any two sources of human induced mortality with different characteristics (e.g. Resident/Non-Resident harvest, First Nations harvest, etc).

The *Mortality Level* section of the screen allows users to set the level of hunting mortality by selecting one of three options: 1) designating the number of animals to be killed each year, 2) the proportion of the initial population to be killed each year, or 3) the proportion of the current population to be killed each year. Additional fields are available for stochastic mode and the Phased In Quota.

The *Relative Selectivity/Vulnerability* section of the *Hunting Mortality* screen allows users to include a measure of the relative likelihood of mortality by hunting for all age class and encumbrance strata in their simulation. There are six command buttons associated with this section of the screen: ***Import***, ***Export***, ***Strata***, ***Normalize***, ***Hunt Data***, and ***Batch***.

There are three ways to establish the harvest selectivity/vulnerability array. The first is to simply enter the relative likelihood values. The second is to import a selectivity/vulnerability array using the ***Import*** function. The third is to create a selectivity/vulnerability array (***Create S-V*** on the ***Hunt Data*** screen) by comparing a harvest data array with the standing age distribution (as specified by the *Relative Distribution* of the ***Initial Population***). The resulting selectivity/vulnerability array is saved in the project file with the rest of the project parameters and is used in simulations.

The *Sample Size* field at the bottom of the *Relative Selectivity/Vulnerability* table shows only when the model is set to run in stochastic mode (see *Preferences* in the **Options** Menu). It provides means to specify the degree of uncertainty in the values in the selectivity/vulnerability matrix.

The numerical values in the Selectivity/Vulnerability matrix do not determine the probability of harvest directly. Rather the values are relative, with high values indicating a particular sex/age/family class is relatively more likely to be harvested than a sex/age/family class with a low value. Typically some sex/age/family class cells may be pooled as a stratum, with all of the values in a given stratum equal. If all values in the selectivity/vulnerability array are equal, the harvest is **proportional** to the relative abundance of the sex/age/family classes. If cells or strata in the selectivity/vulnerability array are not equal the harvest is **selective**. The actual distribution of the harvest is a function of both the relative abundance and the relative selectivity/vulnerability of the sex/age/family classes. Thus the distribution of the harvest varies dynamically as a selective harvest alters the population's sex/age/family class distribution.

The ***Normalize*** function allows resizing the total of the Selectivity/Vulnerability values to the user defined value (e.g. total harvest). This may make it easier to interpret the values within individual cells.

The following is a numerical example with two population strata, their selectivity/vulnerability and the resulting harvest for deterministic runs (the harvest value used is 10).

Population		S/V		Harvest	
100	100	2.0	1.0	6.7	3.3
100	150	1.0	1.0	4.0	6.0
100	150	2.0	1.0	5.7	4.3

**To enter relative likelihood of mortality values:**

1. Start by defining the strata with which you wish to work; re-display the *Relative Selectivity/Vulnerability* matrix in stratified grid format.
2. Enter relative probability of mortality by hunting values for each cell in the resulting matrix.
3. Click on the *Normalize* command button to generate the actual numbers of animals vulnerable to hunting mortality for each cell of the matrix. The sum of all normalized values in the matrix will be equivalent to value entered for *Number of Animals* in the *Mortality Level* section of the screen or another value provided.

*Note: The numeric value of the cells entered in the Relative Selectivity/Vulnerability matrix is unimportant. Hunting mortality values need only be an accurate reflection of relative selectivity/vulnerability for all sex, age, and encumbrance groupings.*

Both harvest and population can have fractional values in the deterministic mode, but are whole numbers in stochastic mode.

Using the *Unselective Harvest* option is equivalent of setting all the selectivity/vulnerability values to 1.0. The original values are preserved in the project file and can be restored by clearing the *Unselective Harvest* check box.

The **Batch** button allows you to specify a series of mortality level values, which will be applied in sequence in successive simulation runs (deterministic or stochastic).

Run	Mean	SE
1	0.000	0.000
2	1.000	0.000
3	2.000	0.000
4	3.000	0.000
5	4.000	0.000
6	5.000	0.000
7	6.000	0.000
8	7.000	0.000
9	8.000	0.000
10	9.000	0.000

Save Results for Each Run

Add Delete OK

The *Mean* and the *SE* specified for the Hunting Mortality Batch can be related to the *Number of Animals*, *Proportion of Initial Population* or *Proportion of Censused Population*.

The *Save Results for Each Run* option tells the system to save full reports for each of the runs into individual files named 'RISKREP\_x.CSV' (where 'x' is the run number).

Information for additional runs can be added or removed using the **Add** and **Delete** buttons.

A Batch option is also available through the **Initial Population** screen. Also see **Running the Model** section for additional details on the Batch option.

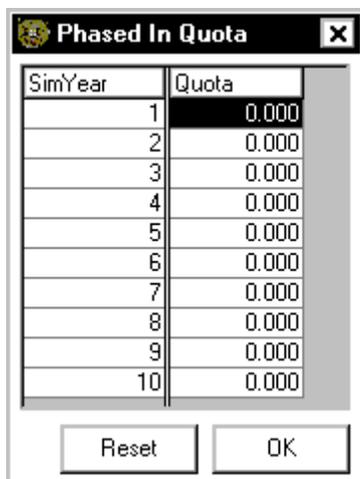
### **Phased In Quota**

The Phased in Quota option allows modifying the harvest values over the course of the simulation.

There are two ways of specifying the changing quota. When the Phased in Quota is set to *Automatic* the harvest value is changed gradually through linear interpolation between the *Initial* and the *Final* value. For the *Number of Animals* option these values are always rounded down to the nearest integer.

In the Manual mode a specific value must be entered for each year of the simulation. The schedule of these values is accessible by clicking the **Set** button. The newly entered values become means in the simulation run.

In stochastic runs the same standard error (entered on the main harvest form) is applied to all of the quota values independently.



The Phased In Quota cannot be used in conjunction with the Batch option.

### ***Application of Uncertainty***

The *Sample Size* field at the bottom of the *Relative Selectivity/Vulnerability* table shows only when the model is set to run in stochastic mode (see *Preferences* in the **Options** Menu). Use the *Sample Size* field to specify the number of times RISKMAN will sample from the *Relative Selectivity/Vulnerability* matrix in order to build each of the distributions it will use in the stochastic run. The size of this parameter determines the degree of deviation between the vulnerability/selectivity distribution entered by the user and the one used in a stochastic run. The higher the value of sample size the closer the derived matrix will be to the original. For example for the sample size of 115 at the beginning of each iteration 115 “individuals” are randomly allocated (multinomial allocation) in the selectivity/vulnerability matrix specified by the user. The resulting distribution forms a new selectivity/vulnerability matrix used for that iteration. Therefore, the higher the sample size the closer the iteration-specific matrices are to the user specified matrix. With a small sample size the matrix has a large variability.

