

Compete ©

An individual-based spatial modelling software to simulate ecological interactions and evolution in sessile organisms

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About *Compete* ©

***Compete* ©** is a spatial individual-based modelling package facilitating study of population and community dynamics and evolution in assemblages of sessile modular organisms competing for space. The kernel of its operation is a probabilistic cellular automaton, but with additional functions for recruitment, mortality, dispersal and disturbance. The model uses synchronous updating of the landscape.

The software provides for:

- up to 40 species
- landscapes up to 800 x 800 cells
- metacommunities of up to 64 landscapes connected by dispersal
- neighbour-specific growth rates for each species
- species-specific recruitment rates
- species-specific mortality rates
- open and closed recruitment regimes
- any network topology describing competitive outcomes among species
- user-defined scenarios of disturbance
- user-defined initial landscapes, including reading maps from file
- single and Monte Carlo runs
- a wide variety of graphical and data file output formats
- open or toroidal (=periodic) boundary conditions
- simulation of the non-spatial equivalent of any defined model structure as difference equations

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Rules and Schedules

1. The **order of events** is:

- Growth and overgrowth of colonies
- Mortality of colonies and disturbance to the landscape
- Dispersal and recruitment, including mutation on growth and interaction parameters

2. Rules for cell and 'colony' **growth**:

- If a ('central') cell is empty then a neighbouring cell is chosen at random; if the neighbour is occupied then that species grows into the empty 'central' cell with probability G_{x_empty} , which is the growth rate of species X into empty space.

By this mechanism 'bays' on the perimeter of colonies fill in more quickly than headlands advance so that 'colonies' grow in an approximately circular shape in free space.

- If a central cell is occupied by a species Y then a neighbouring cell X is chosen at random, and species X overgrows species Y (the central cell) with probability $Pr_{XY} * G_{XY}$ where Pr_{XY} is the probability of X winning an encounter with Y , and G_{XY} is the growth rate of X over Y . Note that $Pr_{XY} + Pr_{YX} + Pr_{standoff} = 1.0$ (Pr_{XY} = probability of X winning in an interaction with Y ; Pr_{YX} = probability of X losing in an interaction with Y ; $Pr_{standoff}$ = probability of there being a standoff between X and Y with neither winning the interaction).
- When the outcomes of pairwise interactions are variable, then every individual of species X can potentially have a different 'genotype' defining its interaction with species Y (and similarly for individuals of species Y interacting with species X). Here the rules for overgrowth need to take into account the different genotypes of the two interacting individuals. If we designate two individuals as individual i of species X and individual j of species Y , then the likelihood of i overgrowing j is $Pr(i>j) = ((Pr(i)_{YX} + Pr(j)_{XY}) / 2)$, and of j overgrowing i is $Pr(j>i) = ((Pr(j)_{XY} + Pr(i)_{YX}) / 2)$.

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Rules and Schedules

3. Rules for Mortality

- Mortality in a given species is defined by (i) the probability of mortality for that species, which applies to every cell of that species in each timestep; and (ii) the size of the mortality event, which defines the maximum number of contiguous cells of the same species that will be removed in a single mortality event. Defining the size of the event invokes a crude form of size-dependent mortality because complete mortality of larger colonies in any one step is unlikely.

4. Rules for Disturbance

- Disturbance occurs randomly on the landscape with a nominated probability applied to every occupied cell. If a random number is less than the nominated probability at a given cell, then that cell marks the centre of the disturbance event. The size (in numbers of contiguous cells that will revert to bare space) and shape (square or random) of the disturbance event are defined by the user.

5. Rules for Dispersal and Recruitment

- Recruitment occurs only in empty cells on the landscape, and is defined as either 'open' or 'closed'. For 'closed' recruitment (i.e. to an empty cell), an occupied cell is chosen at random from the current landscape, and the species occupying the chosen cell recruits to the empty cell with a probability equal to the recruitment rate of the selected species. In contrast, 'open' recruitment does not depend on the relative abundance of species on the current landscape. Instead, a species is selected at random from any that has existed in the system, and the selected species recruits to the empty cell with a probability defined by its recruitment rate. For variable growth and outcome genotypes, if recruitment is 'closed' then the genotype of the selected cell on the landscape is faithfully reproduced in the recruit (but with some probability of mutating up or down by a defined amount), while if recruitment is 'open', the genotype of the recruit is selected randomly from the range of genotypes for growth and 'outcome win' (separately) that have ever existed in the system.
- All recruitment rates can be scaled simultaneously by setting a 'probability of influx' to <1 . In multiple landscapes, recruitment can be derived exclusively from neighbouring landscapes in specified timesteps.

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Menus

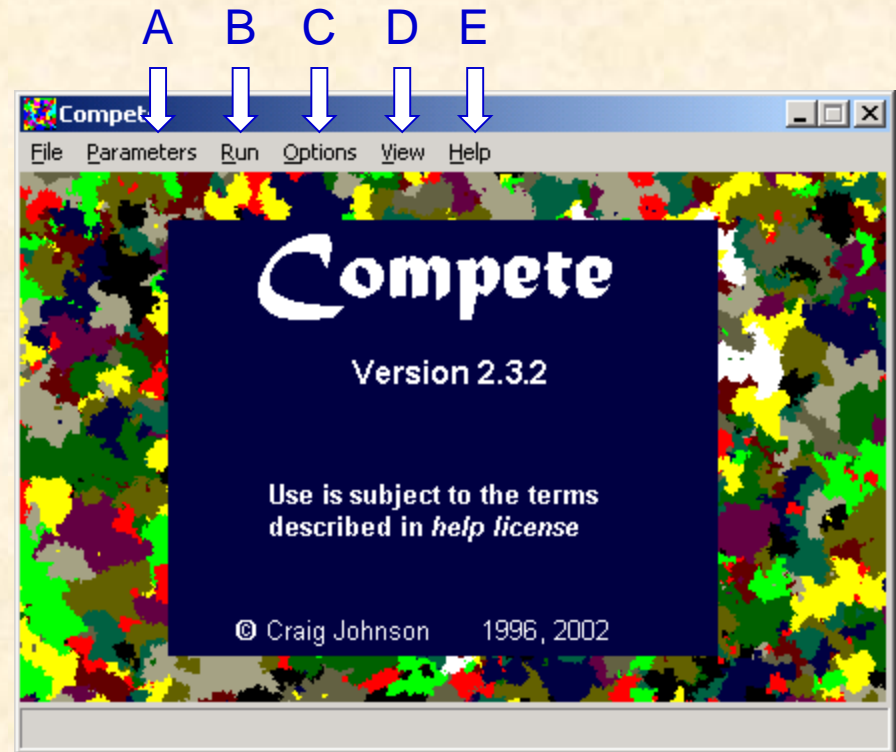
Parameters (A)

Run (B)

Options (C)

View (D)

Help (E)



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Parameters Menu

Use Default

General

Outcome Matrix

Growth Rates

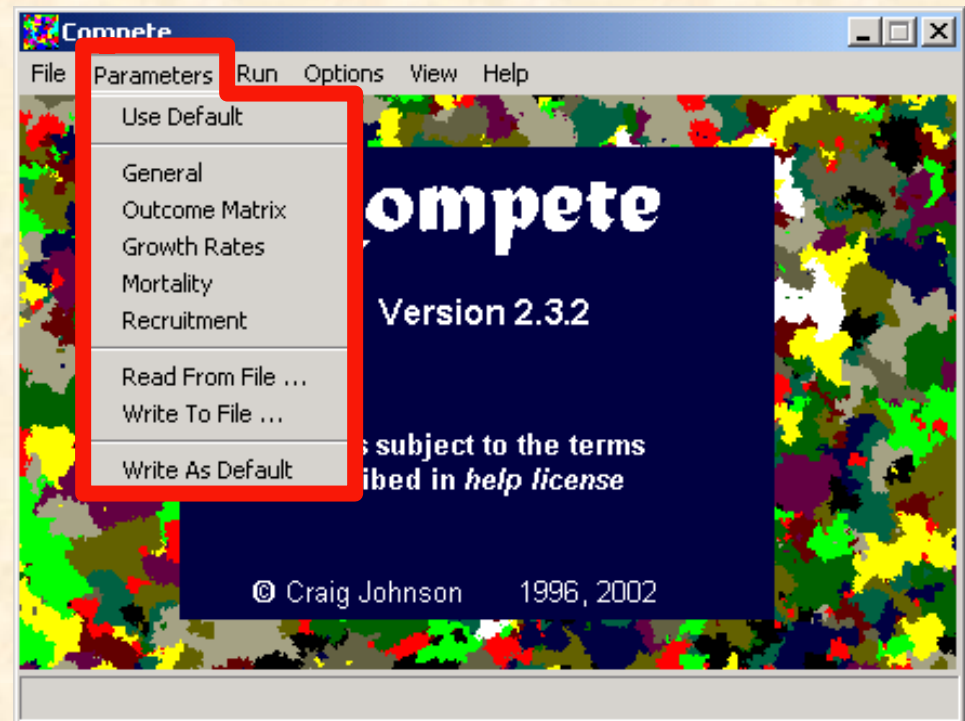
Mortality

Recruitment

Read From File ...

Write To File ...

Write As Default



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Use Default

Selecting this option will retrieve the default parameters. The default parameters are set by selecting [Write As Default](#) from the Parameters menu.

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General

Number of Species: Specify the number of species in the system. The minimum number of species is 3 and the maximum is 40.

Landscape size: Specify the dimensions of the landscape as length x breadth cells. The maximum landscape size is 800 x 800.

Number of pixels per cell: Specify the length of one side of a single cell (in pixels) when displaying the landscape. The model is slowed considerably for values greater than 1, which can be a useful feature to observe detailed dynamics on the landscape.

Number of generations: Specify the number of time steps in the run.

Random number seed: Specify the (pseudo) random number seed. This enables identical repeats of a particular run configuration.

Distribution of initial growth rates: This parameter, which defines the initial spatial distribution of growth rate genotypes when there is a range of growth rate genotypes for one or more species, is **DISABLED in this version**. The default is that genotypes are scattered randomly across the landscape.

Type of initial cover: Specify the initial spatial distribution of species on the landscape. **Random** indicates that species are distributed randomly on the landscape. **Blocks** specifies that a single randomly selected species is distributed into distinct blocks on the landscape. Block sizes range between 15x15 and 25x25, and are adjusted automatically depending on the size of the landscape. Thus, because species are assigned to blocks randomly, if the number of species in the system is large relative to the size of the landscape, then not all species will necessarily occur on the initial landscape. **File** indicates that the initial landscape is read as a map from file. This enables the output of one run to be read in as the initial landscape of another, or for the user to construct any particular initial spatial arrangement.

Initial cover filename: Specify the location (including the path) and filename of the file containing the initial landscape if **File** is chosen as the **Type of initial cover**.

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General

Total initial cover: Specify the total cover of all species combined on the initial landscape. Must be a value between 1-100%. Each species will be distributed in equal abundance on the initial landscape unless a specific initial map is read from [File](#).

