



User's Guide for SIRENA II

A simulation model for the management of natural tropical forests

This document and the SIRENA model have been written by Denis Alder for CODEFORSA (*Comisión para Desarrollo Forestal de San Carlos*) under a consultancy supported by the UK Overseas Development Administration.

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Introduction

SIRENA 2 is a simulation model designed to assist the management of natural tropical forests. It is based on a preceding model, SIRENA 1, which was developed during 1996 for CODEFORSA under the UK/ODA Integrated Forest Management Project. The scientific concepts around which the model are based are discussed in Alder (1995).

This document is a user's guide to the model, written for the forest engineers of CODEFORSA, and for other potential users of the model.

SIRENA 2 is based on the analysis of tree growth patterns from data supplied by CODEFORSA and from plots established and maintained by Portico SA. The data is applicable in the northern zone of Costa Rica, covering drier forests principally in CODEFORSA's management area, and wetter forests under management by Portico. The wetter forests are characterised by a high frequency of *Carapa guianensis*, whilst the drier ones have *Vochysia ferruginea* as an indicator species. These two species do not co-occur with any frequency. *Pentaclethra maculoba* is very common in both types of forest.

Data from secondary forests was also supplied by COSAFORMA for use with the model, but due to limited time, this has not been analysed substantially, and the model will probably not reflect accurately regrowth from abandoned farmlands with its present parameters.

Installation

Initial installation

Initial installation is made by a Microsoft-supplied installation Wizard from a set of three disks. Separate installation kits are available for Windows 3.1 or Windows 95. In each case Disk 1 of the set is placed in the A: drive, and the A:SETUP program run from within Windows.

The SETUP program is automatic except with respect to the target directory. This defaults to C:\SIRENA2, but another directory name can be typed instead if preferred. If the installation is to a network, a directory on a shared drive or network server should be specified.

The installation program copies any required DLL or other system files to the Windows system directories, and creates the program Icon. During this process, error messages may arise. The *Ignore* option should be chosen, and the installation will proceed to completion. These error messages do not appear to affect the operation of the program.

The directory into which SIRENA 2 is installed is called in this guide the *Sirena base directory*.

Setting up the user directory

SIRENA 2 can work with a variety of possible directory arrangements. The simplest is to have all working files within the same directory as the SIRENA program itself. In this case, no command line parameter is needed, and when the login screen appears, it should be left blank, simply clicking OK or typing the {ENTER} key.

A second arrangement is to have several possible users, each with their own working files including species list with customized groupings, scenarios, and outputs. These users can each be assigned a sub-directory to the SIRENA directory. When logging in, the user types his sub-directory name in the login screen.

A third possibility is to have the user directories located on another disk or drive. The command line of SIRENA can have a parameter $D=d:\textit{path}$ added which gives the default base address. The user then only types the sub-directory at login. For example, in the network installation at CODEFORSA, the following arrangement exists:

```
SIRENA base directory .....D:\APLIC\GENER\SIRENA2
User base directory .....X:\USUARIOS
Command line .....D= X:\USUARIOS\
User directories .....X:\USUARIOS\DENIS
                       X:\USUARIOS\MAURICIO
                       X:\USUARIOS\RODOLFO\SIRENA
                       etc.
Login name .....DENIS
                       MAURICIO
                       RODOLFO\SIRENA
                       etc.
```

The command line is set by editing the properties of the program icon from the Program Manager in Windows 3.1. In Windows 95, the *shortcut* to the program is selected, and the *property* keyword clicked from the menu or right mouse button.

When creating a SIRENA user directory, the file DEFAULTS.SN2 must be copied in to the directory from the SIRENA base directory. This file contains details of the user's current preferences for the program.

Updating SIRENA 2

Updated versions can be installed by copying all the files on the update disk into the Sirena base directory. This will usually include:

```
SIRENA2.EXE
IDIOMA.SN2
IDIOMB.SN2
MODELS.SN2
```

Obtaining updates on the Internet

Updates and original installation files can be obtained by E-mailing the author at:

D-ALDER@MAIL.ZYNET.CO.UK

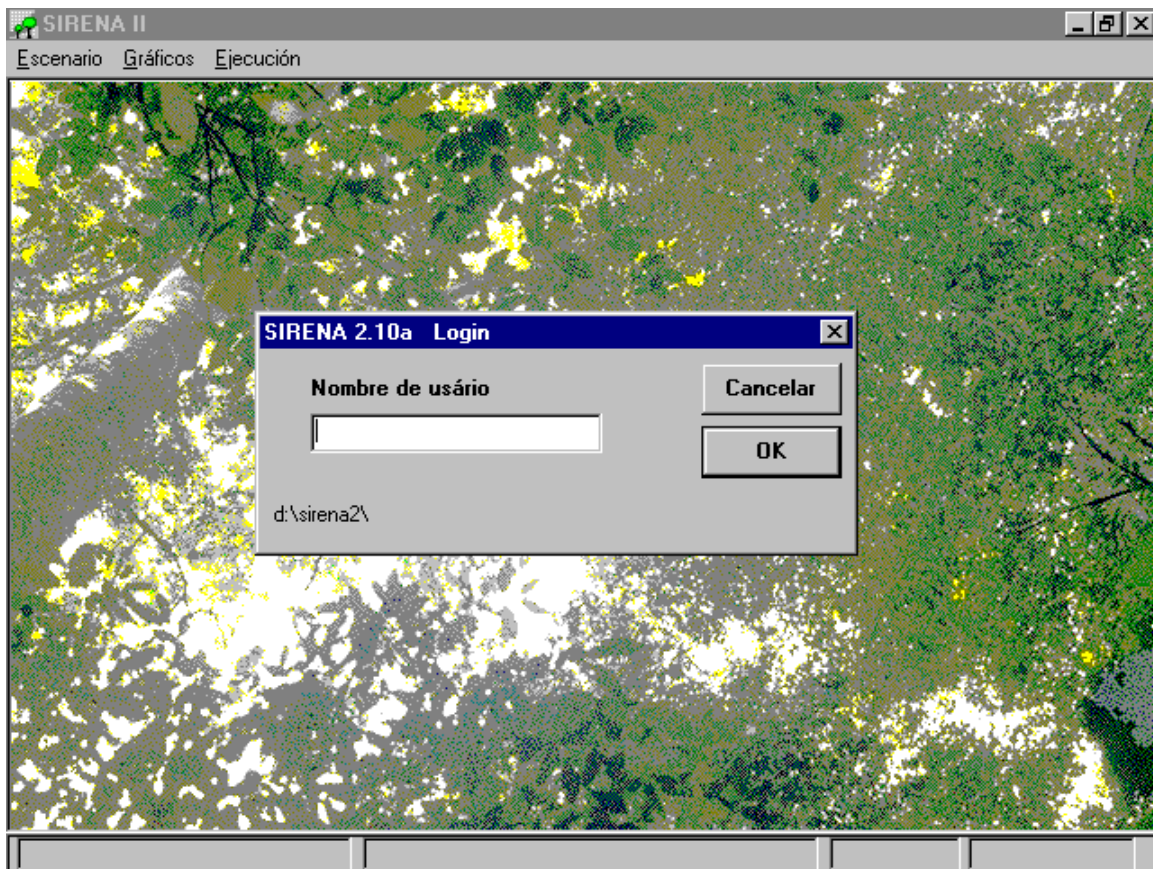
Problems encountered during installation and operation can also be advised to this address.

Starting Sirena 2

The login screen

When the program is started by clicking on its Icon, a screen should appear as shown below.

Figure 1 The login screen



The shows the characteristic background screen of Sirena 2, with a picture of forest canopy. The window controls and text fonts for the main menu differ between Windows 95 and Windows 3.1. The login box offers the following options:

Nombre de usuarioThe user should enter a name corresponding to their user directory.
The base for the user directory is shown at the bottom left of the dialog screen.

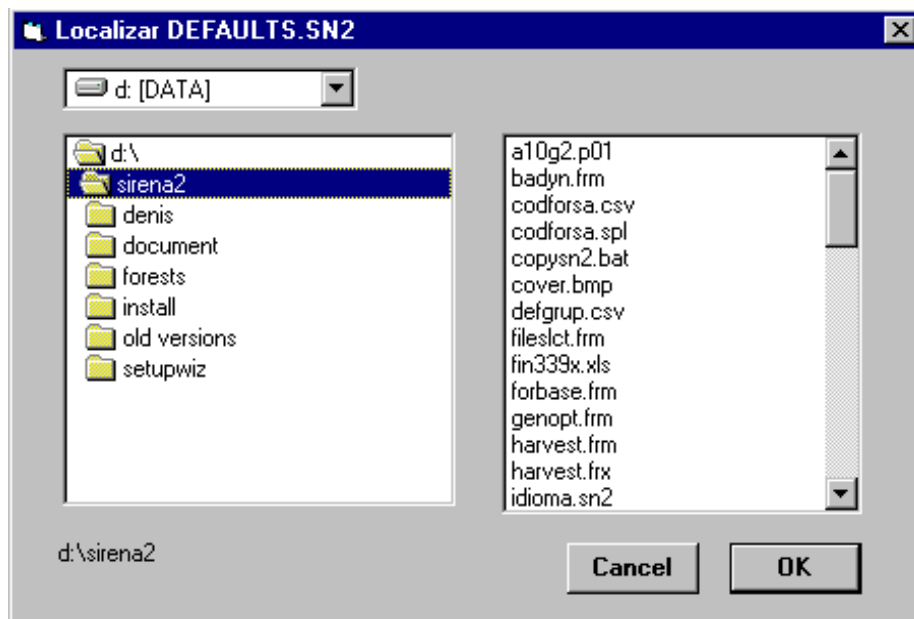
OK..... Clicking this will start the program.

CancelarThe program will close immediately.

The localization dialog

If the user's base directory has not been correctly specified with the D= parameter on the command line (see page 2), then the login screen shown in Figure 1 will not appear immediately. Instead a box will appear as shown below for selection of a directory. The user can navigate this until the correct user directory is found, and then double click on it and close the dialog. In some simple cases the program may then operate correctly. It is more likely that the login screen will appear correctly, but some other file access commands will fail at a later time with a system message such as '*Error 53 File not found*'. If installation has been done correctly, the localization dialog should not appear before the login screen.

Figure 2 The file selection dialog box used to locate a directory



The menu system

Once the login screen has been negotiated, the program's system of menus will be accessible. These appear as shown in Figure 3. The functional groups of menu choices under the main headings are as follows:

EscenariosThis group defines and reads in the forest data to be used as a basis for simulation; establishes options for harvesting and silviculture; allows the definition of species groups; and sets general options for program

control. These details can be saved as either program defaults (for the general options) or as user-defined species lists (for grouping methods), or as scenarios (for combinations of harvesting and silviculture).

Gráficos This displays one of a number of possible charts or tables showing the state of the forest, as the simulation progresses. These include graphs of species abundance, size class distributions, volumes by species groups, basal area by functional components, and a graph comparing successive simulations.

Ejecución This controls the execution of a simulation, starting, pausing, or cancelling it. It also allows the current graphic to be copied to the Windows clipboard for pasting into, for example, a Word document; and allows a graphic to be printed in high quality mode directly to a printer.

Figure 3 The SIRENA 2 menu system

Escenario	Gráficos	Ejecución
Base forestal	Abundancia de especies	Ejecutar
-	Distribución por clase de tamaño	Pausa
Grupos de especies	-	Anular
Aprovechamiento	Volumen por grupos	-
Tratamientos silviculturales	Volumen aprovechados	Copiar
-	Dinámicas de area basal	Imprimir
Manejo de escenarios	Comparaciones de escenarios	-
-	-	Salir
Parámetros de modelo	Cuadro de clases diámétricas	
	Cuadro de aprovechamiento	

Selections from the menu are made in the conventional way with Windows, by pointing and clicking with the mouse, or by using the underlined 'hot keys' from the keyboard. Not all menus are initially accessible. Generally as a minimum, a file of forest data must be read under the *Base forestal* menu before graphics can be displayed or a simulation run.

Defining the forest basis for a simulation

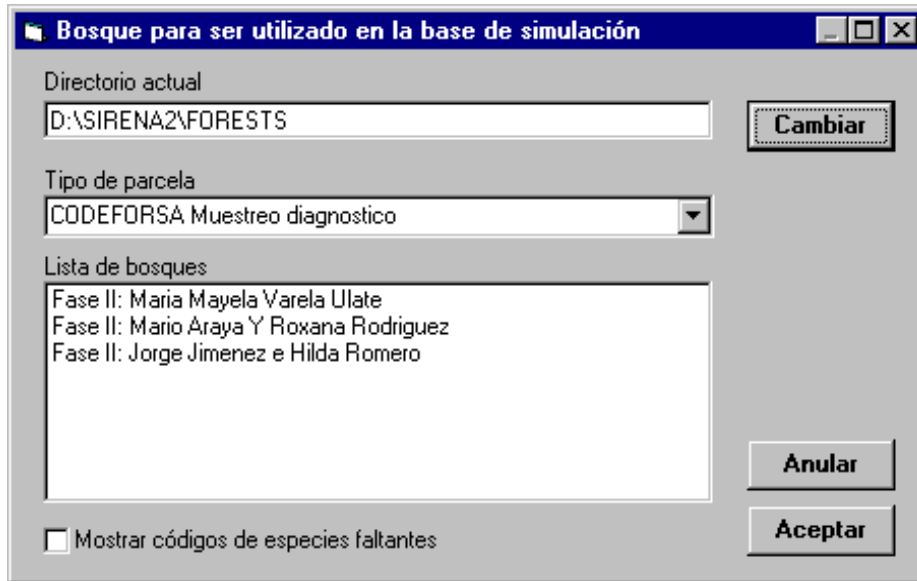
The 'Base forestal' menu

The necessary first step in running SIRENA is to read in forest data that will define a forest to be simulated. The source of this data may be any kind of forest inventory or permanent sample plot. The data is organized into text files with an extension .FBS using a format that is discussed in more detail on page 8.