The value of *Parm SE* is applied at the beginning of each iteration of the simulation. The value of *Parm SE* is considered to be all part of the parameter uncertainty. None of it is applied as environmental uncertainty.

The hunting mortality is calculated by first determining the number of animals to be harvested either by using the number of animals provided by the user or multiplying the specified rate by the initial or the standing population. Each animal is then allocated to a specific sex/age/family status group randomly using multinomial allocation.

If the resulting individual turns out to be a female carrying for dependent offspring, the offspring also die. The final year offspring (ie. all offspring for annual breeders; Age 1 for two year breeding cycle; and Age 2 for three year breeding cycle) are

generally able to survive on their own and are not considered to be under the care of an adult female.

In some cases a young may be harvested while under the care of an adult female, therefore, the encumbrance class of that female must be changed. To do so the model randomly selects females with offspring and removes one of her offspring. For the most senior encumbrance class some of the offspring do not have adults carrying for them. The model randomly determines if the harvested offspring is under a care of an adult female.

### ***Dealing with Over-harvest***

In a declining population scenario some segments of the population may become over-harvested and may not be able to support requested harvest. For example, let's consider two population segments:

Population in the segment	30	4
Selectivity/Vulnerability	4	30
Harvest Weight	120	120

Since the harvest weights are equal for both population segments ideally we would like the harvest to be equal for both segments, however, if the total harvest is too high (say 10 individuals) this cannot be accomplished and the actual harvest would be:

Actual Harvest	6	4
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In a population with two population segments calculating the proper shift of harvest is easy. However, the situation becomes more complicated when more segments are present (e.g. age and encumbrance classes).

Let's consider three classes with total harvest of 15 individuals:

Population in the segment	5	30	4
Selectivity/Vulnerability	24	4	30
Harvest Weight	120	120	120
Initial Harvest Allocation	5	5	5

In the initial allocation the harvest is equal for all segments. During the first pass the system notes that there is need to reallocate harvest from the first segment. The harvest allocation for the second pass becomes:

Harvest Allocation	5.5	5.5	4
--------------------	-----	-----	---

Please note that the over-harvest from the last category has been distributed equally to the remaining population segments since the harvest weights are equal between them.

Shifting the harvest during the first pass has pushed the first segment into over-harvest. Here again we have to shift the over-harvest. There is only one population

segment without the maximum allocation (the middle one); therefore, the over-harvest is pushed to that population segment:

Final Harvest Allocation	5	6	4
--------------------------	---	---	---

Even though the initially we have tried to allocate the harvest equally between the population segments we were unable to do so due to low levels of the population within some of the population segments.

The system has two methods for handling the situation when the overall harvest cannot be supported by the population. By default, the overall harvest is reduced to the total vulnerable population (where Selectivity/Vulnerability is greater than 0). Alternately, the user can select the *End Run with unfilled harv* option, on the Hunting Mortality screen. This truncates the execution of these runs.

The approach described above is used for deterministic calculations. In the stochastic case the individual animals are allocated one at a time, which requires an integer value for the number of animals to be harvested. If the user specified harvest calls for “partial” animals (e.g. as a result of the harvesting a proportion of the total number of animals) the harvest number is randomly rounded up or down. For example, if the harvest being called for is 14.3 animals, the actual harvest has 30% chance of being 15 and 70% chance of being 14).

Once the total number of harvested animals has been selected the Selectivity/Vulnerability matrix is “randomized” as described in the **Application of Uncertainty** section. The relative harvest weights are calculated by multiplying the randomized S/V matrix by the current population for each population segment (age/encumbrance class).

The system then uses the multinomial (Monte Carlo) allocation procedure to allocate harvest to each population segment.

### **Sex Selective Harvest**

The system has two ways of allocating harvest between sexes. The default way is using the relative Selectivity/Vulnerability values (sums for all males and females) as described above. The second is to use the sex selective harvest. In the latter mode the system allocates a fixed proportion of the harvest to each of the sexes (the user provides the proportion of the harvest which is to be allocated females, the rest are allocated to males).

In a declining population scenario allocating the full requested harvest to each category may not be possible. For example for a harvest of 10 individuals we may have the following situation:

Sex	Male	Female
Population Size	6	7
Harvest Allocation Proportion	0.70	0.30
Harvest Allocation	7	3

In the above situation the population cannot support the requested harvest; therefore, the male harvest is reduced to the maximum available. If the *End Run with unfilled harv* option is selected this also ends the run.

Harvest Allocation

6

3

The harvest within each sex is allocated to age and encumbrance classes using the relative Selectivity/Vulnerability values assigned by the user as described above.

### **Hunt Data**

The **Hunt Data** button on the *Hunting Mortality* screen activates the *Hunting Data* screen. This screen features a stratified *Harvest Distribution* matrix into which users can enter actual hunting mortality (harvest) data for the species being modelled.

RISKMAN will use these numbers to calculate the values for the *Relative Selectivity/Vulnerability* table. Clicking on the **Create S-V** command button will invoke the calculation, which will include normalizing (proportion that the hunted population is with respect to the total population in the stratum) based on the user-defined initial population distribution (see *Initial Population* screen). Upon completion of the calculations the user will be returned to the *Hunting Mortality* screen. Selectivity/vulnerability values are generated for the currently selected hunt (spring or fall). The system only holds one set of hunting data at a time, i.e., if you switch from “spring” to “fall” hunting, the hunting data will remain as entered for the spring hunt until you modify them. To save multiple sets of hunting data, use RISKMAN’s **Export** and **Import** features.

For convenience there is a *Strata* button on this screen. It allows the user to define the strata to be used in the entry of the hunting data and in defining the selectivity-vulnerability array. These strata will also be used for the S/V matrix of the currently selected harvest.

The *Import Pop* button allows to import the population distribution matrix as the hunting data array. Using the project’s population distribution matrix instead of actual harvest data to calculate the selectivity/vulnerability is equivalent to using an unselective harvest.