Border type: Define whether the landscape borders are [open](#) or [periodic](#). Borders are periodic when the landscape is a [torus](#), i.e. doughnut shaped.

Mean field approximation: Checking this box activates the model to approximate a mean field system, i.e. a homogeneous system without any spatial structure. It effectively simulates constructing the specified model as difference equations. This is achieved by randomising the position of each cell on the landscape between each time step.

Overgrowth rate: Specify the growth rate of any species in growing over any other species as a proportion of the growth rate over free space. This proportion applies to all species. Note that the individual species and neighbour-specific growth rates specified under the [Growth Rates](#) menu override this. For most applications, it is sensible to set this value at 100%.

Probability of disturbance: Define for each cell the probability of a disturbance event that clears a patch on the landscape, centred on that cell, creating empty space. The size of the disturbed area (number of cleared cells) is defined by the [patch size](#). The shape of the the disturbed patch is chosen under [patch type](#), with options of '[square](#)' (a square patch nearest to the specified size) or '[random](#)' (a random shape of contiguous cells).

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General

Probability of influx: If all species have identical recruitment rates, the recruitment rate can be specified here. However, it is more usual to set this parameter at 1 or 0 (specifying that recruitment does or does not occur, respectively), and specify species-specific recruitment rates under the [Recruitment](#) menu.

An **Open** recruitment type specifies that the likelihood of recruitment of any species to an empty cell is independent of the cover of that species on the landscape. Under this choice, when an empty cell is encountered, a species is chosen at random (all species have equal likelihood of being selected), and the likelihood of recruitment of the selected species to the empty cell is given by the recruitment rate of the selected species (see [Recruitment](#) menu).

In specifying a **Closed** recruitment type, when an empty cell is encountered a species is chosen at random from the landscape. The likelihood of recruitment of the selected species to the empty cell is given by the recruitment rate of the selected species (see [Recruitment](#) menu).

These options work for both [single landscapes](#) and metacommunities of [multiple landscapes](#).

Mutation on growth rates: Specify the [probability of a mutation on the growth rate of a new recruit](#). A mutation event will either reduce or increase the growth rate of the recruit (with equal likelihood) by the quantity specified in [Amount](#). Growth rates are whole numbers between 0 and 100, and the magnitude (= [Amount](#)) of mutation must also be specified by a positive whole number.

The growth rate of a new recruit in which no mutation arises is simply that of its 'parent'. For closed recruitment, the growth rate of the 'parent' is determined as the 'genotype' of a randomly selected individual of that species existing on the landscape. For open recruitment, the growth rate is chosen randomly from the range of genotypes that have existed previously in the system for that species.

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General

Mutation on variable outcome: For new recruits, specify the [probability of a mutation on the likelihood of this species winning a competitive interaction](#) with another species *X* by overgrowth. When interaction outcomes are variable, each individual has a unique probability of a win, loss or standoff in interacting with another individual of another species. Mutation acts only on the likelihood of win and loss, decreasing or increasing (with equal probability) the likelihood of winning by the quantity specified in [Amount](#). The likelihood of win, loss and standoff are positive whole numbers and always sum to 100.

Mutation on variable outcome acts independently on the genotypes specifying the outcomes of interactions with different species. Thus, it is possible that mutation may increase (relative to the genotype of its parent) the likelihood of a particular recruit winning an interaction with species *X*, while the likelihood of the same recruit winning an interaction with species *Y* may decrease relative to the genotype of the parent, and the likelihood of winning an interaction with species *Z* may be identical to that of its parent.

If no mutation arises, then the 'genotype' describing the interaction outcomes of a new recruit is that of its 'parent'. For closed recruitment, the interaction outcome 'genotype' of the 'parent' is determined as the 'genotype' of a randomly selected individual of that species existing on the landscape. For open recruitment, the probabilities defining the interaction outcome against every other species is chosen randomly from the range of genotypes that have existed previously in the system for that species.

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Outcome Matrix

Input Outcome Matrix

... on Species in Column ...

Spec.No.	1	2	3	4	5	6
1	x	44,24,32	66,0,34	46,8,46	82,8,10	70,20,10
2	24,44,32	x	73,11,16	83,9,8	78,20,2	20,15,65
3	0,66,34	11,73,16	x	10,7,83	40,23,37	64,16,20
4	8,46,46	9,83,8	7,10,83	x	44,30,26	56,23,21
5	8,82,10	20,78,2	23,40,37	30,44,26	x	57,0,43
6	20,70,10	15,20,65	16,64,20	23,56,21	0,57,43	x

Effect of Species in Row ...

Variable Outcome

Spec.No.	Win	Loss
1	0 - 100	0 - 100
2	0 - 100	0 - 100
3	0 - 100	0 - 100
4	0 - 100	0 - 100
5	0 - 100	0 - 100
6	0 - 100	0 - 100

Reset to All Fixed

Reset

Cancel

Input Outcome

Outcome of interactions between species 2 and species 4

The probability that:

species 2 overgrows species 4 is % [-1 for variable]

species 4 overgrows species 2 is %

there is a standoff between species 2 and 4 is %

OK Cancel

Clicking on a cell in the top triangle of the matrix enables specifying a fixed genotype describing the outcome of interactions between each pair of species. Probabilities of win+loss+standoff must sum to 100.

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Outcome Matrix

Input Outcome Matrix

... on Species in Column ...

Spec.No.	1	2	3	4	5	6
1	x	44,24,32	66,0,34	46,8,46	82,8,10	70,20,10
2	24,44,32	x	73,11,16	83,9,8	78,20,2	20,15,65
3	0,66,34	11,73,16	x	10,7,83	40,23,37	64,16,20
4	8,46,46	9,83,8	7,10,83	x	44,30,26	56,23,21
5	8,82,10	20,78,2	23,40,37	30,44,26	x	57,0,43
6	20,70,10	15,20,65	16,64,20	23,56,21	0,57,43	x

Effect of Species in Row ...

Variable Outcome

Spec No.	Win	Loss
1	0 - 100	0 - 100
2	0 - 100	0 - 100
3	0 - 100	0 - 100
4	0 - 100	0 - 100
5	0 - 100	0 - 100
6	0 - 100	0 - 100

Random Random (hierarchical) Random without reversals Reset to All Variable Reset to All Fixed

Randomising (hierachical) with 0% standoffs

OK Cancel

Preset options for outcomes. [Random](#) determines each probability of win, loss and standoff at random (but constrained such that they sum to 100); [Random \(hierarchical\)](#) also determines each probability at random but with the constraint that the matrix based on the probability of winning describes a hierarchy; [Random without reversals](#) determines each probability of win:loss as 100:0 or 0:100 with equal likelihood; [Reset to All Variable](#) resets all pairwise interactions as having variable outcomes (see next page); [Reset to all fixed](#) resets all probabilities of win:loss:standoff as 0:0:100 and the user can then alter probabilities manually (see previous page).

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Outcome Matrix

Input Outcome Matrix

... on Species in Column ...

Spec.No.	1	2	3	4	5	6
1	x	Variable	Variable	Variable	Variable	Variable
2	Variable	x	Variable	Variable	Variable	Variable
3	Variable	Variable	x	Variable	Variable	Variable
4	Variable	Variable	Variable	x	Variable	Variable
5	Variable	Variable	Variable	Variable	x	Variable
6	Variable	Variable	Variable	Variable	Variable	x

Variable Outcome

Spec No.	Win	Loss
1	50 - 100	0 - 50
2	0 - 50	0 - 100
3	0 - 100	0 - 100
4	60 - 80	0 - 60
5	40 - 60	0 - 80
6	0 - 100	0 - 100

Input Variable Outcome

Variable Outcome for Species: 4

Probability of Winning

From 60 To 80

OK Cancel

Random Random (hierarchy) Fixed Reset

Not randomising

Selecting cells under **Variable Outcome** enables specifying a range of genotypes for the probability that a particular species will win or lose against another. Individuals on the initial landscape are assigned genotypes from this range at random. Combinations of fixed and variable outcomes are permitted. If any outcomes are designated as variable, this must also be specified under the **run control** options.

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Growth Rates

Growth genotypes must take values between 0 and 100.

Specifying values of both a low and high growth rate indicates that growth rate genotypes are variable. Individuals on the initial landscape are assigned growth genotypes selected randomly from this range. Selecting the **Random** button will specify a random range. If variable growth is selected, species-specific rates in overgrowing other species cannot be specified.

Species	Variable range		Rate against given species					
	Low	High	1	2	3	4	5	6
1	0	40	-	-	-	-	-	-
2	88		-	-	22	95	37	43
3	57			64	-			
4	100			56		-		
5	40				31		-	
6	73							-

Fixed rate if High is blank

Defaults to Low if blank. N/A if variable.

OK Cancel Random Reset Not Randomising

This window denotes species-specific growth rates in interactions with different species. If these cells are left blank and no high growth rate is specified, the default of the low growth rate is used to define growth genotypes of all individuals against all other species. Clearly, this matrix is not necessarily symmetrical. In this example, growth of species 2 over species 3 \neq growth of species 3 over 2.

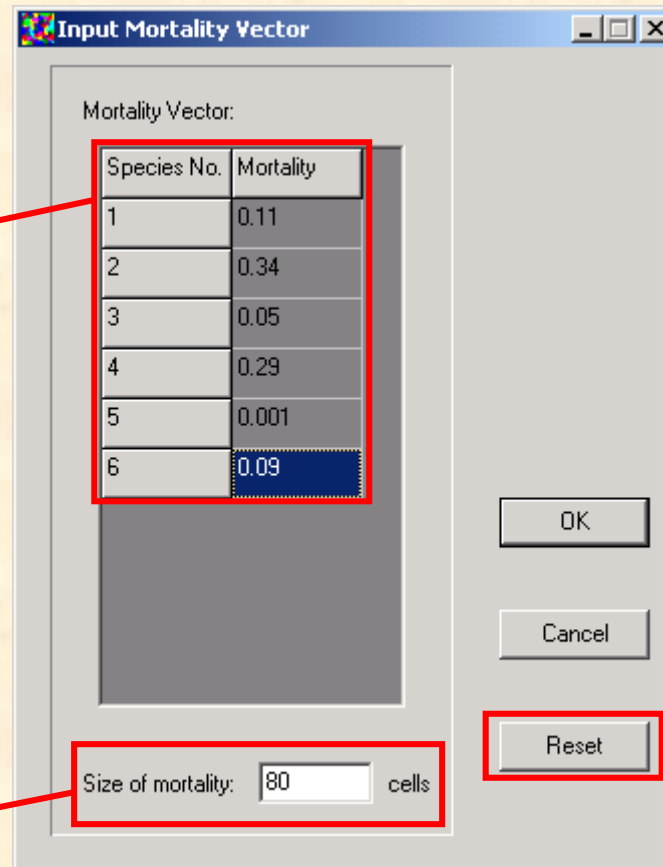
If there is no value for high growth rate, all individuals take the genotype of the low growth rate unless species-specific growth rates are specified in the right-hand matrix..