Sources of data may be of several types. For example, CODEFORSA uses *Inventario preliminar* or *Muestreo diagnostico* data at present. The size, subsampling, and associated species list for each type of plot may vary, and are defined in a control file called *INVTYP.SN2*, which resides in the Sirena base directory. This is a simple text file which can also be edited to add new sample types, as discussed further below.

When the *Base forestal* menu bar is selected, a screen is displayed as shown below.

Figure 4 Dialog to select a forest basis file



The first field shows the current directory for forest files. This can be changed by clicking the *Cambiar* button. A directory selection box appears similar to that in Figure 2, but with the heading *Buscar archivos de inventario*. An alternative directory can be selected, after which the use is returned to the *Base forestal* dialog.

The second field shows the current file type. Clicking the down-arrow at the right will expose a list of available file types. Clicking on a member of this list will update the list of displayed files in the third field.

The third field displays available files of the selected sampling type. Clicking one and pressing *Aceptar* will load that file.

The loading process takes some moments. A count of plot numbers will appear in the status display at the bottom of the screen. This can be used to verify that the file is properly structured. In particular, blank lines in the data may be interpreted as 'false' plots, and will reduce the overall estimates of stocking as a result of an overestimated area figure for the sample.

After loading, the dialog screen will disappear. The name of the selected sample will appear at the bottom left of the status display. All other menu options will then be accessible.

The processing of species codes

When an inventory file is read, SIRENA first reads the species list specified by the corresponding inventory types. This gives the codes used in the inventory, and their corresponding local and latin names, the user-assigned species group, and a growth model number.

SIRENA searches for the species list in two locations. The first is the user directory. This will contain any copies of the species list that have been saved by the user with their own system of species grouping. If no list is found in the user directory, it will then read the list in the Sirena base directory.

The species codes are processed as text items, and may therefore be numeric, hierarchic, or mnemonic codes of any type. CODEFORSA uses simple numeric codes.

If a species code is found in the inventory data which does not exist in the species list, then SIRENA appends it to the internal list of the program. For example if species number 999 was found in the data, but not in the list, it would append an entry with the following details.

- A code number of 999, as found.
- A local name of 'Spp <999>'.
- A scientific name of 'Spp <999>'.
- A species group of 'X'.
- A growth model from the predefined default (from the MODELS.SN2 file).

This internal list is not automatically saved to file. It can be saved from the *Grupos de especies* dialog, as discussed on page 10.

The procedure suggested for dealing with missing species codes and updating the species list is as follows:

- Read several sets of inventory data. After each set, the species list should be saved via the *Grupos de especies* menu. This will build a list of the common missing codes.
- Edit the species list in the user directory to insert correct local and latin names. The species list can be read in to Excel and sorted by latin names to facilitate the editing of an appropriate species group code. If the missing code is in fact a duplicate for an existing code, then the growth model can be altered to that for the pre-existing entry. Otherwise the default value should be left (this will probably be #36, subject to revisions of the MODELS.SN2 file).
- If working with Excel, save the list again as a CSV file to the user directory.
- Check that Sirena reads the list correctly by opening files and viewing the stand table to see that the species are now correctly named.

- From Windows or DOS, copy the species list back from the user directory to overwrite the master list in the Sirena base directory.

Clicking the check box labelled *Mostrar códigos de especies faltantes* in Figure 4 gives a screen displaying missing codes after a file has been read, with a count of the number of occurrences of each code. Its use is not necessary for the operation of the above procedure, but it does provide a quicker check than examining the species list with a text editor.

Creating inventory basis files

The inventory files used by SIRENA are text files which are given the extension .FBS. Normally the data will be extracted from a database file. At CODEFORSA for example, the data may be held in the PLANMAN file called INV.DBF, or a file maintained by the new TREMA system.

The most direct route for creating an FBS file is to extract the data from its DBF format into a text file using FoxPro, and then edit it using a word processor to add the four lines of header information that SIRENA requires.

A limited knowledge of FoxPro is needed to achieve the first step. It is necessary to know the file containing the originating data, its full directory path on the system, and the field names for the plot number, diameter, species code, and form/defect code. Given this information, the following Foxpro commands will extract the data:

```
SET DEFAULT TO userdir
USE invpath\invfile
INDEX ON plot TO ~TEMP FOR forest=id
COPY TO outfile.FBS DELIMITED FIELDS plot, species, diam, form
```

where:

userdir The full path of the user's directory for SIRENA work.
invpath This is the full path of the inventory data file. On a network, the user must have access rights to this path.
invfile This is the name of the .DBF file containing the inventory or sample plot data.
plot This is the field name containing the sample plot number.
forest This is the field name containing the forest name or number.
id This is a number or character string denoting the forest, farm or sample to be extracted. If *forest* is a text field, it must be enclosed in quotes. If *forest* is numeric, it should not be. A FoxPro error message results if *forest* and *id* are not of compatible types.
outfile The name of the output file, with an extension .FBS added.
species The field containing the species codes.
diam The field containing tree diameters.
form The field containing form or defect codes.

This method creates a temporary file ~TEMP.IDX in the user's directory which indexes the required records from the database. This can be deleted if its presence is inconvenient.

After creation of *outfile.FBS* it can be edited with a text editor to add the following lines of information:

1. A code for the inventory type. INV and DIAG are defined for CODEFORSA *inventario preliminar* or *muestreo diagnostico*, for example. New codes and inventory types can be created as described in the following section.
2. A zero or a forest type code. This information is not used by SIRENA 2.
3. The title of the dataset. This can be any text.
4. A zero or the effective forest area. This information is not used by SIRENA 2.

The file should be checked with the text editor to ensure that there are no blank lines between plots. There should also be no spare blank lines at the end of the file. The data should be separated by commas, not semi-colons or any other delimiter. Decimal points must be marked with the dot character, not a comma. None of the data needs to be enclosed in quotation marks. Any quotation marks found should be deleted using the *search and replace* function of the editor.

The file must be saved as a *text only* file. Saving it as a standard word processor file, rich-text file, or other format will cause SIRENA to fail when reading the file.

Defining new inventory or sampling types

New inventory types are created by editing the file INVTYP.SN2 with a text editor. Each line represents one type of plot. There are six items on each line, as follows:

1. The code used for the inventory, eg. INV.
2. The name for the type sample, comprising any descriptive text, eg. *Muestreo diagnostico*.
3. The sample plot size in ha, eg. 0.3.
4. The smallest diameter, in cm, measured on the whole plot, eg. 30.
5. The size of a plot used for subsampling within the main plot to a smaller diameter limit, eg. 0.075.
6. The name of the species list file applicable to the data, excluding the .SPL extension, eg. CODFORSA.

Species groups for forest management

General considerations

Within the SIRENA 2 model, each species is represented individually* . However, natural tropical forests typically comprise 300-400 species of which 50-100 may be of commercial interest. In order to make prescriptions for harvesting and silviculture easy, and in order to present outputs and results simply, species need to be grouped. Generally, the groups should comprise species with similar commercial demand and similar management and silvicultural characteristics.

Groups appear in the legends of graphs and in other contexts where very long names are not very helpful. Generally, the names given to species groups should be short mnemonic codes of not more than 8-10 characters. The name of one group should not be a complete subset of the name of another group. For example A and A+. *SIRENA will confuse group names if one is a subset of another.* Group names are also sorted in outputs and lists in alphabetical order. This may be borne in mind when devising group names.

The graphic outputs use a built in scheme of colouring patterns for up to 6 groups. Thereafter, the system resorts to default colours supplied by the graphics system. These may not be very ideal, and may not be the same for different groups between graphs. It is therefore better if possible to limit the number of groups to not more than 6.

Both these restrictions apply to SIRENA 2.10, and will probably be relaxed on later versions.

Managing species groups in SIRENA

The menu *Grupos de especies* gives access to a dialog screen for moving species between species groups, and for creating and deleting groups. This screen is shown in Figure 5 below.

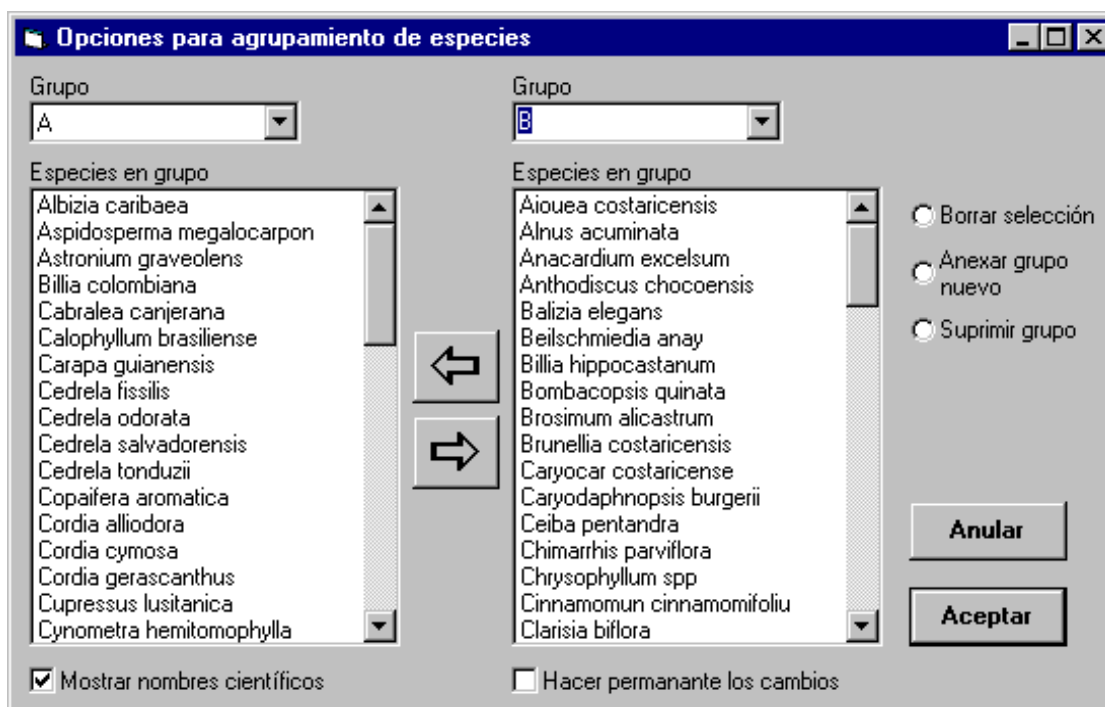
Species can be moved between groups by clicking on them with the mouse to select them, in either the left or right box, and then clicking on either of the arrows in the centre to move them to the alternate box.

The group displayed in either box is selected from the pull down lists at the top.

A new group is created by over-typing the group name *in the right-hand box*, and then clicking the button marked *Anexar grupo nuevo*. If no species have been selected in the left-hand box, an empty group will be created. If species were selected in the left-hand box, they will appear directly in the new group.

* This was not the case with SIRENA 1, which worked only with pre-defined groups, and gave no access to individual species.

Figure 5 Screen for managing species groups



A group is deleted by placing it *in the left-hand box*, removing all species from it into other groups, and then clicking the button *Suprimir grupo*.

The button *Borrar selección* releases any species marked as selected.

If the two groups in the boxes are the same, the message “*Grupos de especies deben ser diferentes*” will appear. Any action will be blocked until one of the groups is changed.

It is not possible with this screen either to duplicate or delete species from the list. They can only be moved from one group to another.

The checkbox labelled *Mostrar nombres científicos* will switch the naming between scientific or vernacular names. However, it should be noted that typically many species will not have vernacular names. For these, the generic name is shown enclosed in brackets. Generally, the scientific names are more useful in this presentation.

The checkbox *Hacer permanente los cambios* is important. It causes the species list in the user’s directory to be overwritten with the new groupings when the *Aceptar* button is pressed. A warning message precedes this to allow the user to change their mind.

With this facility, each user may therefore create a unique set of groupings. If a particular grouping system is determined as being the definitive one, then the relevant

species list file (eg. CODFORSA.SPL) can be copied back into the Sirena base directory from Windows.

There are some deficiencies in this dialog screen that will probably be remedied in later revisions of SIRENA:

- The blocking function when the two lists are for the same group is unduly oppressive. It should be relaxed to apply only to operations that move species.
- It is not possible to directly rename a group. Presently a new group must be created, the species copied to it, and the old group deleted. This is rather tedious, and it is therefore important to spend some time thinking out the nomenclature of groups prior to creating them.

Specification of harvesting operations

The 'Aprovechamiento' dialog

Selecting the menu bar *Aprovechamiento* brings up the dialog screen shown in Figure 6.

Figure 6 Screen to define harvesting options

Control de aprovechamiento

Año del primer aprovechamiento

Ciclo de corta (años)

Área basal requerido antes del aprovechamiento (m2/ha)

Límite de número de árboles a cortar (n/ha)

Límite de área basal a cortar (m2/ha)

Selección de árboles

	Grupo	Diam.Min.	Remanente	¿Cortar?
1	A	50	40	Sí
2	B	50	40	Sí
3	C	50	40	Sí
4	G	50	40	Sí
5	N			
6	P			

remanente especificado por

N %

N/ha

Ordenar la prioridad de grupos

Opciones especiales

Sin aprovechamiento

Normal

Mode de pausa

Cambiar a escenario:

Anular

Aceptar

This screen allows various options relating to harvesting to be specified. The options are divided into three functional boxes:

Control de aprovechamiento

This includes options which control the decision of whether to harvest or not, and general limits on the number of trees or the basal area to be removed.

Selección de árboles

This covers the felling limits and retention specifications by species groups, and determines the order of priority when felling species groups.