The option *Update Sample Size to the Sum of All Elements in the Harvest Distribution Matrix* sums all elements on the Harvest Distribution matrix and places the value as the Sample Size on the Harvest screen.

Hunting Data				
Harvest Distribution:				
Age	Males	Females unenc.	Fem w/1 age0	Fem w/2 age0
0	0.000	0.000		
1	0.000	2.000		
2	8.000	4.000		
3	9.000	2.000		
4	11.000	6.000		
5	5.000	4.000	0.000	0.000
6	3.000	3.000	0.000	0.000
7	9.000	2.000	0.000	0.000
8	3.000	2.000	0.000	0.000
9	4.000	0.000	0.000	0.000
10	1.000	1.000	0.000	0.000
11	3.000	2.000	0.000	0.000
12	2.000	0.000	0.000	0.000
13	2.000	0.000	0.000	0.000
14	2.000	0.000	0.000	0.000
15	2.000	4.000	0.000	0.000
16	3.000	0.000	0.000	0.000
17	2.000	2.000	0.000	0.000
18	2.000	0.000	0.000	0.000
19	1.000	0.000	0.000	0.000
20	0.000	0.000	0.000	0.000

Update Sample Size to the Sum of All Elements in the Harvest Distribution Matrix

OK

Note that use of the *Hunting Data* screen is optional; users should enter data in either the *Relative Selectivity/Vulnerability* table or the *Hunting Data* screen, not both.

## Other Mortality

The **Other Mortality** option in the **Parameters** Menu will activate the *Other Mortality* screen. The screen is only available when the appropriate option is enabled on the **Species Definition** screen

“Other mortality” could include non-hunting human-induced mortality, e.g. defence and/or and road kills. Depending on the species, other mortality occurs either before or after the Fall harvest (see the description for the **Species Definition** screen for more details). Using “other mortality” allows the user up to three unique selective mortality operations that are individually applied to the estimated annual kill for each type.

This screen is similar to the *Hunting Mortality* screen, offering the same opportunities to **Import** and **Export** data, to define **Strata**, to set **Mortality Level**, enter and normalize *Relative Selectivity/Vulnerability* values, and identify the **Sample Size** (for stochastic runs).

**Other Mortality**

Mortality Level

Number of Animals: Mean:  Parm. SE:   
 Proportion of Initial Population:    
 Proportion of Censused Population:

Relative Selectivity/Vulnerability

Age	Males	Females unenc.	Fem w/1 age0	Fem w/2 age0	Fem w/3 age0
0	0.000	0.000			
1	0.000	0.000			
2	0.000	0.000			
3	0.000	0.000	0.000	0.000	
4	0.000	0.000	0.000	0.000	
5	0.000	0.000	0.000	0.000	
6	0.000	0.000	0.000	0.000	
7	0.000	0.000	0.000	0.000	
8	0.000	0.000	0.000	0.000	
9	0.000	0.000	0.000	0.000	
10	0.000	0.000	0.000	0.000	

Sample Size:   Unselective Harvest  Sex Selective Harvest Prop Fem:

Options *Unselective Harvest* and *Sex Selective Harvest* work similarly to on the *Hunting Mortality* screen.

## Initial Population

The **Initial Population** option in the **Parameters** Menu will activate the *Initial Population* screen. This screen describes the initial relative abundance of living animals in all age classes and stratified encumbrance groupings that have been set by the user (i.e., the standing age distribution).

The fields at the top of this screen provide information about the total number of animals in the initial population. Use the *Total Initial Population* field to identify the initial size of the population. The standard errors associated with total population are required only for stochastic runs. All of the standard error is designated as parameter uncertainty.

The *Population Indicator* allows a choice between the mean and median of the population values generated during a stochastic run. The mean is calculated only among the runs not “exceeding criteria” so it is not unusual to observe an increase in the mean population growth rate over time. The median is calculated from among all of the runs. The value of percentile (*%ile*) is required for calculation of and display of stochastic dispersion. The percentile range is distributed evenly on both sides of the median. The percentile range is displayed on the graphs when the *Display Stochastic Error* option is enabled on the graph selection screen.

The thresholds for runs “exceeding criteria” can be specified as reaching below or above a given value.

The threshold criteria setting “below” allows an opportunity to specify the size of the population below which it is considered non-viable. There are two ways to specify the unacceptable criteria. If the value is specified as a number the population will be considered non-viable if it reaches below that value. If the value entered is relatively close to the mean starting population size (e.g. extinct at 500 with 800 starting value and 300 standard error) some of the stochastic runs may start with “unacceptable” populations.

**Initial Population**

Total Initial Population: Value:  Parm. SE:

Population Indicator:  Mean  Median %ile:

The population is considered unacceptable when it reaches

Number:   Proportion of the initial size:   Terminate unacceptable runs

Relative Distribution

Age	Males	Females unenc.	Fem w/1 age0	Fem w/2 age0	Fem
0	105.492	108.488			
1	42.040	43.234			
2	34.414	35.392			
3	30.463	31.328			
4	26.965	25.069	1.099	1.563	
5	23.977	3.659	8.110	11.527	
6	21.224	8.036	1.433	2.036	
7	18.787	2.361	3.604	5.123	
8	16.630	3.687	4.522	6.427	
9	14.720	4.840	2.079	2.955	
10	13.030	2.565	3.494	4.966	
11	11.534	3.656	3.010	4.278	

Sample Size:

Stop the simulation if population reaches upper limit:  times its initial size.

Start with the stable age distribution

OK

If the criteria threshold is entered as a proportion of the initial size, the fraction of the runs that result in unacceptable value is calculated for every iteration of the run based on the proportion specified and the iteration’s initial population size.

Optionally, the runs with non-viable populations can be terminated. All values after the year of termination are set to 0.

A run can also be considered “exceeding criteria” if it reaches above the specified number or proportion. This specification can be used to test population recovery scenarios. All options work similarly to the “below” setting.

The *Relative Distribution* section of the *Initial Population* screen features a matrix that contains unstratified age and encumbrance classes. The number of rows (age classes) depends on the maximum life expectancy of the species being modelled (from the *Species Definition* screen in the **Options** Menu). The *Sample Size* field at the bottom of this matrix shows only when the model is set to run in stochastic mode (see *Preferences* in the **Options** Menu). Use the sample size field to specify the number of times RISKMAN will sample from the *Relative Distribution* matrix in order to build each of the distributions it will use in the stochastic run. This step is similar to the use of uncertainty in the **Hunting Mortality**.