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Mortality Rates

Mortality rates must take values between 0 and 1.

Specify the mortality rate of each species. It defines the probability of mortality of a single cell occupied by the species indicated.



The dialog box titled "Input Mortality Vector" contains a table for specifying mortality rates for six species. The table has two columns: "Species No." and "Mortality". The values for species 1 through 6 are 0.11, 0.34, 0.05, 0.29, 0.001, and 0.09 respectively. The row for species 6 is highlighted in blue. Below the table is a "Size of mortality:" field with the value "80" and the unit "cells". To the right of the table are three buttons: "OK", "Cancel", and "Reset". The "Reset" button is highlighted with a red box.

Species No.	Mortality
1	0.11
2	0.34
3	0.05
4	0.29
5	0.001
6	0.09

Size of mortality: 80 cells

OK
Cancel
Reset

Resets all mortality rates to zero.

The size of the mortality event specifies the number of contiguous cells that die and revert to bare space in a single mortality event. This provides a (blunt) means to specify size-dependent mortality.

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Recruitment Rates

Recruitment rates must take values between 0 and 1.

Specify the recruitment rate of each species. It defines the probability of recruitment of each species to a single cell that is currently unoccupied.

If recruitment is 'open', a species is selected at random and it recruits to the empty cell with the probability specified.

If recruitment is 'closed', an individual is selected at random *from the existing landscape* and that species then recruits to the empty cell with the probability specified for that species.

More complex options are available for multiple landscapes.

Species No.	Prob Recruit
1	0.34
2	0.67
3	1.00
4	0.08
5	0.25
6	0.66

OK

Cancel

Reset

Resets all recruitment rates to unity.

Note: Recruitment rates specified here apply to both single landscapes and to metacommunities of multiple landscapes.

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Reading and writing parameter settings to / from file

Read From File ... enables reading parameters directly from a saved file. Identify the desired file in the 'browse' window which opens automatically on selecting this option.

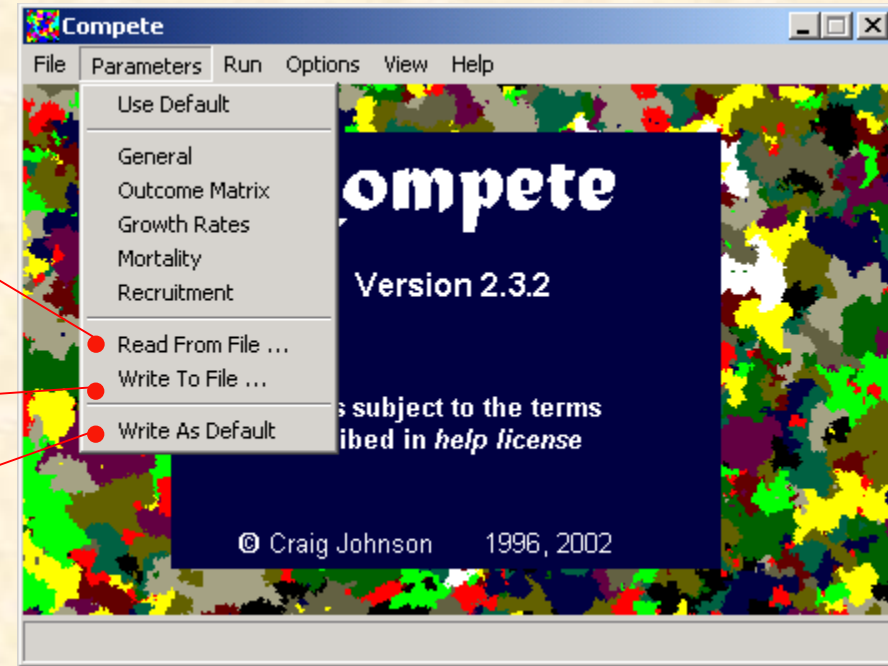
[\[Example of browse window\]](#)

Write To File ... enables saving current parameters by writing to a file. Select the desired location of the file and write its file name in the 'browse' window which opens automatically on selecting this option.

[\[Example of browse window\]](#)

Write As Default

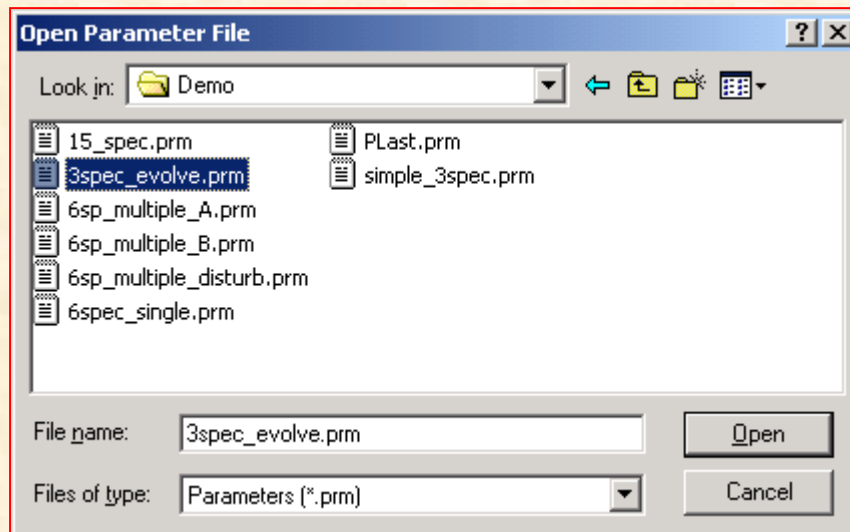
Writes current parameters as the default settings.



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Reading and writing parameter settings to / from file

Read From File ... enables reading parameters directly from a saved file. Identify the desired file in the 'browse' window which opens automatically on selecting this option.



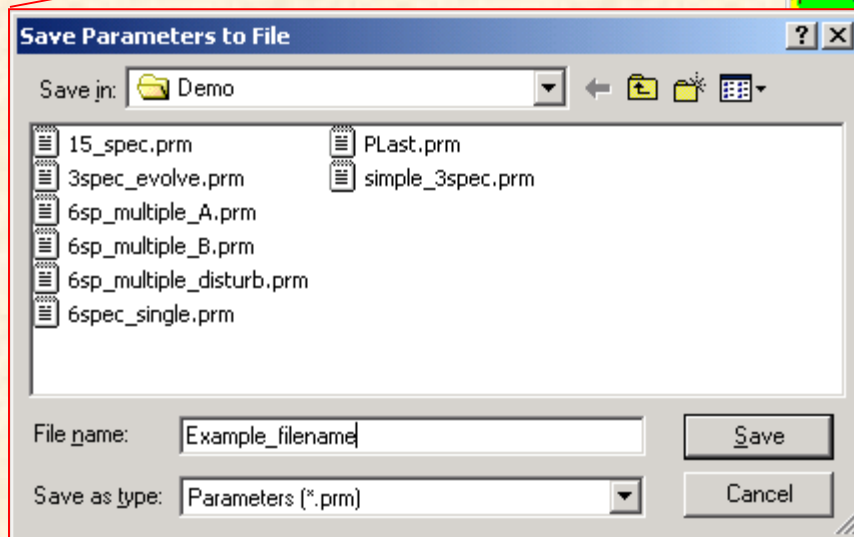
ERASE EXAMPLE

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Reading and writing parameter settings to / from file

Read From File ... enables reading parameters directly from a saved file. Identify the desired file in the 'browse' window which opens automatically on selecting this option.

Write To File ... enables saving current parameters by writing to a file. Select the desired location of the file and write its file name in the 'browse' window which opens automatically on selecting this option.



ERASE EXAMPLE

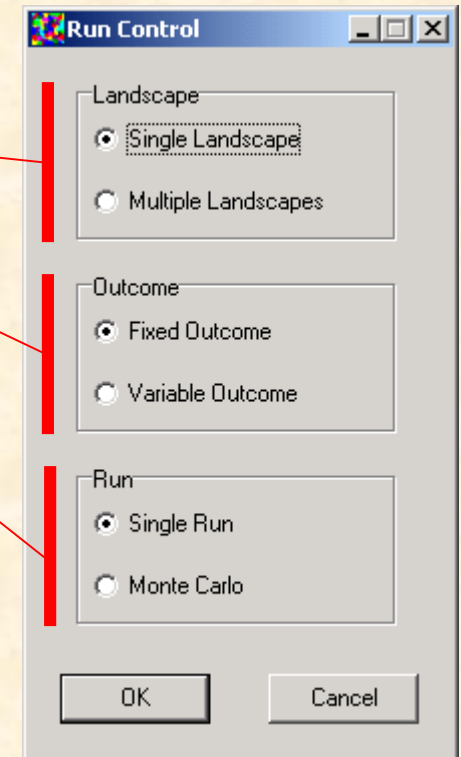
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Run Control Menu

Single vs. multiple landscapes

Fixed vs. variable outcomes

Single run vs. Monte Carlo



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Single vs. multiple landscapes

Selecting [Single Landscape](#) invokes the selected parameters in a single continuous landscape space. All options for run and parameter settings are available for single landscapes.

Selecting [Multiple Landscapes](#) invokes a series of several landscapes connected as a metacommunity. There is no option for running Monte Carlo simulations for multiple landscapes, i.e. single runs are the only options. Selecting this option opens a new window (shown below) in which properties of the metacommunity system, including connectivity, are defined by the user.

The screenshot shows a software window titled "Multiple Landscapes (Single Run)". The window is divided into several sections. On the left, under the heading "Multiple landscapes, Fixed outcome", there is a label "Display landscape every" followed by a text input field containing the number "1" and the word "generations". Below this are two groups of buttons: the first group contains "Start" and "Close" buttons, and the second group contains "Stop", "Continue", and "Reset" buttons. At the bottom left, it displays "Current generation: 0 of total 100" and "Current: Row No. 5 Col No. 5". The right side of the window contains several settings: "Total number of landscapes:" with input fields for "5" Rows and "5" Columns; "Initial distribution of Growth Rates among landscapes: (applies only to variable growth rates)" with a dropdown menu set to "Uniform"; "Output file name for initial growth rates of each landscape:" with an empty text field; "Influx between landscapes" with "Probability:" set to "0.5" and "Time Steps:" set to "100"; and "Influx within a landscape" with "Probability:" set to "0.5".

[Click for more on the window defining metacommunity properties](#)

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Multiple landscapes – defining metacommunity properties

Set frequency of displaying landscapes

Run control buttons

Displays the current generation and the coordinates of the landscape currently being processed

Multiple Landscapes (Single Run)

Multiple landscapes, Fixed outcome

Display landscape every 1 generations

Start Stop

Continue Reset

Close

Current generation: 0 of total 100

Current: Row No. 5 Col No. 5

Total number of landscapes: 5 Rows X 5 Columns

Initial distribution of Growth Rates among landscapes: (applies only to variable growth rates) Uniform

Output file name for initial growth rates of each landscape:

Influx between landscapes

Probability: 0.5

Time Steps: 100

Influx within a landscape

Probability: 0.5

Define the size of the metacommunity as the number of rows and columns of different landscapes.