Opciones especiales

This provides a fast way of selecting a 'no harvesting' option, standard operation, an option to pause the simulation after the harvest has been performed for a more leisurely analysis of the various output screens, and an option to switch to a different management regime (scenario) after the next specified harvest.

These groups will be considered in more detail in the next sections.

Scheduling and controls on the general intensity of harvesting

In Figure 6, the box labelled *Control de aprovechamiento* includes the functions which control the timing of harvesting. Each one has a check box on the left, and a value on the right. Note that if the checkbox is not marked, that particular aspect of scheduling will be ignored, regardless of any value in the field at the right. The options control harvesting as follows:

Año del primer aprovechamiento

This specifies the first year for harvesting. Felling may be delayed after this year if the third option, for basal area control, is also active and the required basal area has not been reached.

Ciclo de corta

This specifies the felling cycle in years. Fellings will not be done over an interval less than this period. If this box is not checked, no felling is done unless the basal area control option is active.

Área basal requerido antes del aprovechamiento

This controls felling by basal area if it is checked. The stand cannot be felled unless the specified basal area has been reached. If a felling cycle has also been specified, then they will act together as constraints on felling, indicating both a minimum period between fellings, and a minimum basal area that must be reached. If no felling cycle is specified, then felling will be done whenever the stand reaches the specified basal area.

Límite de número de árboles a cortar

This places a general limit on the number of trees per hectare that may be removed during felling. It can be given as a fraction if required, representing whole trees over a wider area. For example 2.5/ha indicates 25 trees on 10 ha.

Límite de área basal a cortar

This is an alternative to limiting felling by tree numbers. It specifies the maximum basal area to be removed, in m²/ha. If both tree numbers and basal area constraints are given together, the program will apply whichever

constraint is most severe in a particular harvest. However, this is likely to be confusing to interpret, and is not recommended.

Specifications for the selection of trees

The group of options shown under *Selección de árboles* in Figure 6 determine the specifications for felling. At least one line in this table must be checked with *Sí* in the *¿Cortar?* column for any harvesting to be done.

Specifications for felling trees include the species group to be affected by a given rule, the minimum diameter for trees to be felled, and the number or percentage of trees to be retained. For each group in the table that is to be felled, the *¿Cortar?* box should be clicked with the mouse to show *sí*.

The retention can be specified either as a percentage of the standing trees above the size limit for that species group, or as the total number of trees per hectare to be left. This is done by clicking on one of the buttons to the right of the table.

The species group can be changed by clicking the mouse on the group name to make it active, and then pressing the spacebar to cycle through the list of available groups. Note that if the species grouping is changed, the specifications in this table do not automatically reflect those changes, and it will be necessary to adjust the group names and other details as required.

The order of groups in the table determines the priority of felling when a general limit has been applied. If for example there is a general limit of 2 m²/ha, then all possible trees from the first line of the table will be felled until the limiting basal area is reached. If it has not been reached by felling these, then the process continues with the second line, and so on. To achieve a proportional felling through a range of groups when there is a general limit, a high *Remnante* is needed to ensure all trees are not taken from the group.

The order of species in the table can be changed using the up and down arrow buttons at the lower left. This exchanges cells in a row from the active cell to the left with the row above or below. If the cell selected is in the *Grupo* column, the whole row is exchanged. If it is in the *Diam* column, the groups will remain as ordered, but the specifications will be exchanged.

The current line in the table can be deleted by pressing the *Ctrl+Del* key. A new line will be inserted by pressing *Ctrl+Ins*. A single cell is deleted by pressing *Del*. The deleted text is stored in a memory, and will reappear in the active cell when *Ins* is pressed. This can be used to rapidly enter the same figure in several cells. It is entered in the first cell, and *Del* pressed to place it in the memory. Pressing *Ins* on each of the required cells will then insert the figure.

The last column, header *¿Cortar?*, can be checked or cleared by clicking with the mouse, or by pressing the spacebar.

Special options

There are four special options available as alternatives:

Sin aprovechamiento

When this is checked, no harvesting is done. This is a quick way of establishing a baseline for management without having to reset all the individual options.

Normal

The controls and specifications are applied throughout the simulation.

Mode de pausa

The simulation stops after each harvesting has been done. It can be restarted when required by pressing Ejecutar under the Ejecución menu. This option provides a means of examining the graphs and tables which do not have a time base before they change as the simulation proceeds. While the program is stopped, the details of harvesting, silviculture, etc. may be modified to take effect as the program is re-started.

Cambiar a escenario ...

This mode requires that the scenario manager has been used beforehand (see page 18). If this is the case, then the pull down list will contain a series of codes, which are the file names for scenarios. Selecting a code will cause the program to switch to that felling regime after the *first harvest* in the current specification. This process allows several quite different harvesting schedules to be linked. Note that when a chained scenario is loaded, only the harvesting specifications are updated; any silvicultural treatment will remain the same. Silvicultural details can be chained separately, and operate in a similar fashion, in that they only alter treatment rules and do not affect the harvesting rules.

Specification of silvicultural treatments

The dialog screen

The dialog screen for specifying silvicultural treatments is invoked by clicking the menu bar *Tratamientos silviculturales*. It has the same general layout and functions as the harvesting dialog, with analogous options to control the timing of treatment and the affected species groups.

Figure 7 Dialog for silvicultural treatment options

	Grupo	Dmin	Dmax	% raleo	S/D
1	Comercial	40			Sí
2	Potencial	40			Sí
3	Gavilan	40			Sí
4	Nocomercial	30		40	

Timing of treatments

Figure 7 shows the layout of the screen. There are three checkboxes and associated value fields related to the timing of treatment. Checking the *Tratamiento inicial* box causes an initial treatment to be done in the specified year, irrespective of whether the stand has been harvested or not. If this box is left clear, as in the example, then treatment is done only after harvesting.

Treatment after each harvesting is specified by the second checkbox. The period in years to elapse after each harvest is given in the field to the right of the label *Tratamiento después aprovechamiento*. If this is zero, treatment is done in the same year as harvesting.

Treatments may also be repeated within a felling cycle by checking the third box, labelled *Repetir tratamiento después ...*. A value here of 5, for example, would repeat treatment to the same specifications every 5 years.

Special options

The general options controlling treatment indicated in the group of buttons at the top right of the screen (Figure 7) are the same as for the harvesting screen. The first button provides a quick method of switching off treatment without having to edit the screen in detail. The second button is for normal operation. The third causes the program to pause after each treatment. It can be restarted from the *Ejecutar* menu bar. The fourth button causes a new set of treatment options to be loaded as soon as the first treatment specified has been performed. A more detailed account of these choices is given on page 15.

Specifications for trees to be treated

The table shown within the box labelled *Diámetros y especies* on the *Tratamiento* screen (see Figure 7) allows the selected trees to be specified. Trees are selected by species group (*Grupo* field), and must fall within a range specified by minimum and maximum diameter (*Dmin*, *Dmax* fields). Of the eligible trees, only a certain percentage will normally be treated (*%raleo* field).

For commercial species, it is unlikely that thinning treatment would be applied except to trees of bad form or seriously damaged trees from past logging. This case can be selected by clicking the mouse on the *S/D* field. It is not possible to combine on the same line a phytosanitary specification with a percentage thinning, but it is possible to enter the same group on two different lines. In this case, for example, one could specify the thinning of all defective trees, and then a percentage of the remainder on a second line.

If the *Dmax* field is left blank, then all trees above the specified *Dmin* will be eligible for thinning. If both *Dmin* and *Dmax* are blank, then all trees will be eligible for thinning irrespective of size.

As with the *Aprovechamiento* screen, data can be stored in a memory by pressing *Del*, and then re-inserted to the same and other fields by pressing *Ins* (see page 14). Lines in the table can be deleted by pressing *Ctrl+Del*, and blank lines inserted with *Ctrl+Ins*. Moving the cursor to a cell under the *Grupo* field and pressing the spacebar or clicking the mouse will scroll through the currently defined species groups.

The *S/D* option cannot be toggled on or off (*Sí* or blank) if there is a figure in the adjacent *%raleo* field. Likewise, data cannot be entered in the *%raleo* field if the *S/D* field contains *Sí*.

Because there is no prioritization between groups for treatment, there is no control in this table to change the order of groups, unlike the similar table on the *Aprovechamiento* screen.

The scenario manager

Concepts and definitions

A scenario, in the terminology of SIRENA 2, is a combination of harvesting and silvicultural treatments. The scenario manager allows scenarios to be saved to file, recalled, or deleted from disk.

Each scenario has a title and a code, which is also used as the file name. The file name consists of the code plus an extension of .sc2.

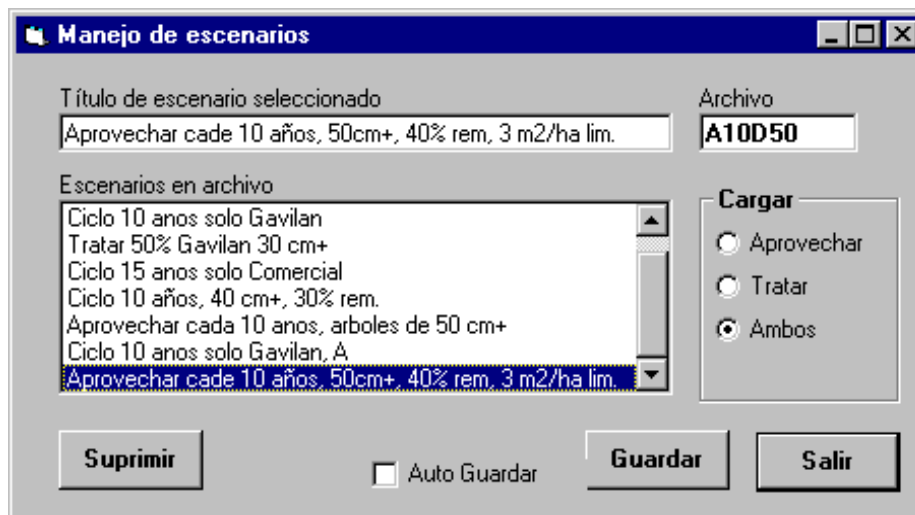
The scenario manager allows a standard list of harvesting and treatment regimes to be kept on disk without needing to re-enter the details each run. As has been noted, both harvesting and treatment specifications can include the linking of one scenario with another, to allow variable specifications which each felling cycle, and to allow variable silvicultural treatments within a cycle. This gives the program almost complete flexibility in the way treatments are specified.

The scenario manager can also be called up at any time while a simulation is running, to introduce an immediate change in the management regime. This can be useful for testing variable treatments and schedules in an *ad hoc* fashion.

Using the scenario manager

The scenario manager is called from the menu bar *manejo de escenarios*. The dialog screen shown in Figure 8 appears.

Figure 8 The scenario manager dialog



A scenario is created by defining harvesting and treatment specifications using the *aprovechamiento* and *tratamiento* screens discussed on pages 12 and 16. Once this has been done, the scenario manager is invoked from the menu. The title box will appear initially blank. A descriptive title of the regime should be typed in, bearing in mind that

this title will appear as a heading on output graphs and tables from the model. The scenario should also be given a code, in a format suitable to serve as a file name. This is typed in the *Archivo* window, which only allows letters and numbers up to a limit of 8 characters to be typed.

The scenario is then saved by pressing the *Guardar* button. If there is an existing scenario with the same file name it will be overwritten without warning; if not, then a new file is created. Checking the box marked *Auto guardar* does not save the scenario immediately, but will cause it to be re-saved automatically in exit from the *Aprovechamiento* or *Tratamiento* screens. This is done without warning regarding the overwriting of the existing values.

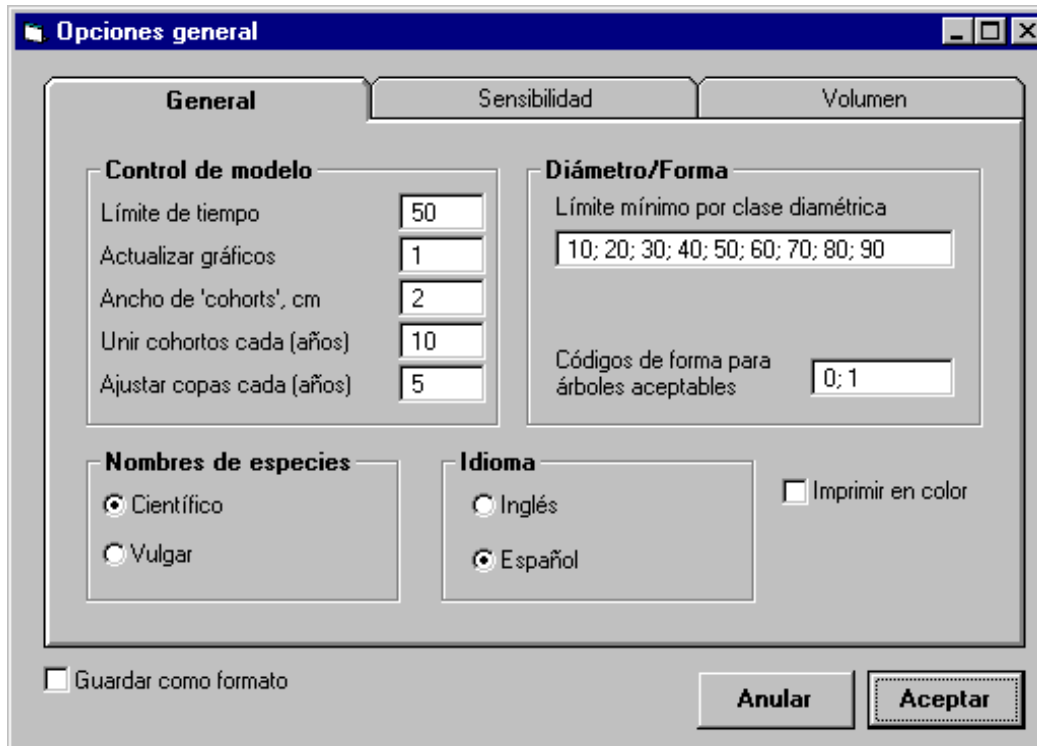
Existing scenarios can be loaded by clicking on them from the list. This immediately loads them in to memory. If the harvesting and treatment regimes have been edited without saving them as a scenario, a warning message appears "*Escenario actual no guardado. ¿Sobre-escribir?*" At this point, the load can be cancelled and the current scenario saved first, if required.