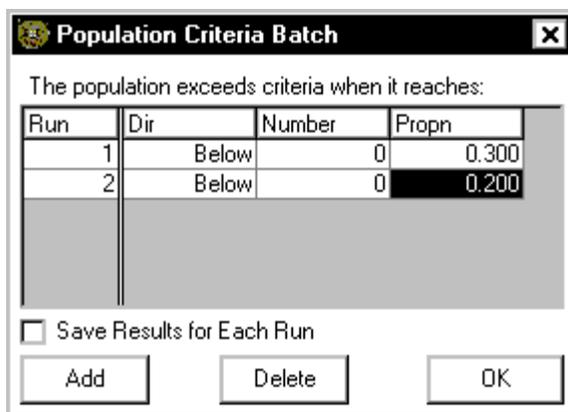
Enter relative abundance values into the matrix (as was the case with the hunting mortality data, magnitude is unimportant) and click on the *Normalize* command button if you wish to generate values based on the user-defined total initial population.

A simulation run can be terminated if the population reaches a specified multiple of the initial size. This feature prevents an apparent “stall” which occurs for large potentially exponentially growing populations. The stall is due to RISKMAN performing stochastic calculations for each individual, which may take a long time for large populations.

The *Start with the stable age distribution* option at the bottom of the *Initial Population* screen allows users to start a simulation run with a stable age population calculated by the system. The calculations incorporate all recruitment and individual survival data entered by the user, and excludes hunting and other (non-natural) mortality. The calculation will run for 100 years, resulting in the distribution to be used as the starting point for the simulation run. Following such a 100-year calculation run, the system will re-set the total initial population to match what had been entered by the user in the *Total Population* field of the *Initial Population* screen. This option can be used to run comparative runs starting with stable and the entered population distribution.

A similar effect can be accomplished by clicking the **Stable Age** button. This replaces the values entered in the *Relative Distribution* table with the stable age distribution calculated as described above. The distribution is normalized to the size of the *Total Initial Population*. However, this distribution will be saved with the project file.

The *Initial Population* screen also features **Import** and **Export** capabilities that function as described for the other screens.



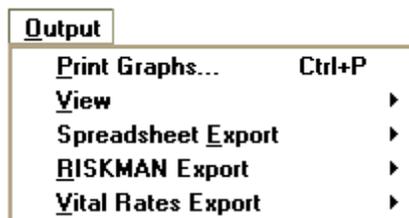
The **Batch** button allows you to specify a series of threshold setting for runs “exceeding criteria”, which will be applied in sequence during a batch run. A batch option is also available for the **Hunting Mortality**. Also, see **Running the Model** section for more details on the Batch option.

The *Save Results for Each Run* option tells the system to save full reports for each of the runs into individual files named 'RISKREP\_x.CSV' (where 'x' is the run number).

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## Output Menu

The **Output** Menu provides users with the opportunity to send graphs to the printer, view and export results.

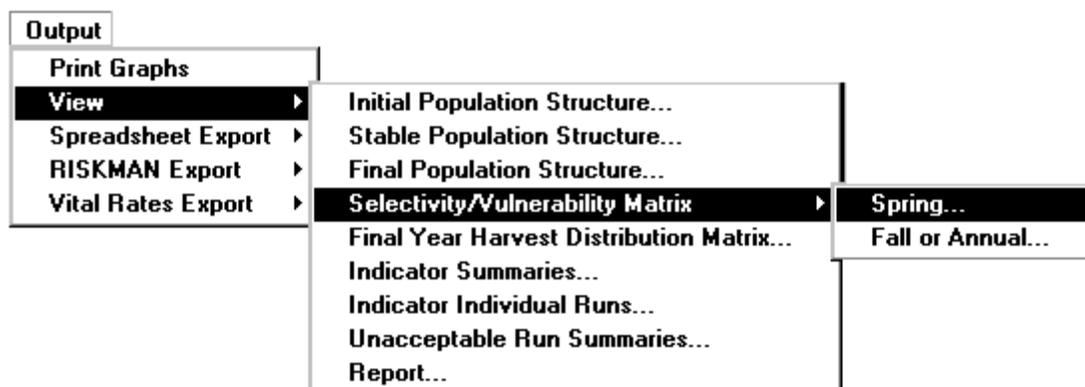


### Print Graphs

The **Print Graphs** option in the **Output** Menu sends all graphs selected for display to the Windows printer. The resulting hard copy includes the name of the project that was printed and identifies the mode in which the model was run (e.g., Deterministic, 3-year Reproductive Cycle).

### View

The **View** and the **Spreadsheet Export** menus contain the same sub-menus and give access to the same data in two different ways.



From the **View** menu the user can immediately display the data on the screen using either the Windows Notepad or a spreadsheet of choice (see the **Preference** option on the **Options** menu). The Spreadsheet Export menu allows the user to write the data to a user defined file in a CSV format (accessible from all major spreadsheet programs).

The options Initial, Stable and Final Population Structure allow review of the population. The population matrix can either be viewed in the normalized (to 1000) or non-normalized format (see the **Preference** option on the **Options** menu).

The **Selectivity/Vulnerability Matrix** option allows review of the *Spring* and *Fall or Annual* matrix.

The **Final Year Harvest Distribution Matrix** option displays the mean and the standard error of the harvest in the final year of the simulation. The mean only includes data for stochastic runs not “exceeding criteria”.

The **Indicator Summaries** menu gives access to year-by-year mean, sum of squares, standard deviation and standard error for all of the indicators defined for graphing. At the end of the indicator summary there is the year-by-year median, lower and upper percentile for the Male, Female, and Total population.