For variable growth rates, define the initial spatial distribution of growth rates across the metacommunity as uniform (i.e. random), clumped ('clumped' growth rates are allocated randomly among landscapes), or a gradient of growth rates.

Specify the name and path of the file to which a summary of the initial growth rate characteristics of each landscape will be written.

Define the pattern of recruitment to empty cells on landscapes in terms of influx from within and between landscapes. Note that the matrix of landscapes is in a toroidal configuration. In any one timestep, recruitment is of either type, never both. For influx between landscapes, specify the influx rate (= probability) and frequency that propagules move between adjacent landscapes (i.e. every n Time Steps). Thus, every n timesteps, a cell is selected at random from a neighbouring north, south, east or west landscape, and the actual recruitment rate of the selected species to the 'central' landscape is the product of the specific recruitment rate of that species and the influx probability. Influx within landscapes is determined by selecting a cell at random, and the selected species recruits at a rate determined by the product of that species' recruitment rate and the probability of influx within landscapes. Thus, influx within landscapes is a form of closed recruitment.

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Fixed vs. variable outcomes ... single run vs. Monte Carlo

To optimise running time, **Compete** © uses different algorithms for models based on fixed and variable interaction outcomes. It is necessary to specify Variable Outcome in the Run Control window if any pair of species is set up as having varying genotypes specifying their interaction outcomes.

For single landscapes with outcomes fixed by the user, repeated runs of the same model can be made by selecting the **Monte Carlo** option. The repeated runs in the **Monte Carlo** will use identical parameter settings, but differ in values of the initial seed of the pseudo-random number generator. Thus, this option enables exploring stochastic variability in model behaviour. For single landscapes with random outcomes, a different random outcome is selected for each run. This option is not available for multiple landscapes. If the **Monte Carlo** option is selected, a new window will appear prompting the user for additional information about the run (as below).

Monte Carlo

Single landscape, Fixed outcome

Repeat for 200 times

Write result to E:\Compete\Demo\3sp_MC run.dat

Start Stop Close

Currently at 56 of 200 runs

Specify the number of repeat runs.

Specify the name and location of the file to which results of the **Monte Carlo** will be written (a 'browse' window will appear). The results file contains a summary of the parameters and, for each run, the:

- outcome matrix of each run (random outcome options only);
- time at which the first species extinction occurs;
- number of species remaining at the end of the run;
- identity of species remaining at the end of the run;
- percentage of runs with no species extinctions;
- identity and time of each species extinction;
- percentage cover of each species at the end of the run.

Informs the user of the stage of the **Monte Carlo**. Note that to indicate that the **Monte Carlo** is still running, information supplied by the user (i.e. number of runs and file name) appears as grey and not black.

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Output Options Menu

Landscape

Cover

Growth Rate

Space-Time Plot

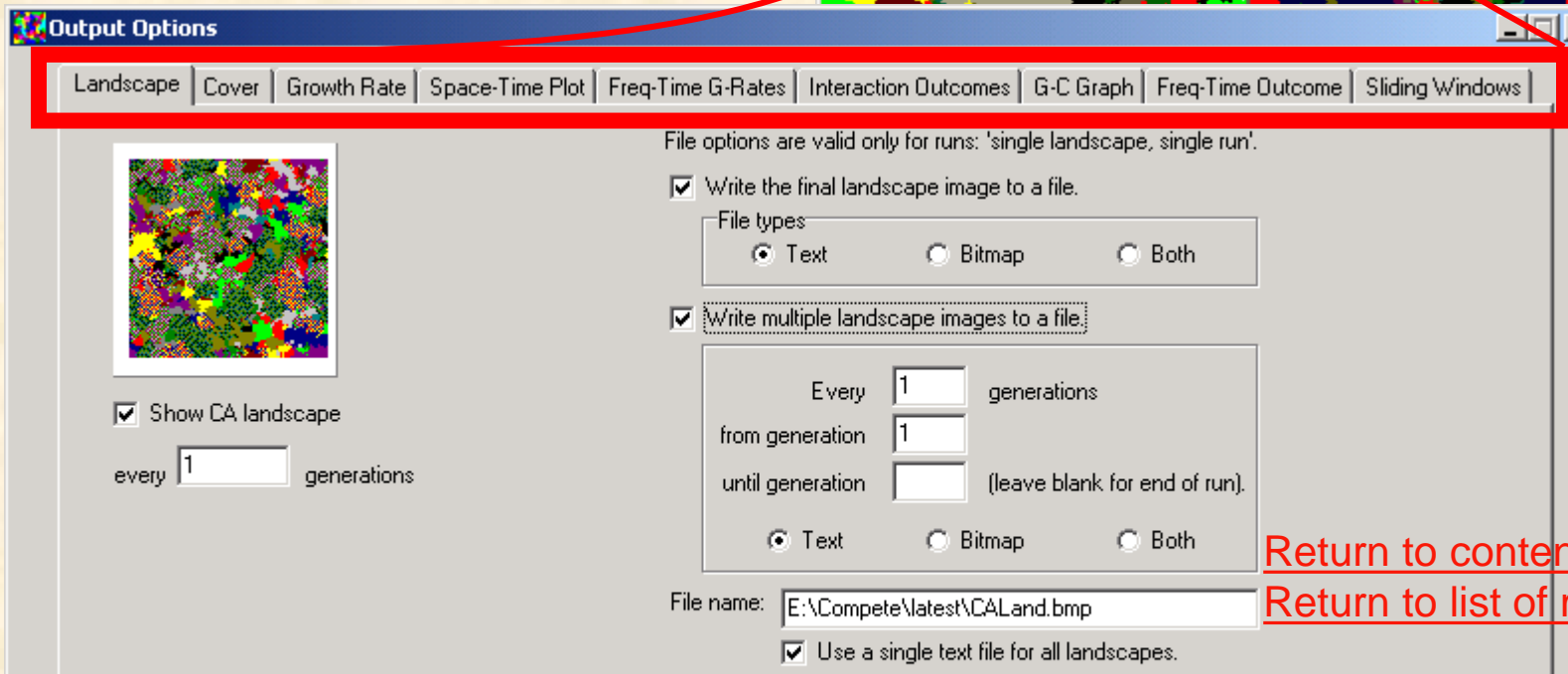
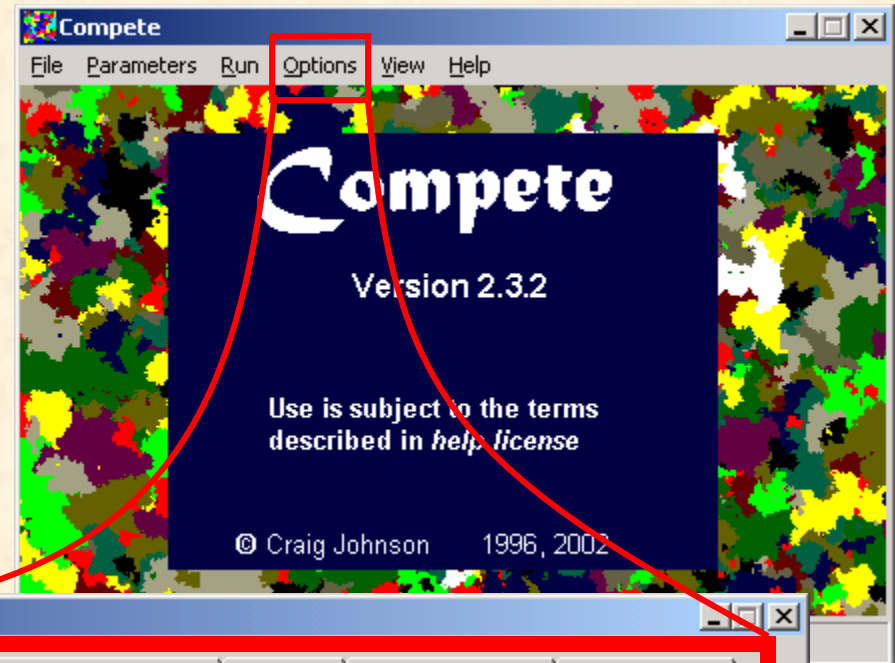
Freq-Time G-Rates

Interaction Outcomes

G-C Graph

Freq-Time Outcome

Sliding Windows



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Landscape: Output options

Select whether to display the landscape (✓) and the frequency of updating the landscape.

Enables saving the final landscape to file as a text file, bitmap or both.

The screenshot shows the 'Output Options' dialog box with several tabs: Landscape, Cover, Growth Rate, Space-Time Plot, Freq-Time G-Rates, Interaction Outcomes, G-C Graph, Freq-Time Outcome, and Sliding Windows. The 'Landscape' tab is selected. On the left, there is a preview window showing a colorful, abstract landscape. Below it, a checkbox labeled 'Show CA landscape' is checked, and a text field labeled 'every' followed by the number '1' and the word 'generations' is present. On the right, a section titled 'File options are valid only for runs: 'single landscape, single run'.' contains two main sections. The first section has a checked checkbox 'Write the final landscape image to a file.' and a 'File types' group box with three radio buttons: 'Text' (selected), 'Bitmap', and 'Both'. The second section has a checked checkbox 'Write multiple landscape images to a file.' and a sub-section with three text fields: 'Every' followed by '1' and 'generations', 'from generation' followed by '1', and 'until generation' followed by a blank field and the text '(leave blank for end of run)'. Below these fields are three radio buttons: 'Text' (selected), 'Bitmap', and 'Both'. At the bottom of this section is a 'File name:' label followed by a text field containing 'E:\Compete\latest\CALand.bmp' and a checked checkbox 'Use a single text file for all landscapes.' At the bottom of the dialog box are three buttons: 'Default', 'OK', and 'Cancel'.