It is possible to load only the treatment, or only the harvesting component of a scenario by checking one of the option buttons at the right of the screen. The default for manually loaded scenarios is to load both components. If only a partial loading is requested, then the part not loaded remains at its current value. For example, if under the *Cargar* options, *Tratar* is selected, and a scenario is loaded by clicking on it, then the current harvesting specifications will remain unchanged, but the treatment specifications will be overwritten with those from the selected scenario.

A scenario is deleted by selecting it and clicking the *Suprimir* button.

Once a scenario has been selected, the dialog can be closed with *Salir* or by using the conventional Windows close control.

Figure 9 The dialog screen for setting general options



Setting general program options

The general options dialog

Clicking the mouse on the menu bar *Parametros de modelo* produces a screen similar to that shown in Figure 9. This is a tabbed dialog with three levels, the first of which is shown when the screen first appears. This tab gives access to the following options:

Language Checking either of the appropriate option buttons switches all texts and menus between the Spanish and English versions. Note that titles created by the user for scenarios or data files are not translated.

Species names These may be either the scientific names of species, or their local names where given in the species list (the name of the genus is substituted in brackets where no local name is present).

Time controls These cover several aspects of model operation. The *Limite de tiempo* is the total simulated time the model will run for. *Actualizar graficos* determines the frequency with which graphs are updated. *Unir cohortos* merges cohorts internally at the intervals indicated. A value of about 10 years will probably give optimal program speed. *Ajustar copas* determines the frequency with which the crown classes of cohorts are recalculated. This should not be more than 5 years, and on faster computers can be

reduced to give smoother lines on the graphs. The *Ancho de cohortas* is not strictly a time control, but effects program speed and resolution. A value of 2 cm is recommended on slower machines, and 1 cm on faster ones with the 32-bit version of the program.

Diameter classes The diameter classes used in output tables and graphs can be set by typing in lower bounds in the box labelled *Límite mínimo por clase diámetrica*. These values *must be separated by semi-colons*, not commas. There is no special limit on the number or size of classes, and these values can be changed while the program is running. However, outputs will become congested if too many classes are chosen; the program may fail if there are less than 2 classes; and the lowest class should not be less than 10 cm, as lower classes are not created by the model with its current growth model calibration.

Form codes The form codes that occur in the inventory data representing trees that are acceptable for harvesting should be shown in the box labelled *Códigos de forma ...*. Several values may be entered, but they must be numeric (not text codes), and they must be separated in the list by semi-colons. Any form codes other than those listed will be deemed to mark a tree as defective, either due to damage or bad form.

Figure 10 Settings for sensitivity analysis

Factor multiplicador a modelo base	
Crecimiento diámetrico	1
Razón de mortalidad	1
Ingresos	1
Daño de aprovechamiento	1
Competencia	1

Colour output Graphs will be printed in colour, as they appear on the screen, if the box labelled *Imprimir en color* is checked. This generally works better than black and white printing with laser and *HP Deskjet*-compatible printers. In the present version, the patterns selected by default for black and white printing are little confusing. When graphs are copied to the clipboard, this is always done in colour as a metafile image. This can be edited with various picture editors, including that in *Microsoft Word*.

Saving options Checking the box labelled *Guardar como formato* will save the options into the file DEFAULTS.SN2 in the user directory when the *Aceptar* button is pressed. The existing file of this name will be renamed as DEFAULTS.01!, 02!, etc., each time the file is saved. These backup copies can be deleted from time to time. They are intended as a safeguard, as inappropriate values for some of these general options can make the program unrunnable.

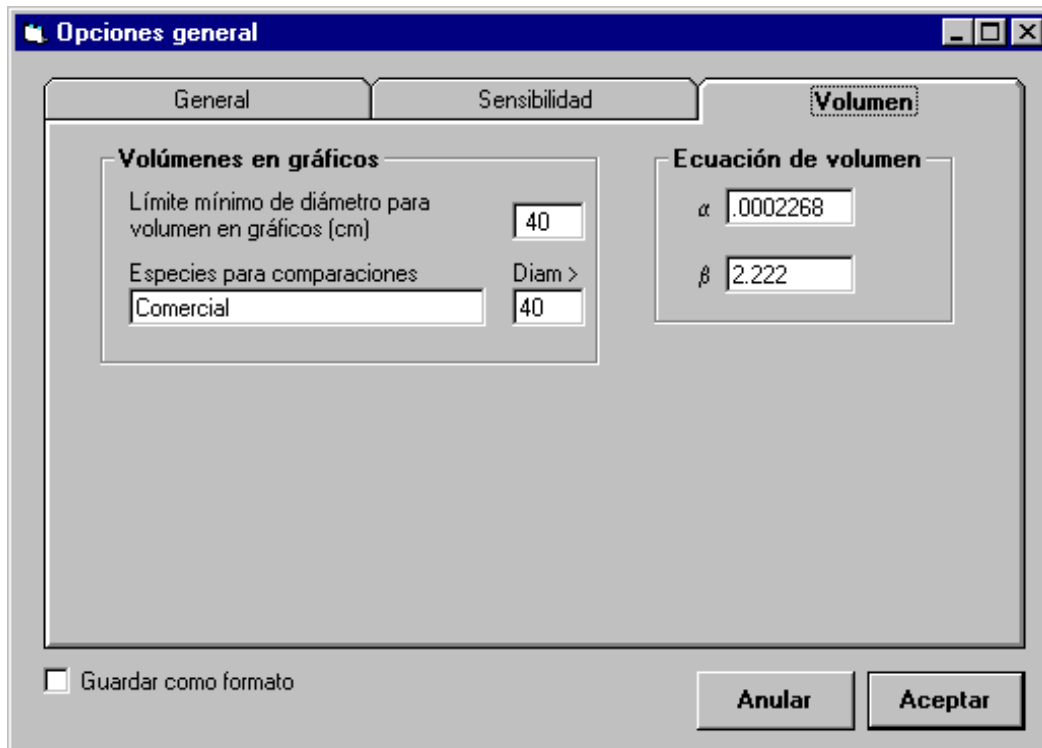
Sensitivity analysis

The second tab of the *Opciones general* screen, labelled *Sensibilidad*, reveals several parameters which can be varied to test the sensitivity of the model, or to adjust its calibration to different sites or situations (see Figure 10). Each value is a multiplier for the basic model referred to. For example, replacing the value of 1 in the *Crecimiento diametrico* with a value of 1.1 will increase all diameter increments by 10%, subject to other constraints in the model.

These factors should not be set to values other than 1 for normal use. The only field that may be applicable for general forest management is that for logging damage (*Daño de aprovechamiento*), which may be adjusted to test the implications of more or less damaging regimes. However, it should be appreciated that coefficients outside the range 0.7 to 1.3, implying a 30% reduction or increase in typical damage, are unlikely to be realistic in any context.

Large values for these sensitivity factors may make the program unrunnable.

Figure 11 Options for volume definitions



Volume options

Selecting the third tab from the *Opciones general* screen, labelled *Volumen*, give access to settings for calculating and displaying volumes. The general volume equation coefficients are for a logarithmic equation with the form:

$$\text{Volume} = \alpha \cdot \text{Diam}^{\beta}$$

with volume in m³, and diameter in cm.

The *Limite mínimo...* field gives the smallest diameter tree that will be included for volume calculations on the graph of standing volumes. The *Especies para comparaciones* should be a list of species groups, separated by commas (*not* semi-colons in this case), to be included in the volume calculation for the lines on the graph comparing successive simulation runs. The group names are case sensitive. If a group is given here which is either misspelt, or does not correspond to an existing group, no error is reported, but no volume is calculated.

The *Diam>* field for the comparisons line shows the tree sizes to be included in calculating the comparisons volumes.

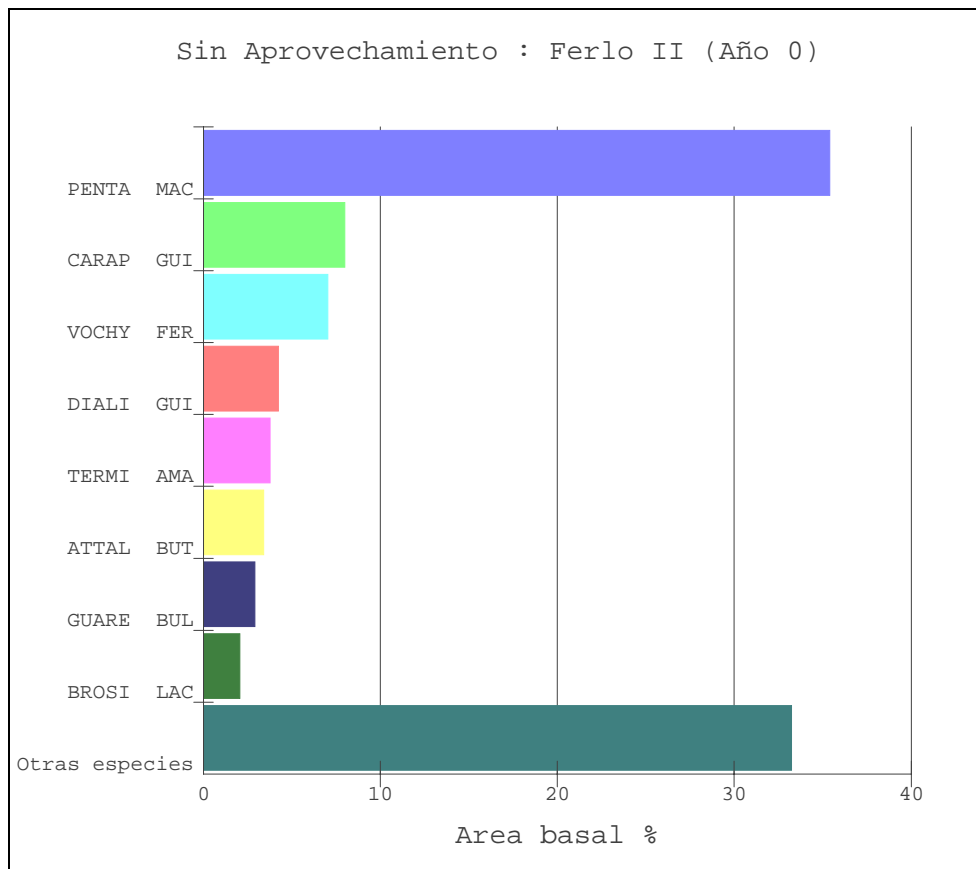
Output graphs

The species abundance graph

The species abundance graph is displayed by clicking the line labelled *Abundancia de especies* under the *Gráficos* menu. An example of this graph is shown in Figure 12 below. The most abundant species is listed first, proceeding down the graph to the least abundant. Scientific names are abbreviated to the first 5 characters of the genus and three of the species, all capitalized. If the use of local names is requested, these are abbreviated to approximately 12 characters where necessary by appending an ellipsis (...). Options appear next to the graph which allow several aspects of its appearance to be changed. The graph can show abundance in terms of numbers per hectare, or basal area %. The trees included can be set to include only those above a specified minimum diameter. The number of species to be shown can be set. In general, with more than 15-20 species shown, the text for the left axis may become too small to be readable.

This graph is a very useful indicator for characterising the type of forest being simulated, with its predominant species. If the model is run while the graph is displayed, it will be seen to change dynamically with each simulated year. The year is shown in brackets on the title line.

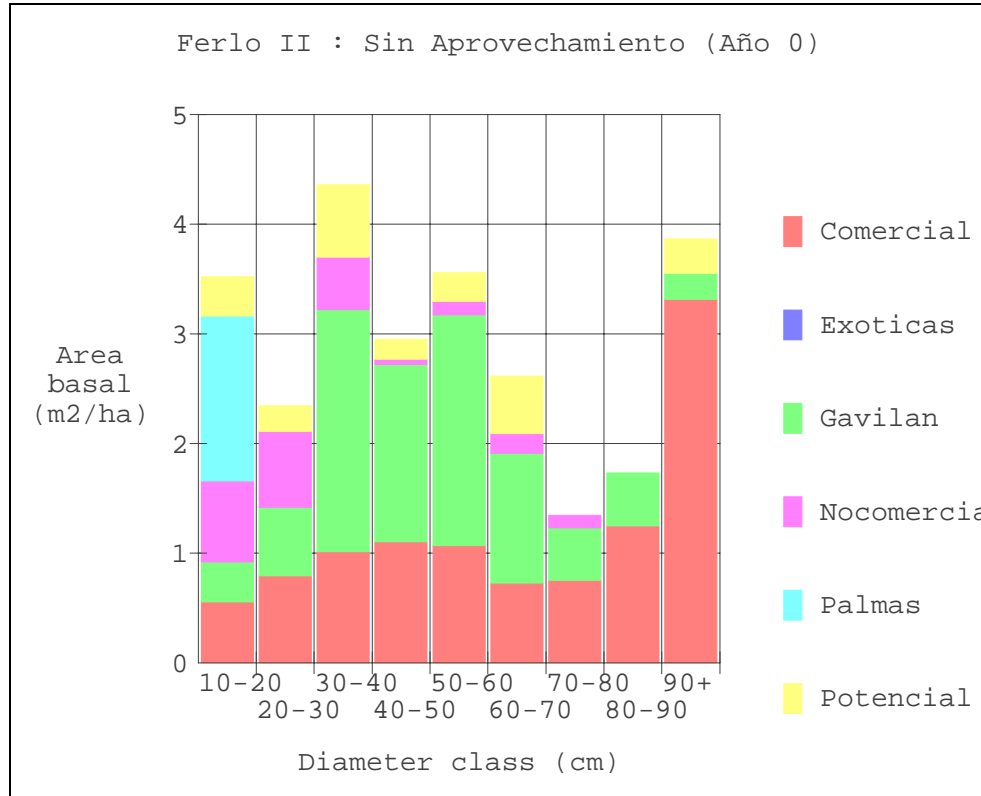
Figure 12 The species abundance graph



Size class distribution

The graph showing size class distributions by species groups is invoked using the menu bar *Distribución por clase de tamaño*. An example is shown in Figure 13 below. The size classes used are set from the general options screen, as discussed on page 20. The left axis can be set to show trees/ha, basal area/ha, or volume/ha. The graph is updated dynamically as the simulation runs, and shows the current year as part of the title.