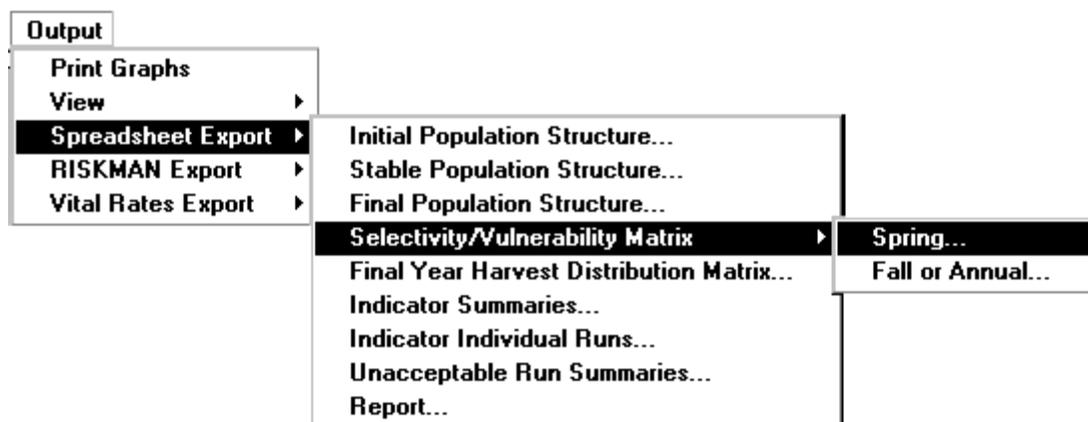
**Indicator Individual Runs** menu lists the values of indicators from up to the first 50 stochastic runs.

**Unacceptable Run Summaries** display the number and proportion of the runs “exceeding criteria” for individual years of the simulation.

The **Report** displays the initial and final population structure followed by the indicators.

## Spreadsheet Export

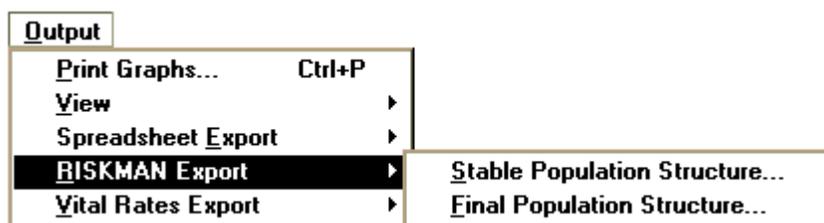
The **Spreadsheet Export** option activates a screen that allows users to select run results for one or more indicators and export them in comma and quote delimited ASCII format suitable for importing into spreadsheet or database applications.



The submenus are the same as for the **View** menu described above.

## RISKMAN Export

The **RISKMAN Export** function allows you to export population structure data resulting from simulation runs in a format suitable for importing into other RISKMAN screens.

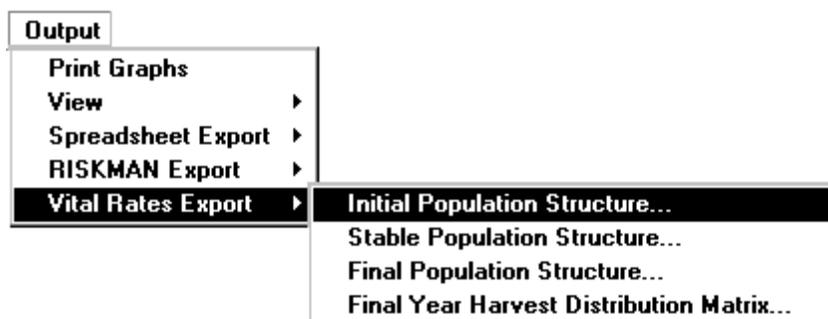


This option allows using the stable or final age distribution as the initial state for other runs. This makes it unnecessary to continue to recalculate the stable age distribution every time you run the model. This is equivalent to clicking the **Stable Age** button on **Initial Population** screen. It also allows to continue a run from the last year simulated.

For example, if you wish to use the final population structure of the species being modelled, start by running the simulation. Following the run, select **RISKMAN Export** and **Final Population Structure** from the **Options** Menu. The export screen offers the opportunity to select the file name. Return to the *Initial Population* screen, click on the **Import** command button, select the file you have just exported and click on **OK**. The values of the final population structure will be inserted into the initial population matrix, overwriting the values that were there before.

## Vital Rates Export

The **Vital Rates Export** function allows the system to export the *Initial*, *Stable* or *Final* age distribution or the *Final Year Harvest Distribution Matrix* in a format compatible to the Vital Rates system.



Vital Rates is a population analysis system for polar bears and other species with three-year reproductive cycles. The Vital Rates system consists of two components: Anursus and its companion program Interval. These two programs allow calculation of the mean and standard error of population parameters for species with three years of parental care (e.g., polar bears, grizzly bears, and walrus).

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## Options Menu

The **Options** Menu provides users with the ability to identify project defaults, mode of operation (i.e., the level of complexity required) and the species to be modelled.



### Preferences

Selecting the **Preferences** option from the **Options** Menu will activate the *Preferences* screen. Here, users will identify project settings.

Currently, there are two run modes available in RISKMAN: *Research-Deterministic* and *Research-Stochastic*. The *Research-Stochastic* mode is the most complex mode and the most capable of mimicking the natural dynamics of populations. When running the model in this mode, users will need to enter the number of Monte Carlo trials they wish the model to execute during a run by entering a value in the *Trials* field. The *Research-Deterministic* mode incorporates all of the aspects of the model simulated in the stochastic mode except the dynamics associated with random variation.

Some project files may be “locked” with a limited access to its parameters. These projects are in a “Management Mode” and are mainly designed for ongoing use in managing populations with few, if any, changes to the parameters.

The stochastic uncertainty is split into two types: the Parameter Uncertainty and the Environmental Uncertainty. The parameter uncertainty is applied only once at the beginning of each stochastic run. The environmental uncertainty is applied each year of the simulation. Both types of uncertainty can be turned on or off and the Standard Error can be apportioned between environmental and parameter uncertainty.

The allocation between the parameter and environmental uncertainty can be changed by entering proportions or picking a value along a slide bar. The proportions set are applied to all of the Standard Error values not allocated specifically to the parameter uncertainty.

The results of the simulations can be viewed in two types of editors: the Notepad or a user selected spreadsheet program.

Turning on the *Prompt for Description on "Save As..."* option box at the bottom of the *Preferences* screen will activate the *Project Description* screen whenever the user saves the project file under a new name.

The screenshot shows the 'Preferences' dialog box with the following settings:

- Simulation Mode:** Radio buttons for 'Research - Deterministic' (unselected) and 'Research - Stochastic' (selected). Below is a text box for 'Trials' containing the value '2500'.
- Apply Parameter/Environmental SE:** A checked checkbox.
- Proportionally Allocate the Uncertainty:** A horizontal slider bar.
- Parameter:** A text box containing '0.0'.
- Environmental:** A text box containing '1.0'.
- Note:** 'When application of Parameter and Environmental uncertainty is disabled only the Demographic Uncertainty is Applied'.
- Simulation Results View Mode:** Radio buttons for 'Text (Notepad)' (selected) and 'Spreadsheet' (unselected). A 'Browse...' button is next to the 'Spreadsheet' option.
- Spreadsheet Path:** A text box containing 'C:\Program Files\Microsoft Office\Office\EXCEL.EXE'.
- Prompt for Description on "Save As...":** A checked checkbox.
- Normalize the Male/Female Population Structures Before Viewing Output:** A checked checkbox.