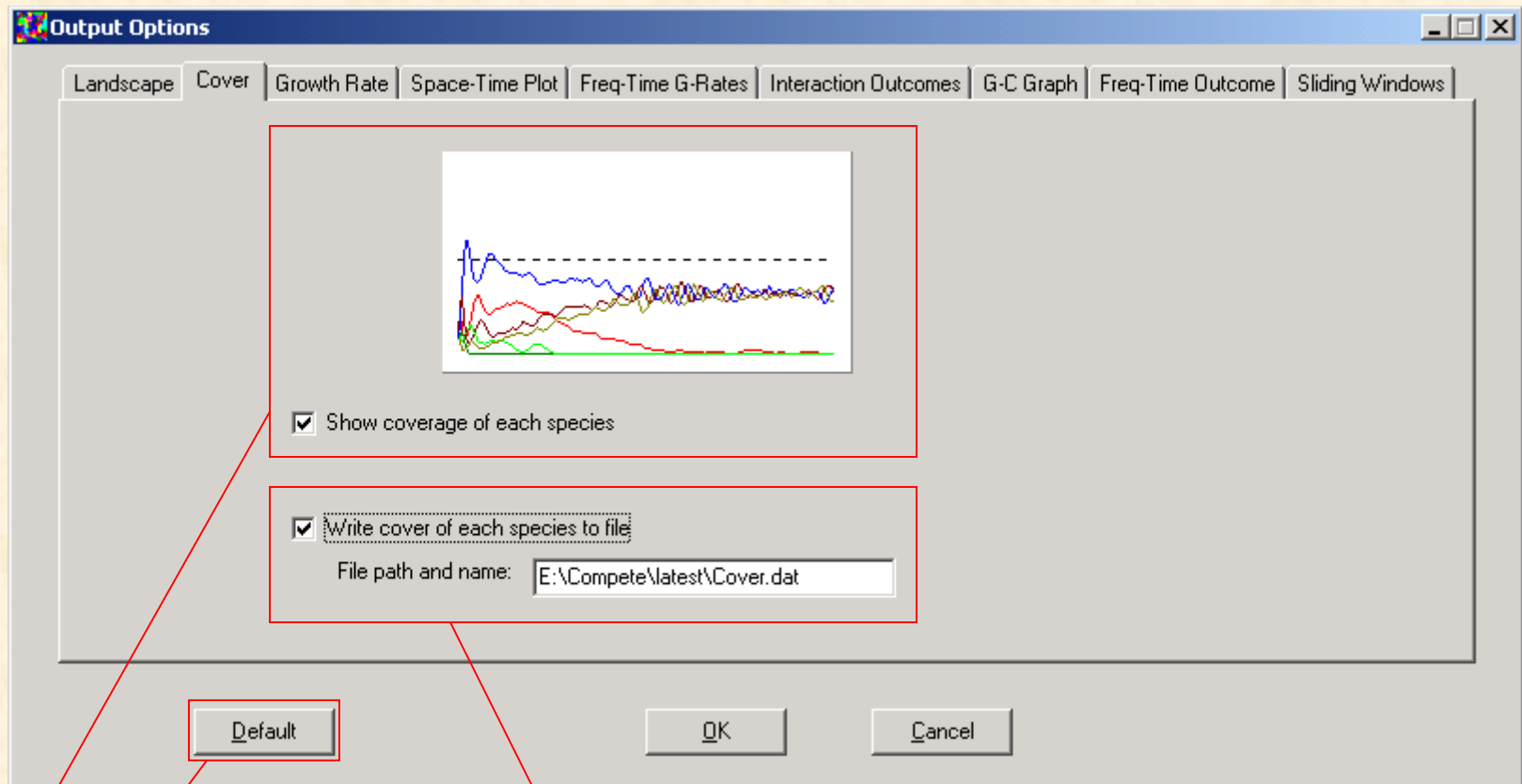
Saves settings as **Default**.

Enables saving multiple images of the landscape to file as a text file, bitmap or both. Specify the frequency to save images and the interval over which images will be saved.

Specify the location of saved files (clicking this area will trigger appearance of a 'browse' box') and whether to save landscapes to a single file (✓). If the latter option is not checked, each landscape will be written to a separate file in a numbered series.

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Total cover of each species: Output options



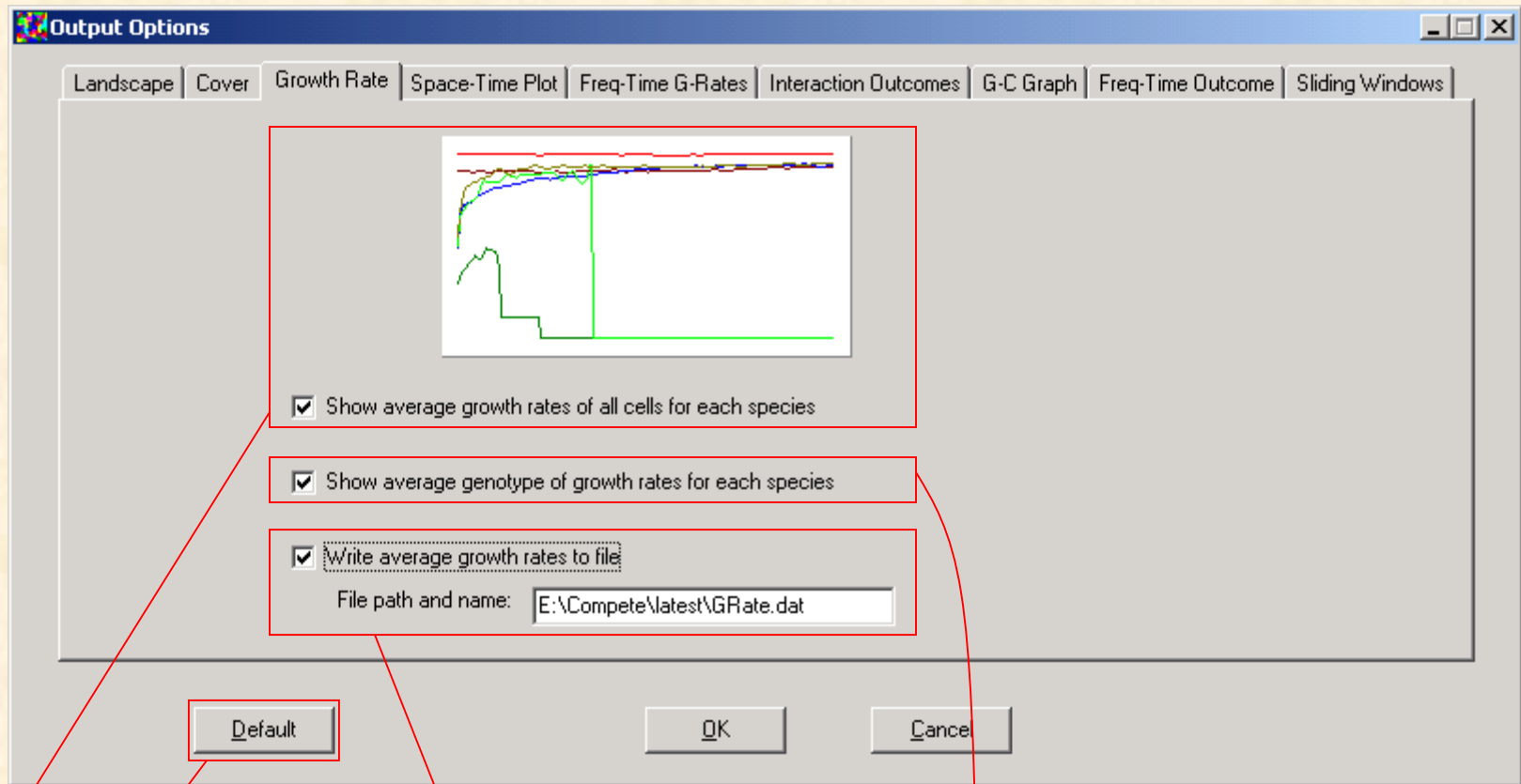
- Select (✓) to graphically display percentage cover of each species on screen.

- Saves settings as **Default**.

- Select (✓) to record to file the temporal changes in percentage cover of each species. Specify the location to save the file (clicking this area will trigger appearance of a 'browse' box').

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Growth rates of each species: Output options



• Saves settings as **Default**.

• Select (✓) to graphically display the mean growth rate of each species on screen (calculated as the mean across all individuals on the landscape)

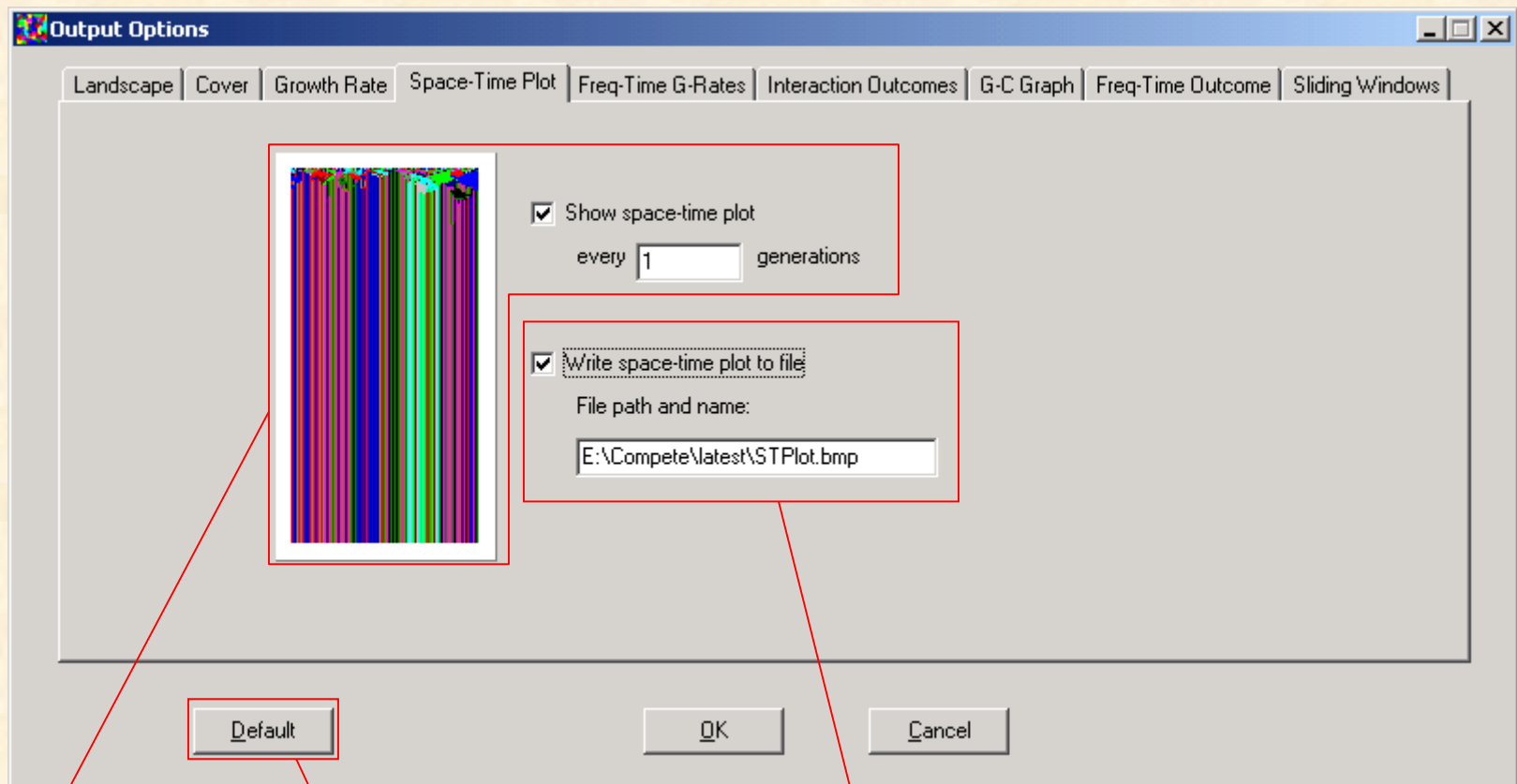
• Select (✓) to record to file the temporal changes in mean growth rate (labelled file#1) and mean growth rate genotype (labelled file #2) of each species. Specify the location to save the files (clicking this area will trigger appearance of a 'browse' box').