Figure 13 Graph of species groups by size classes



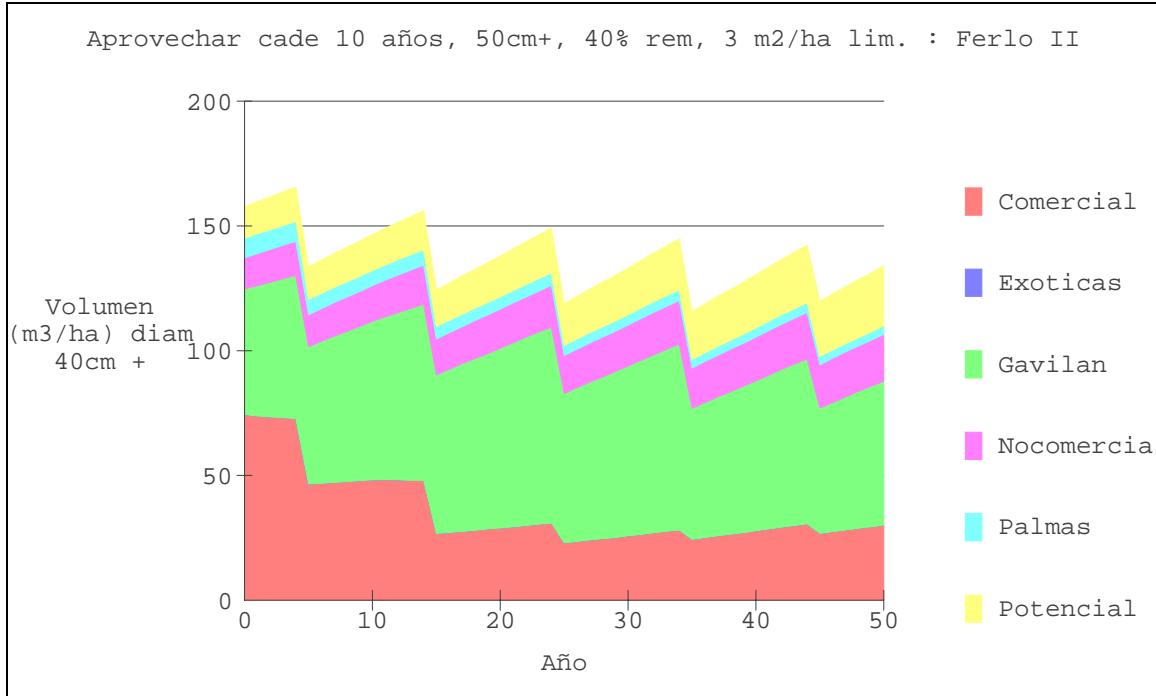
Volume by species groups over time

A graph of standing volume by species groups, as it develops over simulated time, can be shown from the menu selection *Volumen por grupos*. An example of this graph is shown for a regime with a felling cycle of 10 years, and extraction limited to 3 m²/ha in Figure 14. In this example, only *Gavilan* and the *Comercial* group are being felled. There is a decline in the stock over time, but it appears to stabilise over about 50 years. It is probable that a felling controlled to remove a lower basal area would be more suitable on such a short felling cycle.

The volumes are calculated down to the limit specified under the *Volumen* tab of the *Opciones general* screen (see Figure 11). In this case, volumes are shown for all trees above 40 cm diameter. The lines are cumulative, so the volume for an individual species should be worked out by taking the difference between its line and the preceding line

below. The time axis will always depend on the time limit for the simulation, whereas the volume axis is set automatically.

Figure 14 Graph of standing volumes over time, by species groups



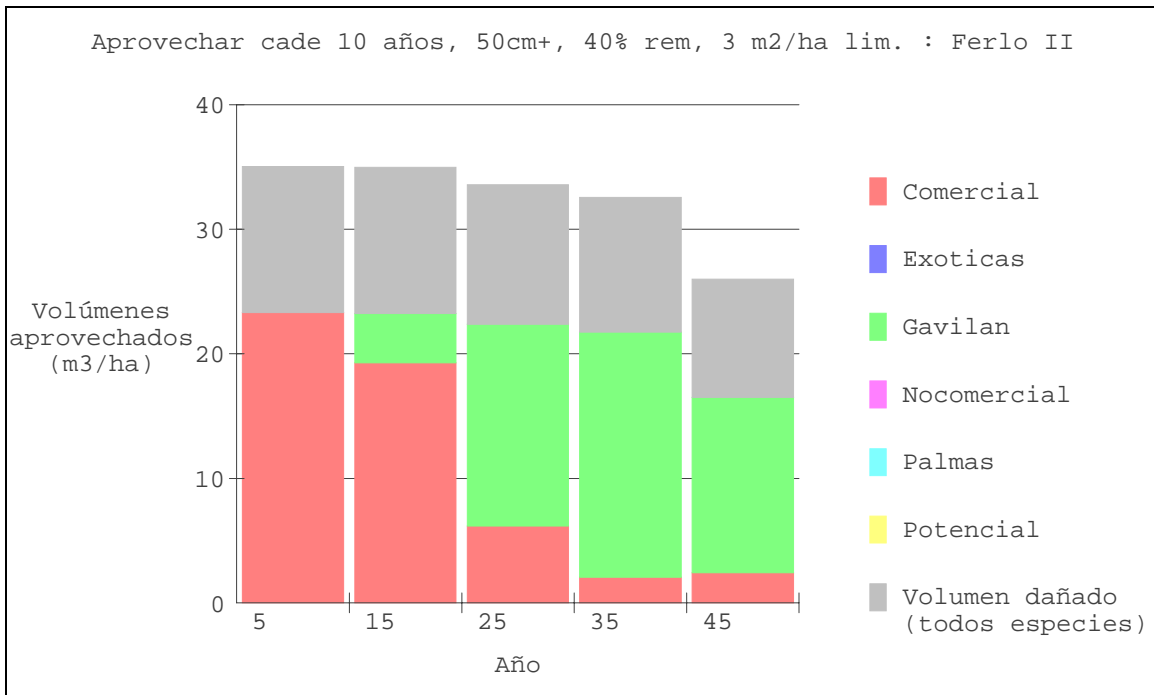
Harvested volumes

The graph of harvested volumes is produced by selecting the menu bar *Volumen aprovechados*. This shows a bar for each felling cycle, subdivided into quantities for each species group, as illustrated in Figure 15. The values are cumulative, and show the volumes actually extracted. The volume of an individual species will be the difference between the top and bottom values for its section of the bar. The topmost section shows volumes destroyed, for all species, among the remnant population, due to skid trails, felling gaps, and severe damage to standing trees.

This example shows a typical pattern of yields in which the most valuable species tend to be taken in the earlier cycles, and less valuable ones in later cycles. The graph also shows a moderate decline in yields over time. These tendencies of a simple management regime can be corrected by placing more stringent limits on the proportion of valuable species removed, and by somewhat reducing the overall level of harvest.

It should be noted that the felling damage shown on this graph is calculated for all species and for all size classes represented in the simulation. This will be down to 10 cm diameter in the present version. It illustrates the point that any felling carries with it a significant cost to the remaining growing stock, in terms of trees and volumes lost.

Figure 15 Graph of harvested volumes



Basal area dynamics

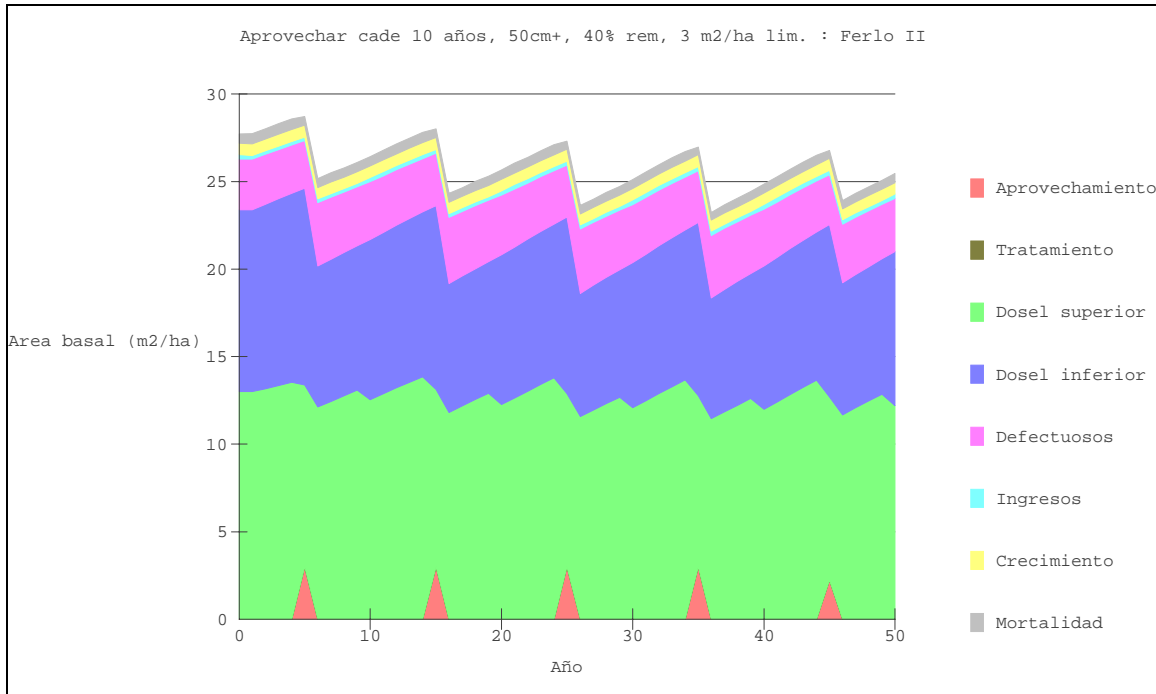
The graph of basal area dynamics is invoked from the menu bar *Dinámicas de area basal*. It illustrates the components of the stand that the model uses in its calculations to estimate growth. An example of this graph, for the same management regime as the preceding cases, is shown in Figure 16.

The standing basal area is subdivided into trees of the upper canopy, corresponding to crown classes 4 and 5 according to Dawkins system, and the lower canopy, or crown classes 1-3. Defective trees of either category are shown above these two layers. This includes trees of bad form, or trees which have been significantly damaged by logging. Each of these three layers has its own distinctive species-dependent growth and mortality function within the model. Generally, most active diameter growth occurs in the upper canopy trees. When running the model, it may appear that the lower canopy basal area is increasing, whilst that of the upper canopy remains relatively constant. This results from the fact that as the upper canopy trees grow, the smaller ones will be pushed into the lower canopy by competition, and hence will become more static in their diameter growth. In the process, the proportion of the stand basal area in the lower canopy will tend to increase.

Above the standing basal areas are shown thin sections which indicate recruitment, increment, and basal area losses through mortality. Harvesting and treatment are shown as triangular peaks on the bottom axis of the graph, which are deducted from the standing basal area.

It will be noticed that the line between upper canopy and lower canopy basal areas tends to be somewhat jagged. This is a function partly of the harvesting process, in this instance, as trees are removed or destroyed, but it is also a function of the frequency with which crown classes are recalculated. The options screen (Figure 9) allows the frequency for recalculating tree canopy positions to be adjusted. This is quite a slow process within the model, and typically can be done on a 5-year cycle. However, if a smoother, more natural looking graph is required, it can be set to an annual basis. This will however slow the model down and does not much influence overall accuracy.