Buttons for 'OK' and 'Cancel' are located on the right side of the dialog.

The option *Normalize the Male/Female Population Structures Before Viewing Output* enables or disables the normalization of matrices to the total population of 1000 before values are viewed or exported.

## Species Definition

The *Species Definition* screen provides users with the opportunity to select species-related parameters that will form the basis for the simulation.

Select the reproductive cycle appropriate for the species being modelled by turning on one of three available choices: 1) annual model (suitable for species with an annual reproductive cycle), 2) black bear (2-year cycle) or 3) polar/grizzly bear (3-year cycle).

Identify the season(s) in which the modelled species will be exposed to hunting. The *Hunting Seasons* section of the screen contains three options: 1) none (i.e., no hunting), 2) annual, and 3) spring and fall.

The order of calculations varies depending on the species selected. For the annual and the 2-year model it is as follows:

- \* Natural Mortality
- \* Aging
- \* Recruitment
- \* Spring Harvest
- \* Other Mortality (if enabled)
- \* Fall Harvest

For 3-year model the order is:

- \* Natural Mortality
- \* Aging
- \* Recruitment
- \* Spring Harvest
- \* Fall Harvest
- \* Other Mortality (if enabled)

The program can simulate other non-hunting mortality. This type of mortality can optionally be turned on or off by clicking the *Apply “Other” Mortality* switch.

Enter the maximum age of individuals in the population to be modelled in the *Maximum Age* field. The *Calc. Reproductive Value for Age* field allows users to enter the age of a female for which they wish reproductive value to be calculated and graphed. Reproductive value can be used to quantify the relative impact on population growth rate of harvesting one particular age (or age strata) versus another by calculating the “present value of future offspring” for that age class (Pianka 1978). That value is generally highest for animals at the age of first reproduction.

The entered value for the age is also used for calculating data for the graph *% Females in Harvest* and the graph *Adult Male/Female Ratio*.

To include density effects in the simulation run, turn on the *Density Dependence* option in this screen. This switch will influence all screens on which density relationships can be defined, i.e., when turned off, the *Density* and *DDPlot* command buttons will disappear and the *Carrying Capacity* and *Shape Factor* data matrices will be disabled.

Typically, density effects are modelled as the effect of total numbers on population growth rate. However, the rationale for an age structured model is that not all individuals (and most particularly not all females) contribute equally to population growth. The mechanism of density effects can be social or nutritional reductions in

recruitment or survival rates of the various sex, age, and family status strata in a given population. Similarly, it may be the density of only one stratum, or some subset of the total population strata, that produce a density effect on the survival and recruitment parameters of one stratum. The manner in which density affects survival and recruitment may be unique for each stratum. RISKMAN allows the user to specify which parameters of which strata are affected, and to identify which strata or stratum caused each specific effect.

A population may be regulated by reductions to recruitment, survival or both. For most harvested populations, the number of density effects options that could regulate a population at a given level is unmanageably large. Eliminating silly options that are inconsistent with the population's biology still leaves a very large number of possibilities. Given the difficulty of accurately measuring a population's survival and recruitment at a constant density, the difficulties of quantifying density effects over a range of densities is prohibitive for most harvested populations. However, an approach is suggested by the equation used to model density effects. If the affected parameter (in the affected strata) is monitored over a range of densities, the "carrying capacity" (CC), and "non-linearity" (KS) values can be estimated by non-linear regression.

For most populations, the data required to identify and quantify the mechanism of density effects will not be available. This is not a deficiency in the simulation model, but rather it is a deficiency in understanding how populations are regulated. This density effects option was developed both to incorporate information on density effects, and to allow the user to game with the model and explore density effects scenarios. When density effects are not included, the user should be aware that the results are valid only for the range of densities that do not trigger density dependent reductions in survival or recruitment (i.e., low to intermediate densities, depending on the biology of the population), and for the density at which the parameter estimates were made.

There is also an option on the *Species Definition* screen to turn on a *Co-variance of recruitment and survival rates* option, because it is likely that variance in recruitment and survival rates is correlated (e.g., a "bad" year would reduce both recruitment and survival). When turned on, this option causes the system to synchronize the environmental component of variance for recruitment and individual survival rates. Synchronization of environmental variability is accomplished by using the same random deviate for all parameters in a given year. The parameter uncertainty is considered to be entirely due to sampling error and thus is independent. The alternative (i.e., independent parameters) is modelled by drawing a different random deviate for each parameter each year. RISKMAN is an individual based model in stochastic mode. Demographic uncertainty is modelled using Bernoulli trials.

In the *Recruitment* section of the *Species Definition* screen, users define *Maximum Litter Size*, *Minimum Age of Reproduction* and *Maximum Age of Reproduction*. These values set the boundaries for the *Recruitment by Age* matrix of the *Recruitment* screen (**Parameters** Menu) and directly influence strata defined by the user.

*Note: When changes are made to any of the recruitment parameters in the Species Definition screen, or to Maximum Age, existing strata become invalid and will automatically be deleted (i.e., recruitment, individual survival, hunting mortality, natural mortality).*

## Setup Graphs

The **Setup Graphs** option in the **Output** Menu activates the *Setup Graphs* screen.

With this screen, users can select indicators to be graphed, a subset of lines for those indicators, set numerical boundaries for the Y axis and identify formatting preferences.

The *Indicator* column of the *Setup Graphs* screen lists all the indicators available for graphing. Each of the eight rows in this column contain a full list of indicators, available in a drop-down list.