• Select (✓) to graphically display the mean growth rate genotype of each species on screen. This is the mean of all genotypes existing on the landscape ignoring their abundance.

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Space-Time plot: Output options

The Space-Time plot samples a 'slice' through the middle of the landscape (= space on the x-axis) and plots it successively through time (= time on the y-axis). It is a useful means to visualise spatial self-organisation.



- Select (✓) to display the Space-Time plot, and specify the frequency (= every n^{th} timestep) of plotting.

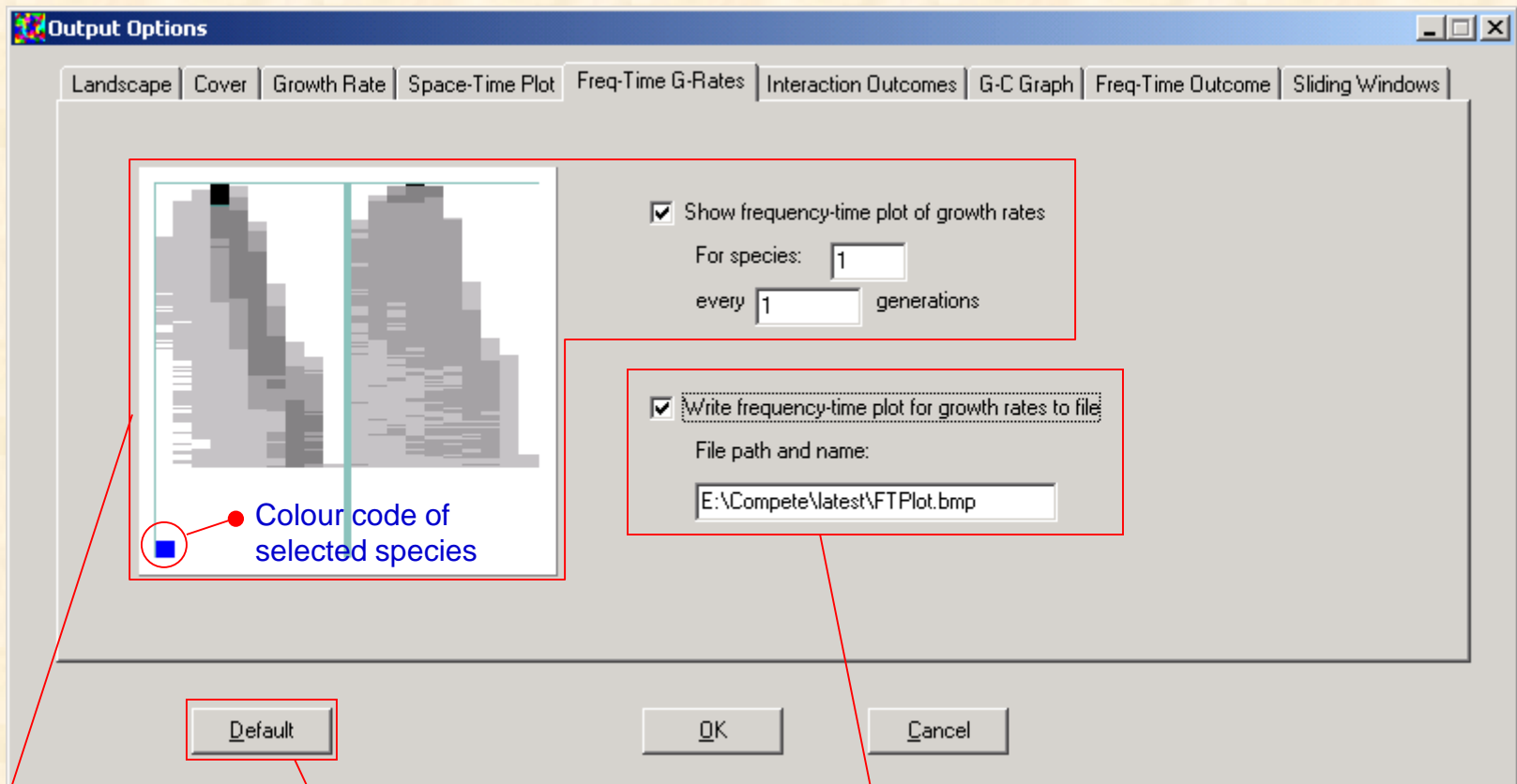
- Saves settings as **Default**.

- Select (✓) to record **Space-Time** plot to file as a bitmap. Specify the location to save the file (clicking this area will trigger appearance of a 'browse' box').

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Frequency-Time plot of growth rate genotypes: Output options

This plot shows temporal changes in the frequency of growth-rate genotypes for a selected species. Growth rate is shown on the x-axis (0-100 in 10 class intervals) and time on the y-axis. Frequency is indicated by the intensity of the grey-scale (white = 0; black = 100). The left graph depicts absolute frequencies of growth rates of all individuals on the landscape (i.e. is weighted by the number of individuals with particular genotypes). The right graph depicts the 'binary' frequency of genotypes, i.e. it scores the occurrence of a genotype but ignores the total number of individuals with that genotype.



- Select (✓) to display the **Freq-Time G-Rate** plot, and specify the species and frequency of plotting.

- Saves settings as **Default**.

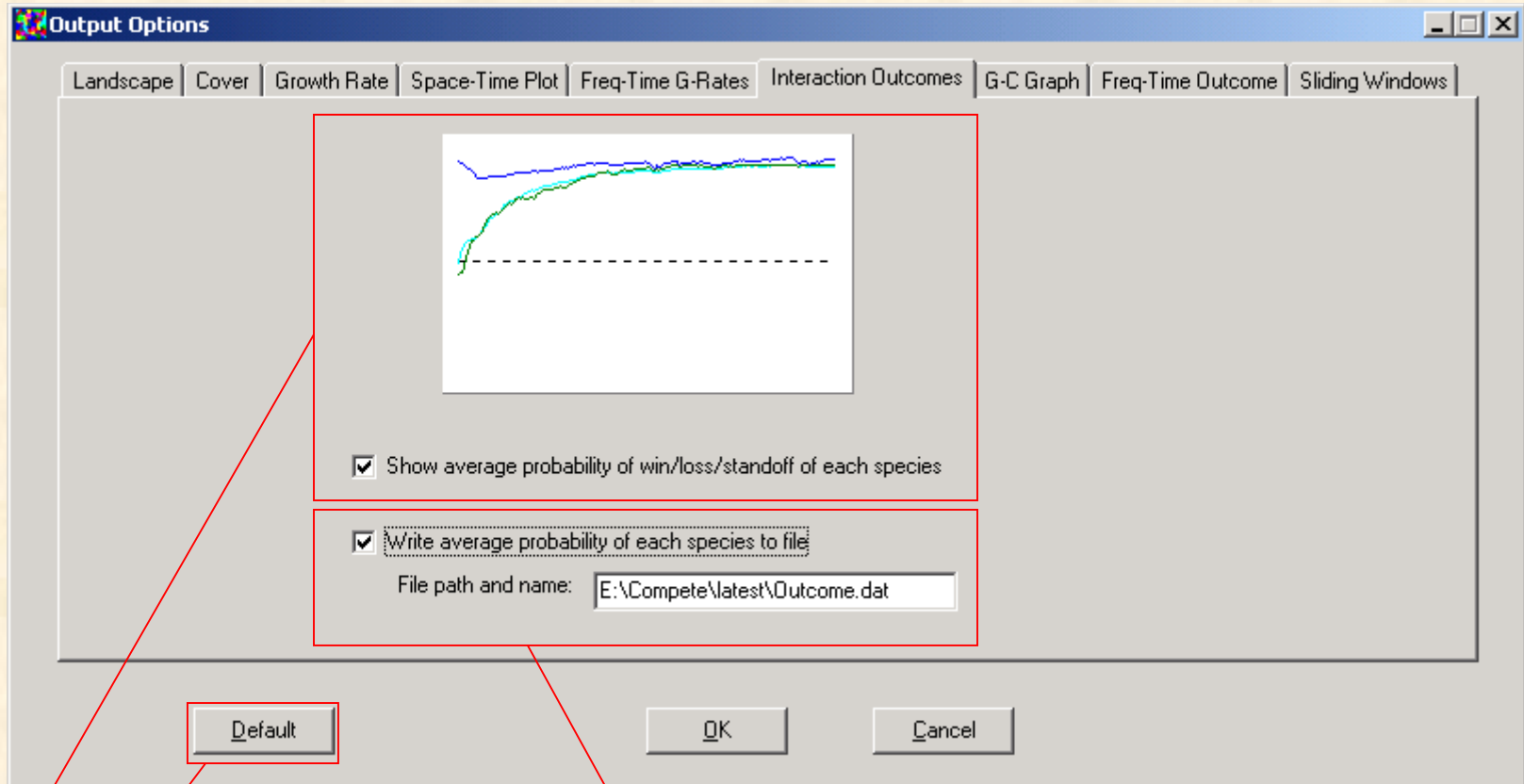
- Select (✓) to record **Freq-Time G-Rate** plot to file as a bitmap. Specify the location to save the file (clicking this area will trigger appearance of a 'browse' box').

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Probabilities of Interaction Outcomes for each species: Output options



- Saves settings as **Default**.