Figure 16 Graph of basal area dynamics



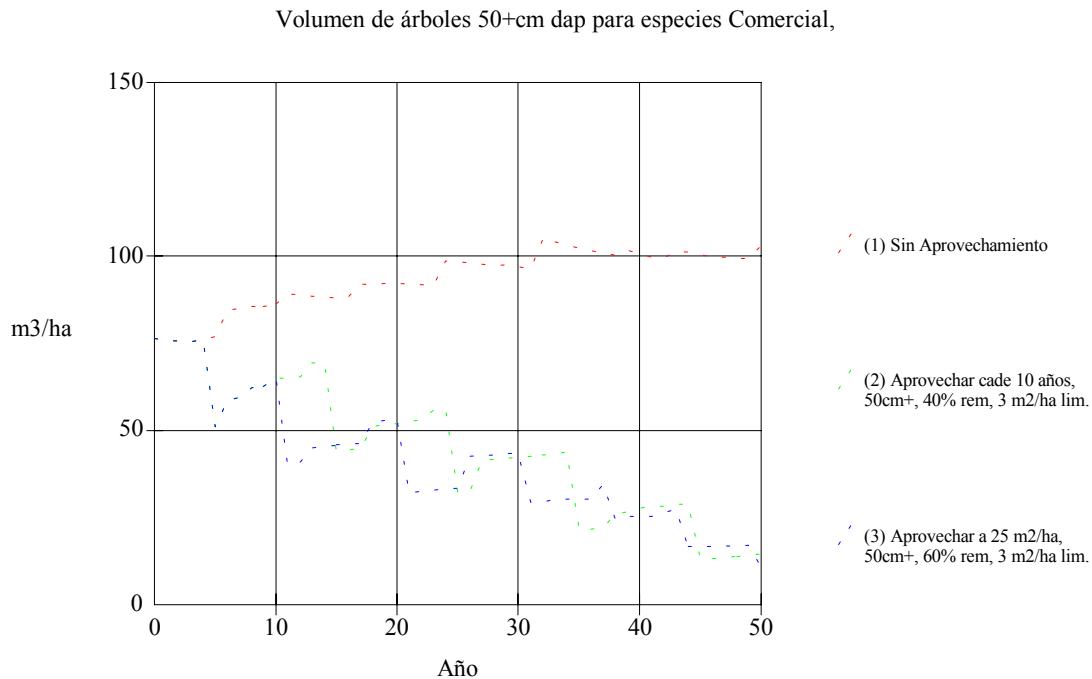
Regardless of the adjustment frequency set, crown positions are always recalculated following any disturbance of the stand due to logging or treatment. Some trees will then be promoted to upper canopy status to compensate for losses, in effect simulating the process of gap formation.

Comparison of scenarios

When successive simulations are run, the volumes for a defined component of the forest in each trial are plotted on the *comparison of scenarios* graph. This is invoked from the menu bar by clicking on *Comparaciones de escenarios*. The actual volumes included in this graph are determined from the settings in the *Opciones general : Volumen* screen, discussed on page 23. This determines the lower diameter limit for the volume shown, and the list of species groups to be shown. It is important that the names of the species groups correspond exactly with current groups, as otherwise nothing may appear and the comparisons line will simply lie along the zero axis. These names are cases sensitive, so that capital and small letters must correspond.

The example shows three regimes. The first is for the forest without harvesting. This shows a rise in volumes over 50 cm to about 100 m³/ha after some 35 years, where it stabilises. The second corresponds to the preceding examples, with 3 m²/ha being removed on a 10-year cycle. The third is an attempt at a more sustainable method of harvesting. The retention percentage is increased to 60%, and felling is scheduled when the stand reaches 25 m²/ha, but removals are still 3 m²/ha. It shows a very similar pattern to the second regime, with declining large tree volumes over time, as the stock is effectively consumed non-renewably.

Figure 17 Example of the comparisons graph for three scenarios



The title to the comparisons graph will show the volume limit and the species groups selected in the *Opciones general* screen. The legend shows the individual scenario titles. This requires that the scenario is saved via the *Manejo de escenarios*; otherwise, only run numbers are shown, and the legend text is blank. This graph is not well suited for monochrome reproduction, due to the similarity of the lines.

Output tables

Table of species by diameter classes

Clicking on the menu bar *Cuadro de clases diámétricas* brings up a screen like the example shown in Figure 18. This displays initially a stand table for species groups. It has several active functions. The statistic shown in the table may be N/ha, volume, or basal area. Volumes, if selected, are calculated to the lower diameter limit set under the *Opciones general : Volumen* screen.

Figure 18 Screen showing the table of diameter classes

Grupos	Clases diámétricas (cm)								
	10-20	20-30	30-40	40-50	50-60	60-70	70-80	80-90	90+
Comercial	23.03	16.97	11.21	6.97	4.85	2.42	1.82	2.42	3.64
Gavilan	23.03	9.70	24.55	10.00	6.36	3.03	1.21	0.61	
Nocomercial	40.00	16.97	5.15		0.61	0.61	0.30		
Palmas	95.76								
Potencial	23.03	6.06	5.76	0.61	1.21	1.82			
Total	204.85	49.7	46.67	17.58	13.03	7.88	3.33	3.03	3.64

Totales
 Selección: 21.21 Acumulado: N/ha

The table shows data for trees of acceptable form only, defective trees only, or both, depending on the value selected under *Forma*.

The boxes labelled *Totales* provide a calculator function that is useful for analysing harvesting and treatment specifications. If a group of cells are selected with the mouse, as shown in the example, then the totals for this group will be displayed in the box labelled *Selección*. Clicking on the *Selección* field adds this total to any value already in the *Acumulado* field, and clears the *Selección* field for a new value. The *Acumulado* field itself can be cleared by double-clicking it. These functions are useful for totalling values for particular species within a range of diameter classes.

The table initially shows summaries by species groups. Double clicking the mouse on a line expands the table for that group to show the data species by species. Double clicking again causes the table to revert to its original form, showing group summaries.

The stand table data can be saved to a text file that is readable by Excel. It is necessary before doing this to assign a scenario name to the simulation, using the scenario manager. The check box labelled *Escribir cuadro a archivo* will then become accessible. A default file name consisting of the scenario code, followed by the year as an extension, will be shown in the text box. This name can be edited manually. When the check box is clicked, the file is written, and at the bottom of the screen, the full output path and file name will be shown.

The file contains heading information giving the forest and scenario name, the statistic used (N/ha, volume, or basal area), and the type of trees included (acceptable, defective, or both), as well as the current year. It then lists each species with its code, name, and group, and the stock by diameter classes.

This table can be imported into Excel very easily using default options. The file is opened as if it were a spreadsheet. A 'Wizard' will then appear. Select immediately the 'Finished' button at the lower right to indicate acceptance of all default settings, and the table will be imported correctly. The table can then be formatted, edited and sorted as required, and saved as an Excel workbook under another name.

If the screen is displayed while the model is running a simulation, then the displayed values will be updated automatically for growth, mortality, etc. The model can be paused and the table saved to file as required. Each time it is saved, the file name extension will automatically be adjusted to reflect the simulation year.

The yield table

All the figures that underlie the graphs of standing and harvested volumes can also be saved to file as the model is run. This requires that a scenario name is selected beforehand using the scenario manager. The menu bar *Cuadro de aprovechamiento* is then chosen. A tick will appear beside the bar in the menu to show that this feature is active. Outputs from the model will be saved into a file with the same name as the scenario code, but with an extension .SY2.

This file can be imported into Excel in the same way as the diameter class table, as noted above. The file is opened in Excel, and the text import Wizard will automatically format the file using its default options. The file contains a heading giving the forest name, the scenario title, and the headings for the various data columns. The rows in the file correspond to years in the simulation. The data can be edited as required for presentation.

Executive menu functions

Running, pausing and cancelling simulations

Under the menu heading *Ejecución* will be found three groups of functions which control execution of the model, exportation of outputs, or the exit from the program

Ejecutar runs the model with currently defined parameters. If the model has not yet been started, or has finished (with FIN displayed in the lower right box of the status bar), then it will start from year zero. If the model has been paused, then it will continue from the year at which it paused.

Pausa halts the model temporarily. It can be restarted by clicking on *Ejecutar* again. It will continue from the year in which it was paused. While the model is paused, harvesting and silvicultural options can be changed, the scenario manager accessed, and any of the output screens examined. Outputs can be printed or copied to the clipboard as required.

It is also possible to change species groups while the model is running or to import new forest data. This is definitely not recommended however, and may cause the program to fail. If it is desired to do this, then the *Anular* option should be used beforehand, or the model allowed to finish its run (indicated by FIN on the status line).

Anular cancels an active simulation and returns the year to zero, reloading the base line data for the forest.

Exporting and printing outputs

The menu bars *Copiar* and *Imprimir* act on a currently displayed graph, if there is one. *Copiar* copies the graph to the Windows clipboard as a metafile. This can be imported into Microsoft Word as a picture object, and may be edited within Word to a limited extent. A number of graphics packages can also import this format and may allow more facile editing. Using Word, it is simply necessary to click the *Copiar* bar, switch to Word, and press CTRL+V at the point where the graph is to be pasted in to the document. Double clicking on the graph will invoke the Word picture editor for minor embellishments.

The *Imprimir* function sends a high-quality image of the graph to the system default printer.

These functions work only on graphs. They do not print or copy either the stand table, or any of the input screens. The stand table can be output via Excel, as discussed on page 30 above.

Exiting from Sirena 2

Clicking the *Salir* menu bar causes the program to be terminated. This can also be effected by closing the main program window, or with the ALT+F4 key.

Technical basis of the model

Introduction

It is not necessary to read this section in order to use SIRENA. It is intended to provide background information on how the model works. A more technical discussion of cohort modelling in general will be found in Alder (1995).

The data base

The basis for analysing the growth functions in the model were 9 1-ha and 27 ¼-ha plots established by CODEFORSA since 1991, with an average remeasurement period of about 4 years, and 17 1-ha plots established by Portico SA since 1989, measured over about 7 years, in all cases with 2 or 3 intermediate measurements. The same data was used in the SIRENA I model, but in this instance intermediate measurements have been used, and the latest remeasurements for 1995 and 1996 added to the data set.

In addition to this, COSAFORMA provided measurements from 34 plots of 600 m² established in secondary forest. These plots were included in the tree increment analysis, but were not used in the basal area functions due to their small size. These plots were measured annually over a 4-year period from 1992.

In all, a total of 64,678 tree records exist in the database, covering 624 species. There are three distinctive types of forest:

- The CODEFORSA plots occur mainly in the central northern zone of Costa Rica, and are characterised by somewhat lower basal areas (typically 20-25 m²/ha), the presence of *Vochysia ferruginea* as an indicator, and the relative absence of *Carapa guianensis*. The forests in which the plots are located are mostly smaller fragments of about 50-100 ha.
- The Portico plots occur further to the east, in higher rainfall areas, in larger continuous tracts of forest, and are characterised by a high frequency of *Carapa guianensis* and the absence *Vochysia ferruginea*.
- In both types of forests, *Pentaclethra macroloba* is a very common component, typically constituting 30-40% of the basal area in many cases. Its abundance is generally lower in the Portico forests, however.
- The secondary forests of the COSAFORMA data set are young regrowth stands of various pioneer species. A distinctive aspect is the frequency of *Cordia alliodora*, and the relative absence of *Pentaclethra*, *Vochysia*, or *Carapa*. These plots are also located in the central northern zone of Costa Rica.

The present version of the model is therefore limited in its applicability to these forests of the northern zone of Costa Rica.

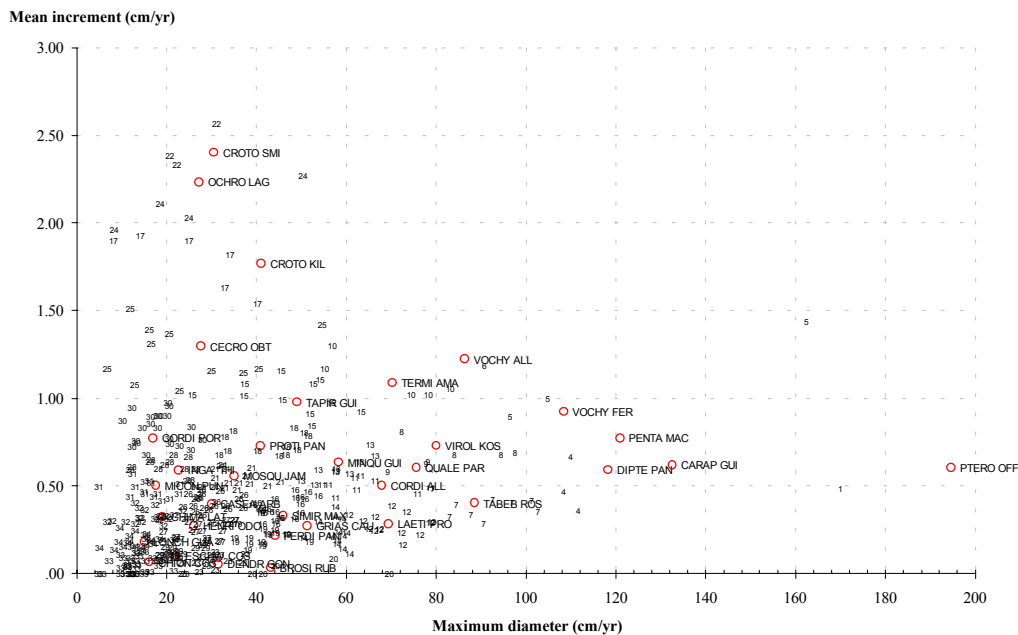
The formation of species groups

The formation of species groups is a necessary first step in analysing growth functions for any tropical forest data. This is because there are a large number of species, many of which are represented in the data by only a few individuals.

For the SIRENA 2 data, methods were tried based on statistical comparisons of regressions between species. Initially, species that were rare were grouped by genera to achieve at least 5 or 6 individuals. A logarithmic regression of basal area increment on tree basal area was then fitted. Using as a discrimination factor a 95% probability that two groups differed, some twenty groups were formed, containing very unequal numbers of trees, and combining species with no apparently similar attributes. The method was not felt to be very useful as it did not combine naturally species that ought to be similar, such as fast growing, shorter lived species, or slower growing, longer lived types.

As with past modelling efforts with SIRENA 1, and the CAFOGROM models for Brazil, a more pragmatic method was eventually used, in which mean increment of upper canopy trees (classes 3-5) was graphed against the largest observed individual for each species. This naturally groups short-lived, fast growing ephemerals, and larger, slower growing forest trees. In order to make the grouping as consistent as possible with common-sense, the groups were formed by identifying key species scattered over the ordination space. Other species were then assigned to the groups seeded from these key species on the basis of their distance in ordination space. Thus each non-key species was attached to a group formed by the nearest key species.

Figure 19 Species groups formed around key species



The results of this ordination are shown in Figure 19. The key species that ‘seed’ each group are shown by a circle, with their abbreviated species name. The small numbers show the position of other species associated with each group. The table below lists the groups, with their key species and other statistics.