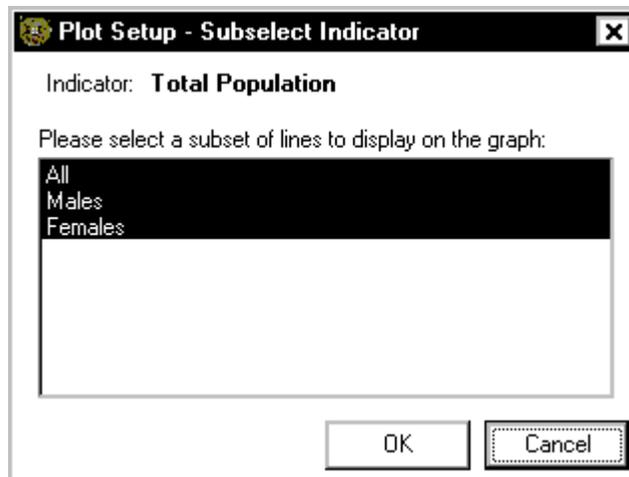
Graph Pane	Indicator	Y Minimum	Y Maximum	Y Ticks	Dynamic Y Axis	X Axis Labels	Visible
1	Total Population	2	3	2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
2	Total Harvest	4	6	3	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
3	Mean Age of Pop.	6	9	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
4	Mean Age of Harvest	8	12	5	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
5	Pop. Growth Rate	10	15	6	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
6	% Exceeding Criteria	12	18	7	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
7	% Females in Harvest	14	21	8	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
8	% Adult (>=12yr) Fem.	16	24	9	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

Display Stochastic Error   
 Display Stochastic Error As:    
 Std Dev   
 Std Error

Display Stochastic Run Preview (after 10% of the iterations)

Select the indicator to be graphed by simply highlighting the choice with a click of the mouse. Each of the indicators has up to four lines that describe it. You can select a subset of those lines by clicking on the **Sub** button. The indicator chosen will dictate the setup of the Y axis. The columns labelled *Y Minimum*, *Y Maximum* and *Y Ticks* allow users to select range and tick interval values to be displayed on the Y axis. For example, setting *Y Minimum* = 0, *Y Maximum* = 80 and *Y Ticks* = 4 generates a graph with a Y axis displaying ticks (and values) every 20 places from 0 to 80. Alternatively, users can instruct RISKMAN to select the Y axis parameters by clicking on the *Dynamic Y Axis* option box.



The X axis for each graph shows the number of years being simulated in the current run. Choose whether or not to display values and ticks on the X axis by clicking on the *X Axis Labels* option box in the next column.

The *Visible* column on the far right of the *Setup Graphs* screen allows users to select which graphs they wish to see displayed with the **Main Menu** screen when the system is launched. The system can display from one to eight graphs at the same time.

At the bottom of the screen the user has an opportunity to choose to display stochastic error (this option is only available in the stochastic mode). The user also has a choice to display the error as a line with one or two standard deviations (*Std Dev*) or Standard Errors (*Std Error*) away from the mean. A standard error is a measure of dispersion of means of distributions of observations while the standard deviation measures observations themselves.

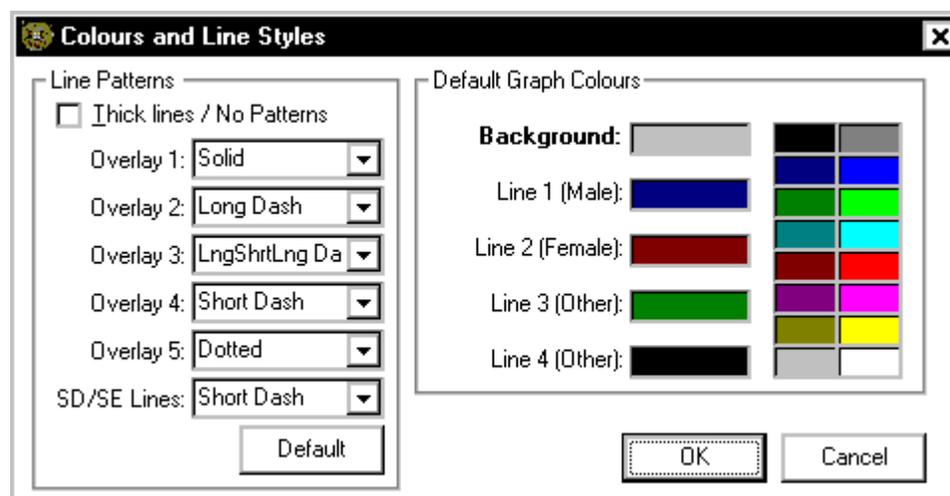
The *Overlay* option cannot be used while the stochastic variability (SD/SE) is displayed on the graphs. When the SD/SE is off you can use runs with a single or a small number of iterations to visually gauge the degree of variability in the results caused by the current set of parameters.

The central tendency and the variability characteristic for the total population can also be displayed as a median and a percentile by making the appropriate choice on the *Initial Population* screen. The settings there will overwrite the values selected here, but only for the population panel.

For long stochastic runs it may be worth displaying a “preview” of the results using the *Display Stochastic Run Preview* option. A summary of the results of the first 10% of the runs are displayed.

## Colours and Line Styles

The *Styles* command button at the bottom of the Setup Graphs screen activates the *Colours and Line Styles* screen with which users can customize the appearance of their graphs.



Here you can select different colours and line attributes for up to four graph lines per graph.

---

## Help Menu

Windows Help offers a quick way to find information, such as how to perform a particular task. Within a Help topic there may be one or more jumps or pop-up links which you can click to display additional information about the topic. The mouse pointer changes from an arrow to a pointing finger when it is over a link. Simply click on any link to activate it.



Jumps to tables or figures within the body of the text will display a secondary window in which the table or figure will appear, with the original window remaining visible. You can click on the x in the button in the upper right corner of a secondary window to put it away, so that you can continue reading the original window.

In a button bar at the top of the Help main window, there are four command buttons: *Contents*, *Search*, *Back*, *Print*, << and >>.

- *Contents* returns you to the Contents topic page;
- the *Search* command button activates a window that allows you to enter keywords to search for help on a particular topic;
- the *Back* command button displays the last topic viewed, moving back one topic at a time in the order in which they were viewed;
- use the *Print* command button to print the currently active Help topic;
- use << and >> to move backward and forward in the "browse" sequence, which is the sequence in which the author organized the text. You can use these buttons to move through the documentation to read it as a conventional paper.