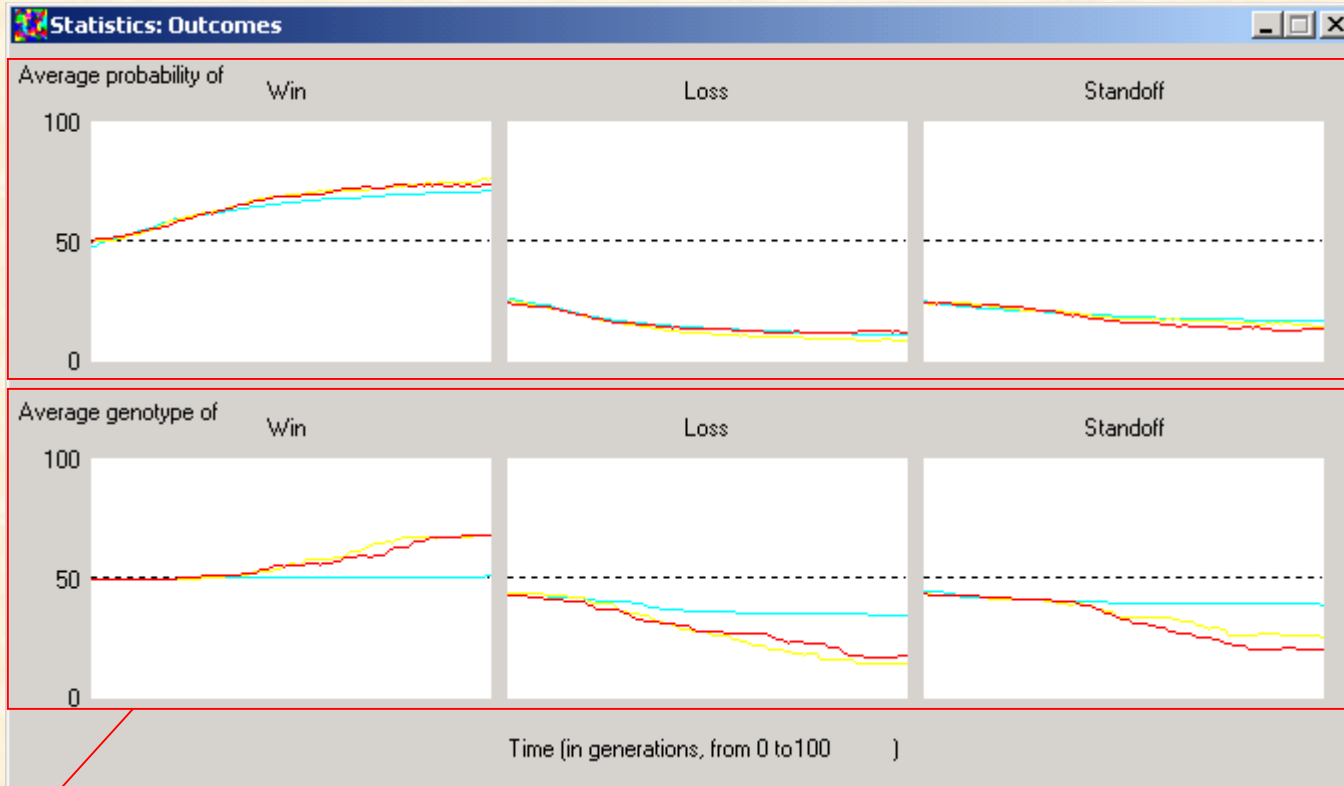
Select (✓) to display on screen the temporal change in the average probabilities of win, loss and standoff of each species against all others for which the outcome is variable (see [NOTE](#)). This option provides graphs of both '[absolute averages](#)' and (binary) '[genotype averages](#)'. Note that species with fixed outcomes against all others show as zero.

- Select (✓) to record to file the temporal changes in the mean probability of each species realising a win, loss or standoff against each other species. Two files are produced, one for the '[absolute average](#)' of outcomes of all individuals of each species against all others on the landscape (File Type #1), and one for the mean (binary) '[genotype frequency](#)' (File Type #2) in which the number of individuals with each genotype is ignored. Specify the location to save the file (clicking this area will trigger appearance of a 'browse' box').

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Example: Graphs of Interaction Outcomes

In these plots, the x-axis shows time (in generations), and the y-axis is mean probability.



These graphs show the mean probability of win, loss and standoff of each species against all other species combined, weighted by the number of individuals carrying each genotype. The calculation is performed only for those interactions that have a variable outcome (see [NOTE](#)). The mean is calculated from all individuals of each species on the landscape. Each colour is for a different species.

NOTE: To obtain 'absolute means' for interaction outcomes of each species against every other species separately, choose 'write to file' under the [Output Options for Interaction Outcomes](#).

These graphs show the unweighted mean genotype of the probability of win, loss and standoff of each species against all other species combined. This mean considers only the presence and absence of genotypes, and so is not influenced by how many individuals on the landscape have a particular genotype. Each colour is for a different species. The calculation is performed only for those interactions that have a variable outcome (see [NOTE](#)). To obtain 'genotype means' for interaction outcomes of each species against every other species separately, choose 'write to file' under the [Output Options for Interaction Outcomes](#).

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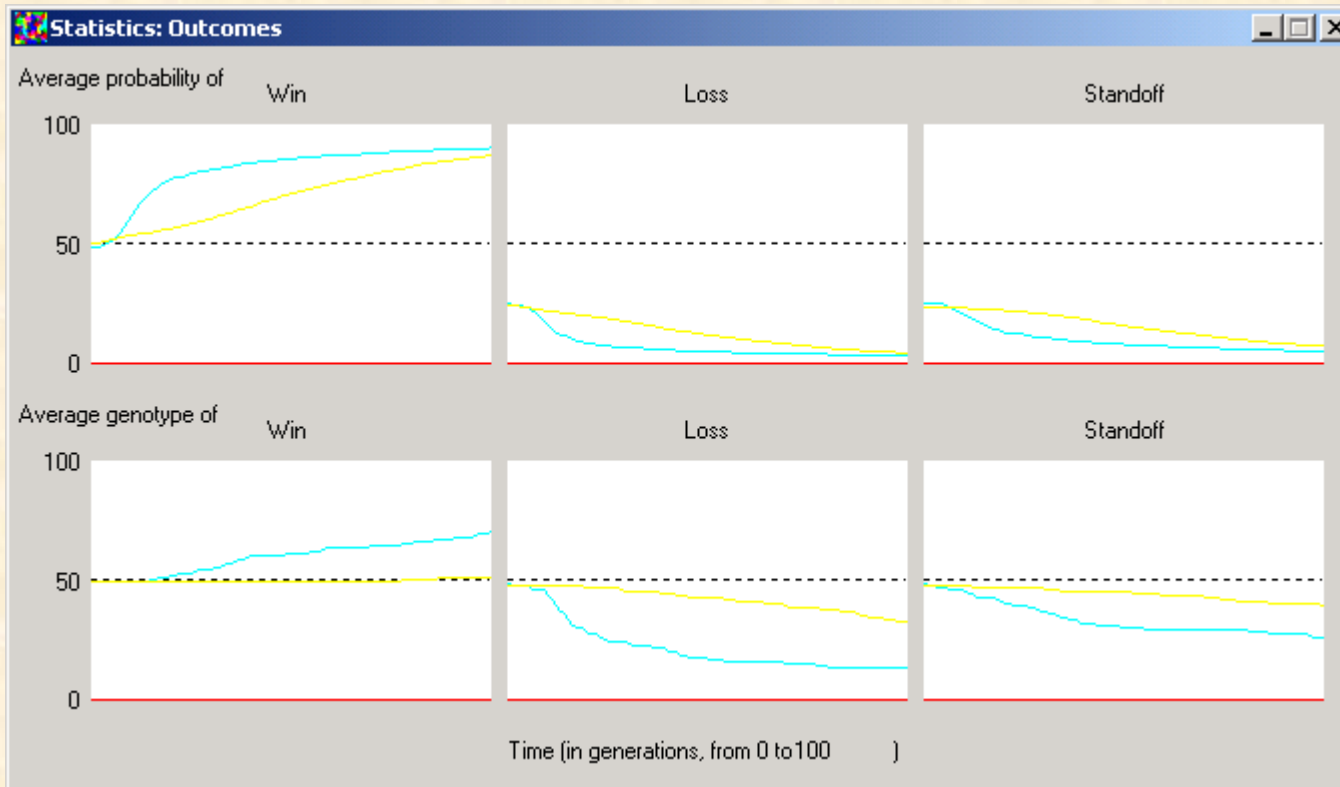
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NOTES on Probabilities of Interaction Outcomes for each species

- Average probabilities of win, loss and standoff of each species are calculated against all other species for which interaction outcomes have a variable component. Thus, if S1 vs. S2 is variable but S1 vs. S3 and S2 vs. S3 are fixed, in producing the statistics for S1 only the interaction of S1 with S2 is considered, and for S2 only the interaction with S1 is considered.
- Species with fixed outcomes of either win or loss against all other species are ignored in calculations, and on the graphs these species are shown as zero.



In the example output on the left, the probability of S1 (blue) winning over S2 (yellow) is set to variable (initially between 1 and 100%); while S2 has a 100% probability of overgrowing S3 (red); and S3 has a 100% probability of overgrowing S1. S3 is shown as zero since its relationship with S1 and S2 is fixed. Genotype frequencies of the outcome of S1 interacting with S2 change through time as selection acts; the same must therefore be true of S2. Wins for S2 are those against S1 only since the interaction of S2 with S3 is fixed.

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Files recording details of Interaction Outcomes

Two types of files are produced when the option to save data to file is selected. They are labelled as [filename1.dat](#) (Type #1 files) and [filename2.dat](#) (Type #2 files), and contain information about mean outcomes of each species against every other species combined, and against every other species separately.

For each species, Type #1 files summarise mean probabilities of win, loss and standoff calculated as the mean of all individuals of that species on the landscape at the specified timestep.

Type #2 files summarise mean probabilities of win, loss and standoff calculated as the mean of all different genotypes that exist on the landscape at the specified timestep, but ignoring that several individuals may have the same genotype. Thus, this mean considers only the presence and absence of different genotypes, and is not influenced by how many individuals on the landscape have a particular genotype.

Basic parameters of the run are recorded at the beginning of both types of file. For examples and an explanation of the file format, click on either:

[Type #1 file](#) OR [Type #2 file](#)

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Files recording details of Interaction Outcomes: Example of Type #1 file

Average Probabilities of Species (Normal)									
Gen No.	1			2			3		
	Win	Loss	S/O	Win	Loss	S/O	Win	Loss	S/O
0	48.7	25.8	25.5	50.3	25.0	24.7	50.3	24.8	25.0
1	48.6	26.2	25.2	50.6	25.2	24.2	51.3	24.1	24.6

Generation 1

Speci specj win loss stand-off

1 1 -1.0 -1.0 -1.0

1 2 45.8 27.5 26.7

1 3 51.4 24.9 23.7

2 1 47.7 25.5 26.8

2 2 -1.0 -1.0 -1.0

2 3 53.5 25.0 21.6

3 1 51.7 23.1 25.2

3 2 50.9 25.2 23.9

3 3 -1.0 -1.0 -1.0

2 50.0 25.5 24.5 51.2 24.8 24.0 51.8 23.8 24.4

3 50.0 25.4 24.6 51.1 24.6 24.4 51.9 23.8 24.3

4 51.3 24.8 23.9 51.1 24.4 24.4 51.8 23.6 24.6

5 ... etc.

Heading .. 'Normal' indicates absolute average where means are calculated on the basis of all individuals.

Species identification.

Average probabilities of win, loss and standoff of each species against ALL other species with which that species interacts and for which the interaction outcomes are set to 'variable' (i.e. fixed outcomes are ignored).

For generation 1, and every 100 generations thereafter, the mean genotype of the probability of win, loss and stand-off of every species against each other species separately is given (means are based on variable interaction outcomes only).