Figure 20 List of key species for Sirena 2 model groups

Group	Key species	Trees	Dmax	Dinc	Nsp
0	Palms	-	-	-	18
1	<i>Pterocarpus officinalis</i>	247	195	0.61	3
2	<i>Carapa guianensis</i>	1147	133	0.62	1
3	<i>Pentaclethra macroloba</i>	1651	121	0.77	1
4	<i>Dipteryx panamensis</i>	52	118	0.59	4
5	<i>Vochysia ferruginea</i>	221	108	0.93	4
6	<i>Vochysia allenii</i>	156	86	1.23	2
7	<i>Tabebuia rosea</i>	60	89	0.41	10
8	<i>Virola koschnyi</i>	133	80	0.73	5
9	<i>Qualea paraensis</i>	150	76	0.61	4
10	<i>Terminalia amazonia</i>	16	70	1.09	6
11	<i>Cordia alliodora</i>	118	68	0.51	10
12	<i>Laetia procera</i>	242	69	0.29	15
13	<i>Minquartia guianensis</i>	16	58	0.64	11
14	<i>Grias cauliflora</i>	110	51	0.28	14
15	<i>Tapirira guianensis</i>	80	49	0.98	13
16	<i>Simira maxoni</i>	267	46	0.34	26
17	<i>Croton killipianus</i>	28	41	1.77	7
18	<i>Protium panamense</i>	110	41	0.73	14
19	<i>Ferdinandusa panamensis</i>	276	44	0.22	18
20	<i>Brosimum rubescens</i>	14	43	0.04	7
21	<i>Mosquitoxylon jamaicense</i>	55	35	0.56	17
22	<i>Croton smithianus</i>	52	30	2.41	6
23	<i>Dendropanax gonatopodus</i>	30	31	0.06	16
24	<i>Ochroma lagopus</i>	59	27	2.24	5
25	<i>Cecropia obtusifolia</i>	15	28	1.30	15
26	<i>Casearia arborea</i>	98	30	0.40	24
27	<i>Henriettea odorata</i>	94	26	0.28	27
28	<i>Inga thibaudiana</i>	52	23	0.59	17
29	<i>Eschweilera costaricensis</i>	28	22	0.10	25
30	<i>Cordia porcata</i>	17	17	0.78	31
31	<i>Miconia punctata</i>	50	18	0.51	22
32	<i>Chimarrhys latifolia</i>	57	19	0.33	33
33	<i>Chione costarricense</i>	17	16	0.07	65
34	<i>Lonchocarpus guatema</i>	44	15	0.18	44

The number of trees shown under the *Trees* heading refers only to the number of trees for the key species, not for all the species in the group. Likewise, the statistics shown are for the key species only, not group means. The last column shows the number of species in each group. Statistics are not shown for palms, as these were grouped on the basis of their botanical affinity, rather than via the ordination process.

The species group that each individual species belongs to is contained in a database file called GROUPS. This has two fields, GENSP and GRUP, which give the abbreviated scientific name of the species, and its allocated group. This file can be used as a resource to add group numbers to any species list that is being prepared for use by SIRENA.

Growth and mortality rates by species groups

Once species groups had been determined, it was possible to compile increment and mortality data and fit regressions. In the event, it was found that tree size was not a significant factor in tree increment regressions once canopy position and defect status had been accounted for. Increment statistics were therefore compiled as a simple table of mean increments for lower canopy trees (crown classes 1-3), upper canopy trees (crown classes 4-5), and defective trees (malformed, damaged, or trees which died over the period). Mortality statistics were compiled on a similar basis. The coefficients are shown by species groups in the table below.

Figure 21 Diameter increment and mortality coefficients by species groups

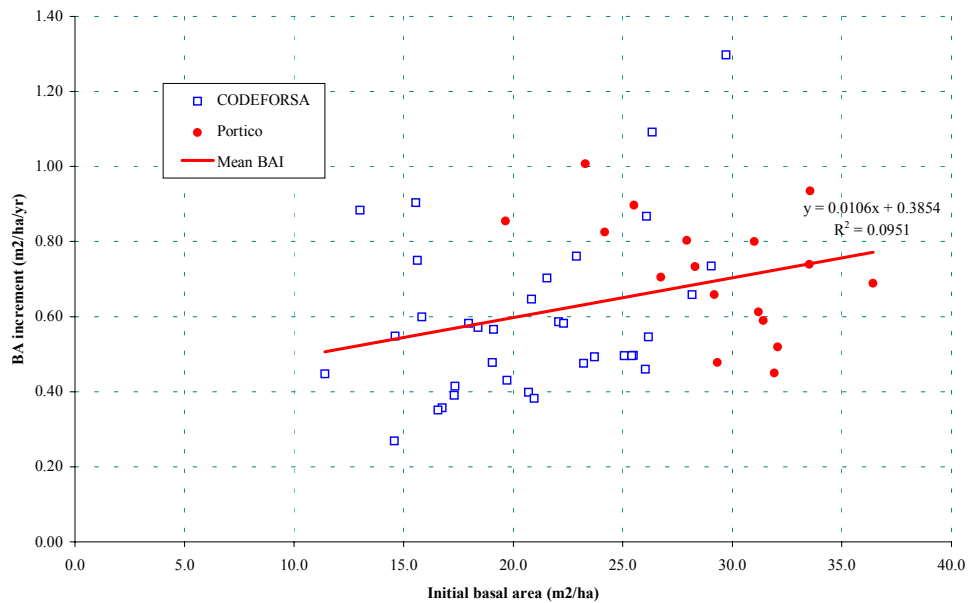
Species group	Total trees	Dbh increment, cm/yr			Dmax	Annual Mortality Rate		
		U/S	Canopy	Defective		U/S	Canopy	Defective
0	7370	0.083	0.061	0.027	34	0.042	0.042	0.268
1	952	0.323	0.706	0.518	192	0.021	0.035	0.042
2	2754	0.230	0.629	0.293	134	0.016	0.014	0.014
3	4326	0.656	0.866	0.467	124	0.026	0.023	0.050
4	636	0.297	0.430	0.463	125	0.012	0.001	0.025
5	636	0.560	1.029	0.467	131	0.030	0.034	0.318
6	443	0.525	1.375	0.344	94	0.007	0.000	
7	565	0.194	0.346	0.156	104	0.010	0.019	0.023
8	568	0.404	0.754	0.117	155	0.014	0.005	0.036
9	621	0.344	0.645	0.354	89	0.026	0.033	0.079
10	282	0.876	1.161	0.342	86	0.029	0.023	0.414
11	944	0.384	0.511	0.571	95	0.019	0.025	0.067
12	1225	0.200	0.341	0.115	81	0.036	0.016	0.056
13	453	0.401	0.652	0.375	110	0.026	0.011	0.023
14	784	0.226	0.276	0.138	71	0.024	0.017	0.052
15	479	0.543	1.033	0.616	70	0.011	0.021	0.104
16	1665	0.272	0.392	0.155	55	0.045	0.028	0.127
17	24	0.476	1.457	3.425	44	0.121	0.000	
18	511	0.368	0.924	0.672	76	0.037	0.035	0.117
19	1792	0.178	0.198	0.133	72	0.019	0.015	0.081
20	100	0.233	0.124	0.051	120	0.057	0.030	
21	520	0.318	0.657	0.167	72	0.035	0.019	0.077
22	149	1.164	2.683	1.507	53	0.084	0.144	0.058
23	693	0.199	0.102	0.088	45	0.021	0.028	0.044
24	118	0.953	2.387	1.755	56	0.547	0.073	
25	78	1.099	1.227	0.000	58	0.208	0.151	0.761
26	910	0.379	0.391	0.253	41	0.018	0.004	0.071
27	1413	0.256	0.257	0.213	48	0.013	0.025	0.037
28	353	0.466	0.757	0.388	50	0.097	0.104	0.220
29	930	0.176	0.142	0.021	31	0.011	0.027	0.027
30	269	0.466	0.904	0.384	31	0.013	0.023	
31	320	0.366	0.406	0.301	29	0.011	0.026	
32	445	0.335	0.280	0.178	41	0.026	0.041	
33	534	0.101	0.104	0.118	38	0.047	0.070	0.066
34	560	0.220	0.168	0.090	38	0.041	0.169	0.129

This table shows the total number of trees for each species group. Not all trees are useable for all analyses. Dead trees cannot be used in increment studies, for example. The *Dmax* figure was compiled as either twice the 95% order statistic of the diameter distribution, or the actual largest diameter, whichever was smaller. This was designed to give an estimate that avoided excessive values due to eccentrically large individuals.

The basal area increment model

It was found in initial trials of the model that simulated increment tended to be excessive after heavy disturbance and regeneration of large numbers of trees. As in the earlier SIRENA 1 model, it was decided to add a basal area increment function for the stand as a whole that would be used to condition individual tree increments whilst preserving the relative differences between species and stand components (lower and upper canopy, defectives). This function is shown in Figure 22 below.

Figure 22 The basal area increment model



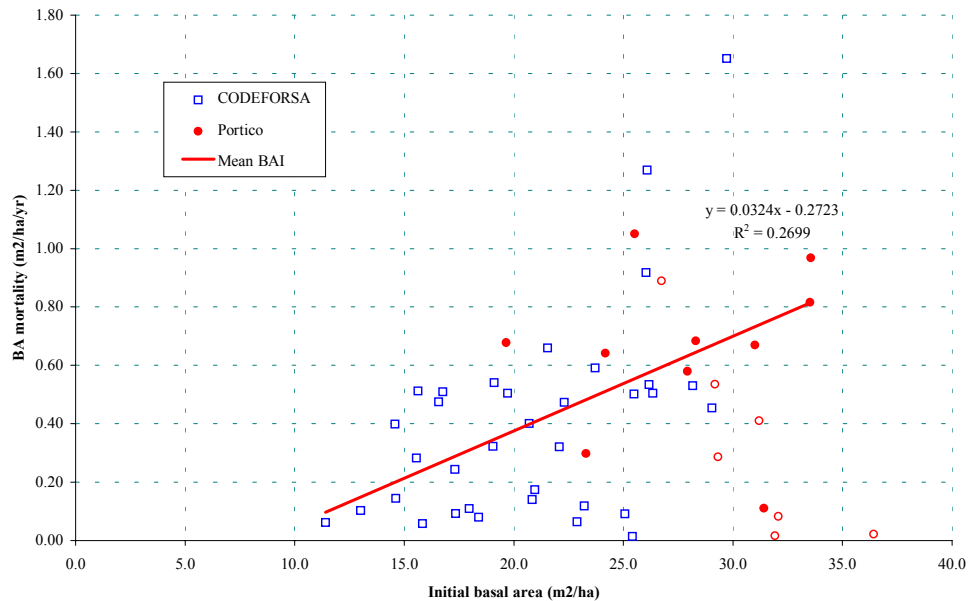
The correlation between basal area increment and stand basal area at the start of a period is very weak. The calculations here are done over the whole measurement period, and are gross increments on live trees. The average period was 4.83 years for all plots. The data for CODEFORSA and Portico are shown with separate symbols. The COSAFORMA data was not used due to the small plot size.

Although the correlation is low, this function is useful in showing that increment is relatively constant over a range of basal areas, and implies higher net per tree growth at lower stockings. It is used as a moderating and conditioning function for the individual species and stand component growth models.

Basal area mortality

A function for basal area mortality was used in a similar way to that for basal area increment. This conditions individual species group and stand component mortalities, from Figure 21, so that their relative values are preserved whilst total mortality agrees with the stand level function.

Figure 23 The basal area mortality model



As with the earlier regression, the R^2 is very low. Nonetheless this function greatly improves the behaviour of the model, which otherwise does not show a sufficient tendency to increasing mortality with stand density.

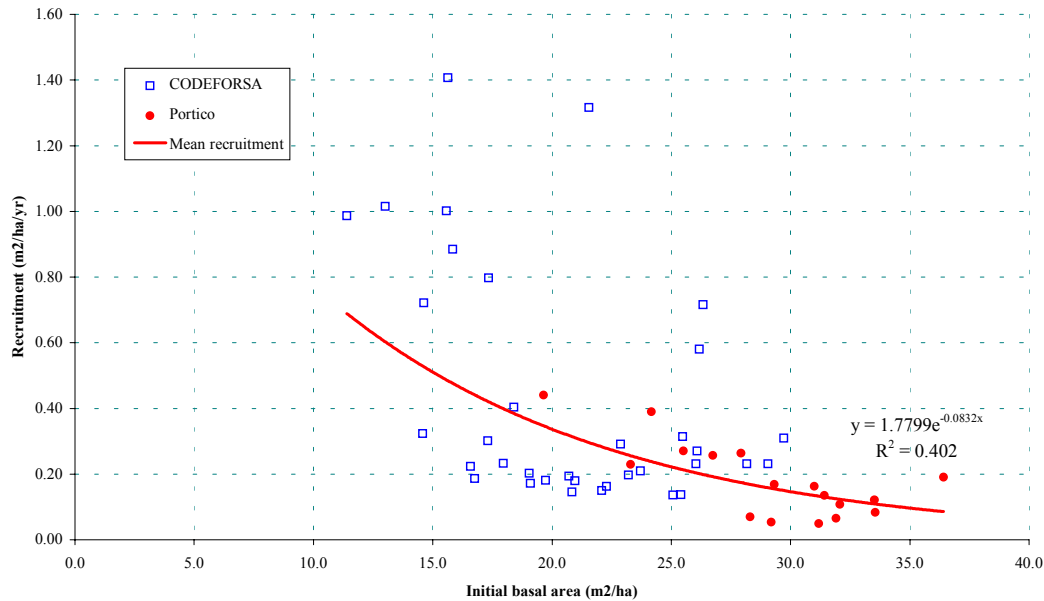
Recruitment basal area

Whereas the mortality and increment functions for basal area condition individual tree models, the recruitment basal area model is the primary method of predicting recruitment. The data and function are shown in Figure 24. This is a more clearly defined function than the others, showing a definite decline in recruitment with increasing stand basal area.