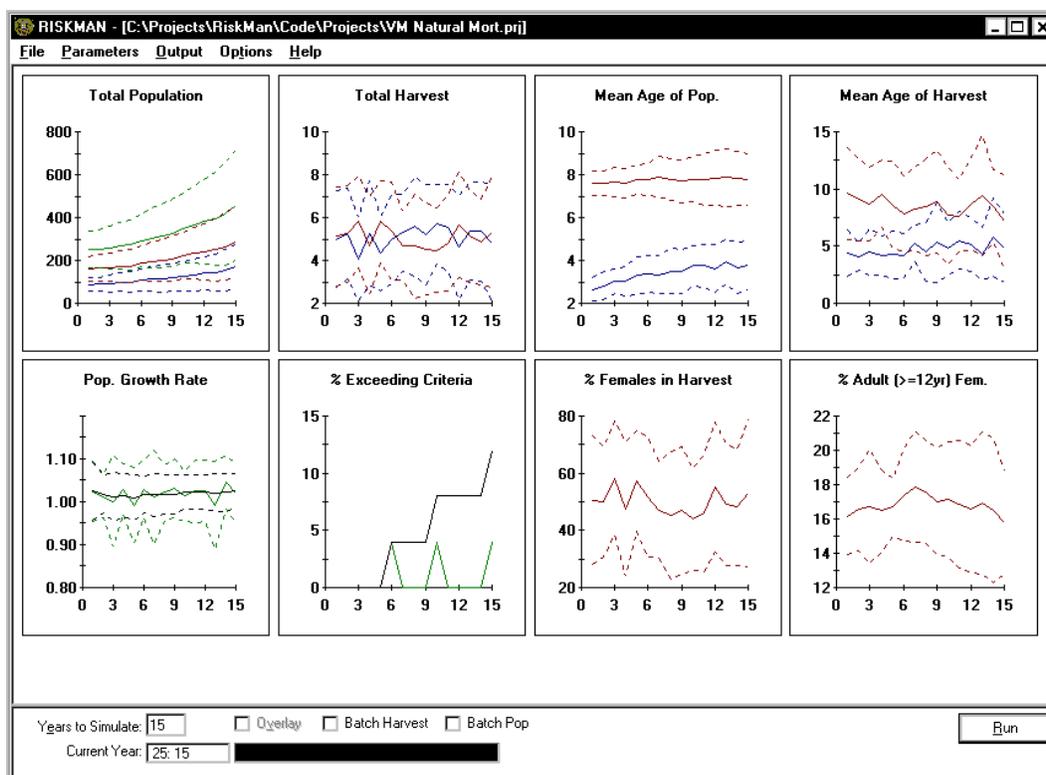
You can also move, resize, maximize, or minimize the Help window, just as you would any other window.

---

## Running the Model

In addition to displaying from one to eight graph panes at a time, the main window displays several other options. Users can designate the number of years to run a simulation by entering a value in the *Years to Simulate* field. The *Overlay* option allows users to run up to four additional simulations (each with a different set of recruitment, survival and/or mortality parameters but over the same number of years) and have the results displayed along with those of the first run.

The *Overlay* option cannot be used while the stochastic variability (SD/SE) is displayed on the graphs. When the SD/SE is off you can use runs with a single or a small number of iterations to visually gauge the degree of variability in the results caused by the current set of parameters.



The **Run** command button initiates the simulation run and generates graphs according to the user's instructions in *Setup Graphs*. The button's description changes to *Interrupt* for stochastic runs. Clicking this button instructs the system to complete the current stochastic trial then stop. The number of years simulated up to the point of interruption will appear in the *Current Year* box. Clicking on **Run** again will re-start the simulation from the beginning rather than from the point of interruption. Deterministic runs of the model cannot be interrupted.

*Note: The results of simulation runs are not saved as part of the project files. To save run results, use the options available in the **Output Menu**.*

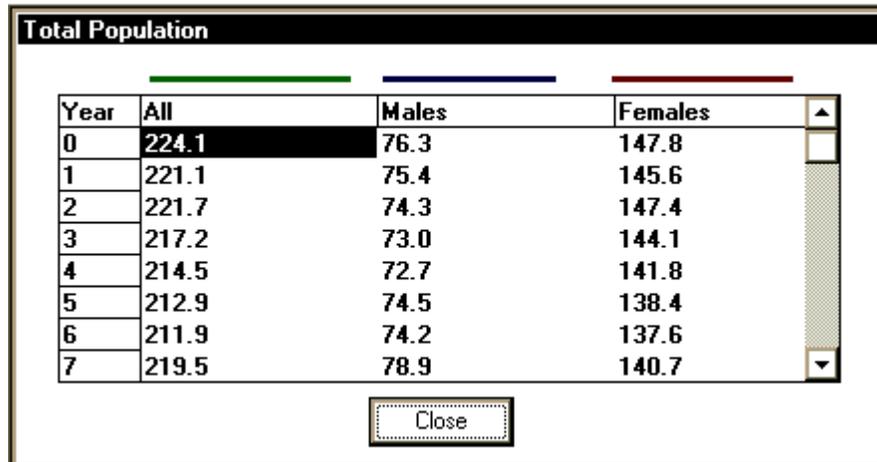
The **Batch** toggles allow the user to utilize a series of harvest levels (specified in *Hunting Mortality*), and also utilize a series of criteria for runs "exceeding criteria" (in *Initial Population*). This allows the user to explore a range of harvest values over a range of acceptable outcomes in a single run. The probabilities may be defined as a fraction of Monte Carlo simulations that exceed a given proportion of the initial number, or a fraction of runs that are less than a stated proportion of the initial number. Thus both recovery and decline scenarios can be evaluated. See description for the **Hunting Mortality** screen and the **Initial Population** screen for details on the two available batch options.

A large number of iterations is required when the distribution of outcomes are spread out over time. The **Batch** options allow more efficient scheduling by identifying a set of simulations that are processed sequentially and automatically. The simulations

can run unsupervised over-night, or in the background. The results are saved in a .CSV file to allow easy use in other programs or reports.

## Display Graphs

Graphs are displayed in the space under the **Main** Menu bar.



Year	All	Males	Females
0	224.1	76.3	147.8
1	221.1	75.4	145.6
2	221.7	74.3	147.4
3	217.2	73.0	144.1
4	214.5	72.7	141.8
5	212.9	74.5	138.4
6	211.9	74.2	137.6
7	219.5	78.9	140.7

Close

For each graph shown on this screen, a legend listing all data points, and identifying data groupings along with their associated line colours is accessible by double-clicking anywhere on the graph pane.

# Schedule A

---

## End User Licence

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# Glossary of Terms

## **Bernoulli trials**

Random events characterised by 1) their results must be a success or failure, 2) the probability of success (or failure) must be the same for all trials, 3) all trials must be independent from one another. The probability of obtaining a given number of successes in a given number of trials is represented by a binomial distribution.

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