The number of recruits is calculated from the mean diameter of all recruitment, excepting the COSAFORMA plots, which was 12.68 cm, relative to a minimum measurement diameter of 10 cm. The function shown is based on a 4.8 year lag between the initial basal area and the accumulated recruitment. In the model, this lag period is used to input to the function basal area at an earlier date when calculating the current recruitment. It will be seen for example that if a heavy harvesting is done, recruitment does not respond until 4 years after the event. This reflects the average time for trees to enter the measurement limit of 10 cm plus.

Recruitment is apportioned among species based on these present in the inventory data. As this is read, a frequency table is built up of pioneer and non-pioneer species. This is used to determine relative frequencies of recruits. A bias function is applied to increase the proportion of pioneers, and decrease that of non-pioneers, at lower basal areas.

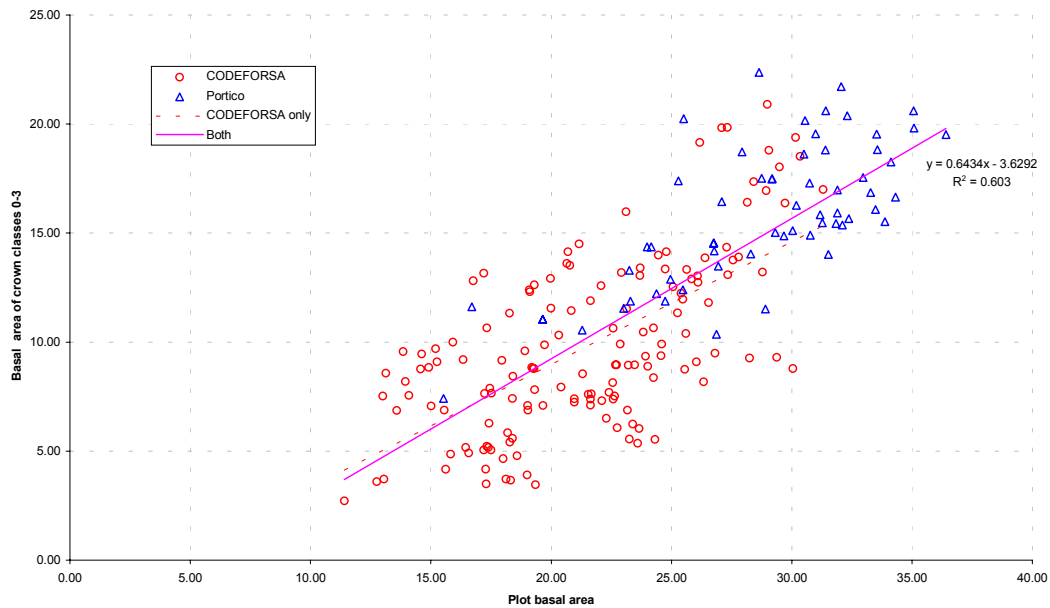
Figure 24 The basal area recruitment model



Crown classification of trees

A key element of the growth model is the assignment of a canopy position to each cohort, in order to select the appropriate increment and mortality coefficient. The crown positions are simplified into two categories: Lower canopy, comprising crown classes 1-3, and upper canopy, including crown classes 4 and 5. The model uses the relationship shown in Figure 25 to determine the basal area which is comprised of lower canopy trees, given the total stand basal area. Individual cohorts are sorted by size, and allocated to the upper canopy until the quota of available basal area is satisfied. The smaller diameter trees are then assigned to the lower canopy. Defective trees are included as part of the lower canopy in the regression and in its application within the model, although they draw on their own distinct mortality and growth coefficients.

Figure 25 Model for crown class classification



Logging damage

The logging damage functions are based on surveys carried out by CODEFORSA, with ODA assistance, which related the volume removed from seven farms to the area impact, in terms of gaps and trails, and to the percentage of severely damaged residual trees. Simple linear regressions were used, as the data was too sparse to justify curvilinear relationships. The functions are similar to those used in SIRENA 1, and have been reported elsewhere (Maginnis, 1997).

Supplying coefficients to the model

The coefficients for the above models are supplied in a file called MODELS.SN2 which should be in the same directory as the SIRENA program. This is a simple file of comma separated values which can be amended by text editor. A listing is shown in Figure 26. The values in this file are as follows:

- The coefficients (intercept and slope) for the linear basal area increment function.
- The coefficients for the linear mortality function.
- The coefficients of the negative exponential recruitment function, the time lag in years, and the mean diameter of recruits.
- The number of pioneer groups, and the model numbers applicable.
- The area and tree functions for logging damage, and the 'avoidance diameter' for skid trails.
- The linear coefficients of the crown class function.

- For each species model, the model number, diameter coefficients, maximum diameter, and mortality coefficients, as set out in the table in Figure 21.
- A final default model, here number 36, which is assigned to all species not found in the species list, but occurring in the inventory data. This will be seen to replicate model 21, which is for trees of medium size and growth rate (see Figure 19).

Figure 26 Listing of the MODELS.SN2 coefficients file

0.3854, 0.0106
-3.6292, .6434
1.7799, .0832, 4, 12.68
8, 22, 24, 17, 25, 15, 18, 30, 28
.0807, .0055, .0211, .0017, 20
-.2723, .0324
0,0.083,0.061,0.027,34,0.0416,0.0418,0.2676
1,0.323,0.706,0.518,192,0.0212,0.0354,0.0423
2,0.230,0.629,0.293,134,0.0155,0.0140,0.0142
3,0.656,0.866,0.467,124,0.0263,0.0231,0.0499
4,0.297,0.430,0.463,125,0.0117,0.0013,0.0252
5,0.560,1.029,0.467,131,0.0297,0.0338,0.3179
6,0.525,1.375,0.344,94,0.0071,0.0000,0.0071
7,0.194,0.346,0.156,104,0.0098,0.0194,0.0229
8,0.404,0.754,0.117,155,0.0140,0.0054,0.0363
9,0.344,0.645,0.354,89,0.0255,0.0328,0.0785
10,0.876,1.161,0.342,86,0.0292,0.0228,0.4143
11,0.384,0.511,0.571,95,0.0192,0.0245,0.0669
12,0.200,0.341,0.115,81,0.0356,0.0160,0.0563
13,0.401,0.652,0.375,110,0.0257,0.0107,0.0231
14,0.226,0.276,0.138,71,0.0241,0.0166,0.0522
15,0.543,1.033,0.616,70,0.0114,0.0214,0.1043
16,0.272,0.392,0.155,55,0.0446,0.0283,0.1270
17,0.476,1.457,3.425,44,0.1211,0.0000,0.1211
18,0.368,0.924,0.672,76,0.0370,0.0352,0.1171
19,0.178,0.198,0.133,72,0.0189,0.0149,0.0809
20,0.233,0.124,0.051,120,0.0572,0.0303,0.0572
21,0.318,0.657,0.167,72,0.0352,0.0186,0.0765
22,1.164,2.683,1.507,53,0.0841,0.1444,0.0583
23,0.199,0.102,0.088,45,0.0205,0.0279,0.0440
24,0.953,2.387,1.755,56,0.5466,0.0730,0.5466
25,1.099,1.227,0.000,58,0.2083,0.1510,0.7614
26,0.379,0.391,0.253,41,0.0184,0.0037,0.0713
27,0.256,0.257,0.213,48,0.0128,0.0246,0.0369
28,0.466,0.757,0.388,50,0.0971,0.1035,0.2197
29,0.176,0.142,0.021,31,0.0112,0.0271,0.0270
30,0.466,0.904,0.384,31,0.0125,0.0230,0.0125
31,0.366,0.406,0.301,29,0.0106,0.0260,0.0106
32,0.335,0.280,0.178,41,0.0263,0.0414,0.0263
33,0.101,0.104,0.118,38,0.0471,0.0695,0.0657
34,0.220,0.168,0.090,38,0.0409,0.1689,0.1293
36,0.318,0.657,0.167,72,0.0352,0.0186,0.0765

Conclusion: The application of SIRENA

SIRENA 2, like its predecessor, is designed to supplement forest management plans by allowing the sustainability of proposed harvesting regimes to be tested over time. It gives due weight to the influence of logging damage, and reflects the influence of stand density variations on growth and mortality. It also shows how different policies for retaining and selecting species can influence the mixture that is harvested at each successive cycle.

The model's accuracy is uncertain, and it will require more and longer measured series of permanent plots to test it thoroughly. However, tree growth is not especially sensitive, and over moderate periods of up to thirty years, its predictions are unlikely to greatly in error. Beyond this, species composition may change as a result of different patterns of recruitment, and the model's ultimate accuracy is unlikely to be very great until more data is available.

Certain aspects of the model are not essentially dynamic and predictive, but are simple data processing functions. The effects of selective harvesting or treatment on species composition, for example, or the various short-term graphs available of volume, basal area, and size class distribution. These are likely to be useful under any circumstances.

The model also provides a very useful teaching tool for forest management. It is not easy to envisage the important variables that may influence forest growth and composition, or the implications of stand treatments or harvesting. SIRENA allows these questions to be explored in an interactive way. The strong influence of felling damage on short-cycle logging is clearly shown. The possibilities for manipulating species composition, or for reducing accumulated defect, through stand treatment, can be readily studied.

Every effort has been made to make the model as easy to use and as interactive as possible. Given the complexity of modern operating systems, this is certainly a non-trivial task. Hopefully users will find SIRENA as 'friendly' as its short development cycle may permit.

The model does emphasise the importance of permanent sample plot work. It is only from this type of data that we will learn enough about natural forest dynamics to be able to manage them with any confidence for the longer term.

Appendix: Troubleshooting

This Appendix summarises some common problems that will be found when installing and running SIRENA, and suggests some possible solutions. If all else fails, please contact the author by E-mail to D-ALDER@MAIL.ZYNET.CO.UK and attach copies of the current files you are using, especially:

IDIOMA.SN2

IDIOMB.SN2

MODELS.SN2

DEFAULTS.SN2

The scenario file(.sc2)

The forest basis file (.FBS)

The species list file (.SPL)

The date of the Sirena .EXE file and the version number shown.

Missing files

A message on start-up that the file VB40016.DLL or VB40032.DLL is missing indicates that the program has not been installed properly. It cannot be installed by simply copying the .EXE files, but requires a number of library files. The original installation disks are needed for this purpose.

Missing files with extensions .OCX or .DLL may be reported later, when particular functions are accessed. This is the same problem.

Copies of the Windows 3.1 compatible installation disks are available from CODEFORSA. This version can also run on Windows 95.

The Windows 95 installation process with the 32-bit version is problematic due to a fault in the Microsoft installation Wizard for this version. Please contact the author by E-mail for current advice.

Wrong Windows version

The Windows 95 version cannot be run under Windows 3.1. The file is called SIRENA95.EXE to distinguish it from SIRENA2.EXE, which is the Windows 3.1 version. The latter can however run on Windows 95 and is certainly easier to install.

Continued appearance of the localizer screen

If the screen shown in Figure 2, page 4 appears repeatedly before the login screen, then the program cannot find the files IDIOMA.SN2 and IDIOMB2.SN2, which should be in the same directory as SIRENA2.EXE. Setting the working directory on the program startup icon should cure this if the files do exist.

If the Localizer screen appears repeatedly after login then either:

- The wrong user directory has been given

- The base directory for users has not been properly specified on the D= parameters (for network use).
- The files DEFAULTS.SN2 (in the user directory) or MODELS.SN2 (in the Sirena directory) cannot be found.

Review the installation method discussed from 1.

The program will normally fail with an error 53 or 76 if it is unable to find the necessary files after one or two attempts.

The program crashes immediately after login

With versions before 2.11c, this will happen with execution error 13. With later versions, it will advise that the decimal point must be set to ‘.’. Systems which are configured to use the comma as the decimal usually give problems with a variety of software. It is strongly recommended that the control panel international settings are used to set the decimal to a point (.), the list separator to a comma (,), and the thousands separator to a comma or a space. The Spanish (Mexico) settings give this by default.

Various violation errors are reported erratically when running the program

The Windows installation is probably corrupt. It should be re-installed from original manufacturers disks. This is especially likely to be true if similar problems occur with other Windows software. Virus attacks in particular can leave corrupted files even if anti-virus software has ‘cleaned’ the system.

‘Access denied’ errors occur when saving species lists or scenarios

Under a network, this will probably occur because you are working in a network directory to which you only have read access. Modify the installation setup for directories. The D= parameter on the command line can be used to direct your work by default to a local disk or user directory (see page 2).

If it is a stand-alone system, then you may be running two copies of SIRENA simultaneously, or may have the required file opened by another program such as Excel or Word.

Sirena2 runs excruciatingly slowly

Sirena 2 should not be run on an SX machine, as this lacks a co-processor and does arithmetic about 10 times slower than DX machines. Simulation is very arithmetic-intensive. The lowest standard processor useable is a DX2-66. A Pentium is recommended.

The model crashes with a ‘division by zero’ message when running simulations

If any of the update frequencies on the General Options screen (Figure 9) are zero, then the program will crash when a simulation is started.

The program runs but produces ridiculous values

There could be a number of reasons. The MODELS.SN2 file could have been modified. Check it carefully against Figure 26. The sensitivity parameters could be zero, negative or extreme values. Check the screen shown in Figure 10. All the values should be 1.

The comparisons graph is always zero

The species groups listed for the comparisons line must agree with the current groups. See page 23.

Treatments or harvesting are not as expected

Read pages 12-18 carefully. The species groups must agree with you current groups, the '*Normal*' option button should be checked, and you should have indicated *Si* against those species which you wish to harvest.