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Files recording details of Interaction Outcomes: Example of Type #2 file

Average Probabilities of Species (Genotype)

	1			2			3		
Gen No.	Win	Loss	S/O	Win	Loss	S/O	Win	Loss	S/O
0	50.0	49.5	50.0	50.0	49.5	49.5	50.0	49.5	49.5
1	50.0	49.5	50.0	50.0	49.5	49.5	50.0	49.5	49.5

Generation 1

specI specJ win loss stand-off

1	1	-1.0	-1.0	-1.0
1	2	50.0	48.6	49.1
1	3	50.0	47.6	49.0
2	1	50.0	47.6	48.2
2	2	-1.0	-1.0	-1.0
2	3	50.0	49.5	49.0
3	1	50.0	49.0	49.0
3	2	50.0	48.6	48.5
3	3	-1.0	-1.0	-1.0

2	50.0	49.5	50.0	50.0	49.5	49.5	50.0	49.5	49.5
3	50.0	49.5	50.0	50.0	49.5	49.5	50.0	49.5	49.5
4	50.0	49.5	50.0	50.0	49.5	49.5	50.0	49.5	49.5

5 ... etc.

Heading .. 'Genotype' indicates averages are calculated from all different genotypes present, but where the number of individuals of each genotype is not considered.

Species identification.

Average 'genotype' of win, loss and standoff of each species against ALL other species with which that species interacts and for which the interaction outcomes are set to 'variable' (i.e. fixed outcomes are ignored). Only different genotypes are considered in calculating these averages, and the number of individuals of each genotype is ignored.

For generation 1, and every 100 generations thereafter, the mean genotype of the probability of win, loss and stand-off of every species (*i*) against each other species (*j*) is given separately (means are based on variable interaction outcomes only, and are based only on the different genotypes present and not the number of individuals that possess a particular genotype).

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G-C plot: Output options

This plot shows the distribution of growth and outcome genotypes for a selected species at the beginning and end of the run. Thus, these graphs enable examining the joint evolution of growth and outcome genotypes. Outcome genotypes give the probability of winning, and are for the selected species over other nominated competitors. Two types of graph are shown: the Competitive Graph shows the overall mean growth and outcomes against all other species with variable outcomes; 'Competitive Graph A' gives results against each species separately.

- Select (✓) to display the **Growth Rate-Competition Outcome plots**. Specify the 'winning' (=overgrowing) and competitor species of interest and frequency of plotting. If "against species" = 0, then graphs are produced for every species.

• Saves settings as **Default**.

• Select (✓) to record **Growth Rate-Competition Outcomes** data to **file**. Specify the location to save the file (clicking this area will trigger appearance of a 'browse' box').

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Selection on growth rate and competitiveness: description of plots

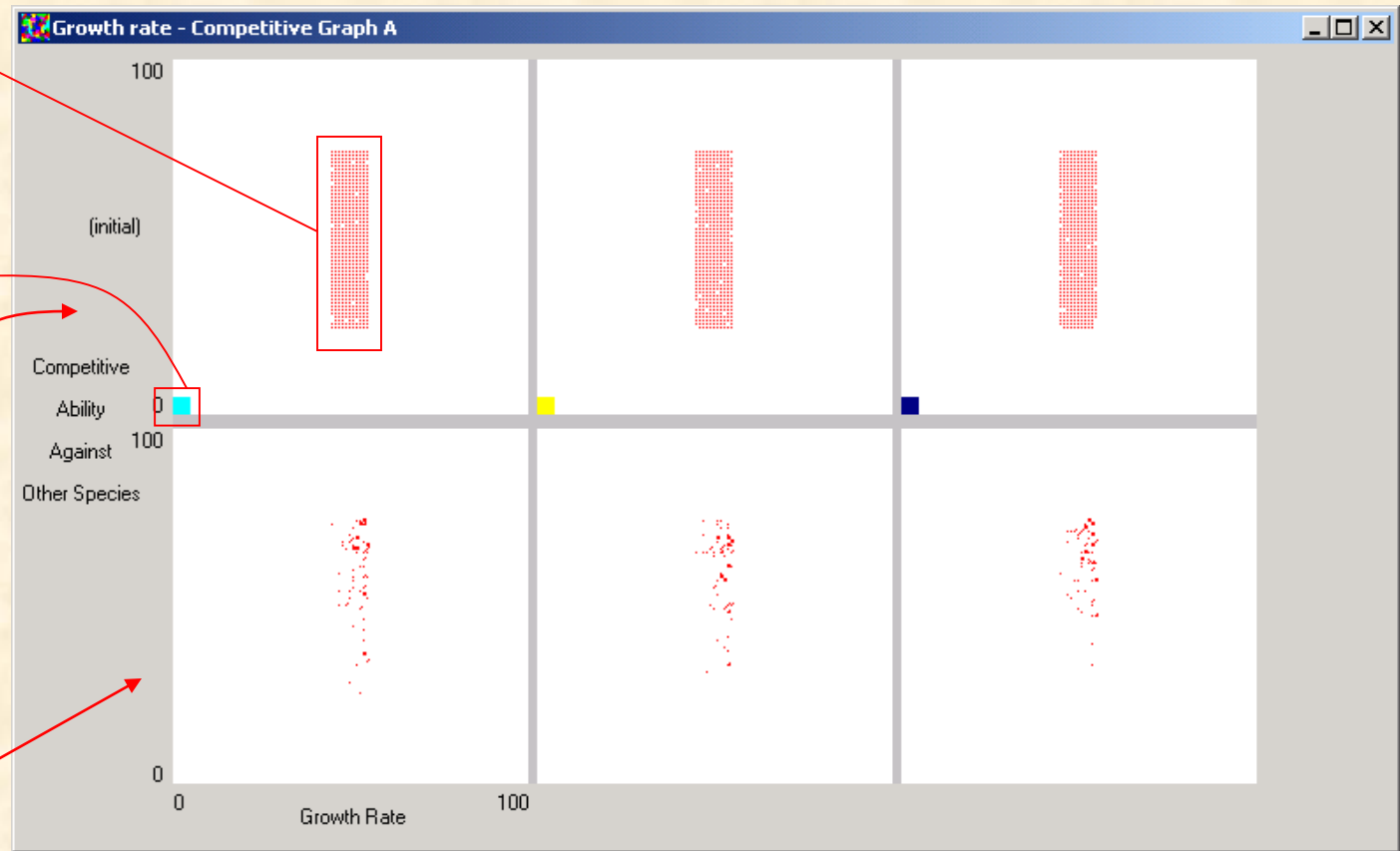
Two plots are produced. 'Competitive Graph A' (shown here) summarises the initial and final distribution of growth rate and competitiveness genotypes of the nominated species against all others separately (if 'against species' is selected as zero). The size of the points indicates relative frequency. The selected species is indicated by the colour of the points on the graph (view colour map to see colour code of each species). The identity of competitor species is indicated by the colour of small squares in the bottom left corner of the upper figures in the 'Competitive Graph A' window. The second plot shows the pooled result of the selected species of interest against all others.

Identity of species of interest is indicated by the colour of the points

Identity of competitor species is indicated by the colour of the square in the bottom left corner

Distribution of genotypes at generation = 0

Distribution of genotypes after the last generation of the run



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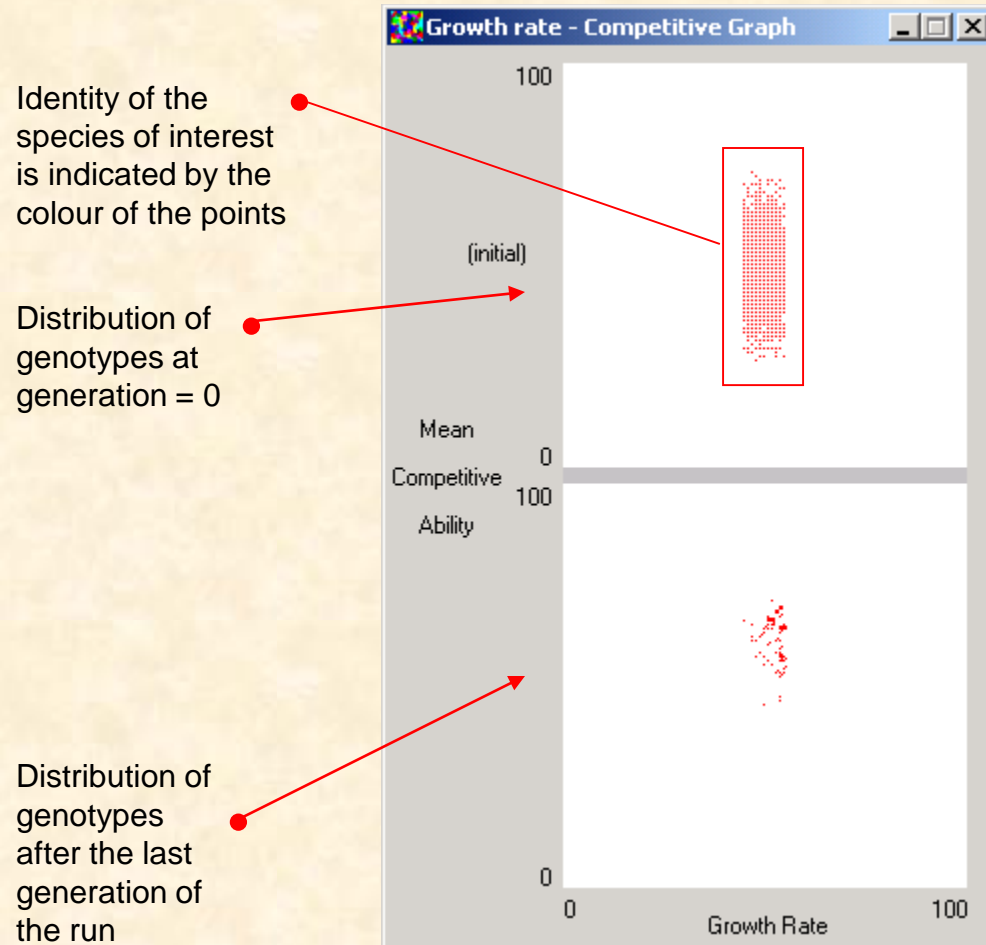
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Selection on growth rate and competitiveness: description of plots

Two plots are produced. The second, shown here, summarises the collective initial and final distribution of growth rate and 'competitiveness' genotypes across all other species simultaneously. The size of the points indicates relative frequency. The selected species is indicated by the colour of the points on the graph.



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Selection on growth rate and competitiveness: format of output file

This first part of the file contains a summary of the parameters used to generate the file. The body of the file contains information on all growth rate-competitiveness genotypes and their frequency at each nominated n^{th} timestep of the model:

Identity of the species of interest, i.e. the 'overgrowing' species.

Growth Rate -- Competitive

For species: 1

G-Rates Competitive(win) Number of Cells

Gen = 0

0	42	1
0	45	1
0	82	1
0	87	1
1	18	1
1	30	1
1	35	1
1	42	2

... etc.

Generation number. Data are recorded for generation 0 and then every n^{th} generation as specified on the [output options form](#).

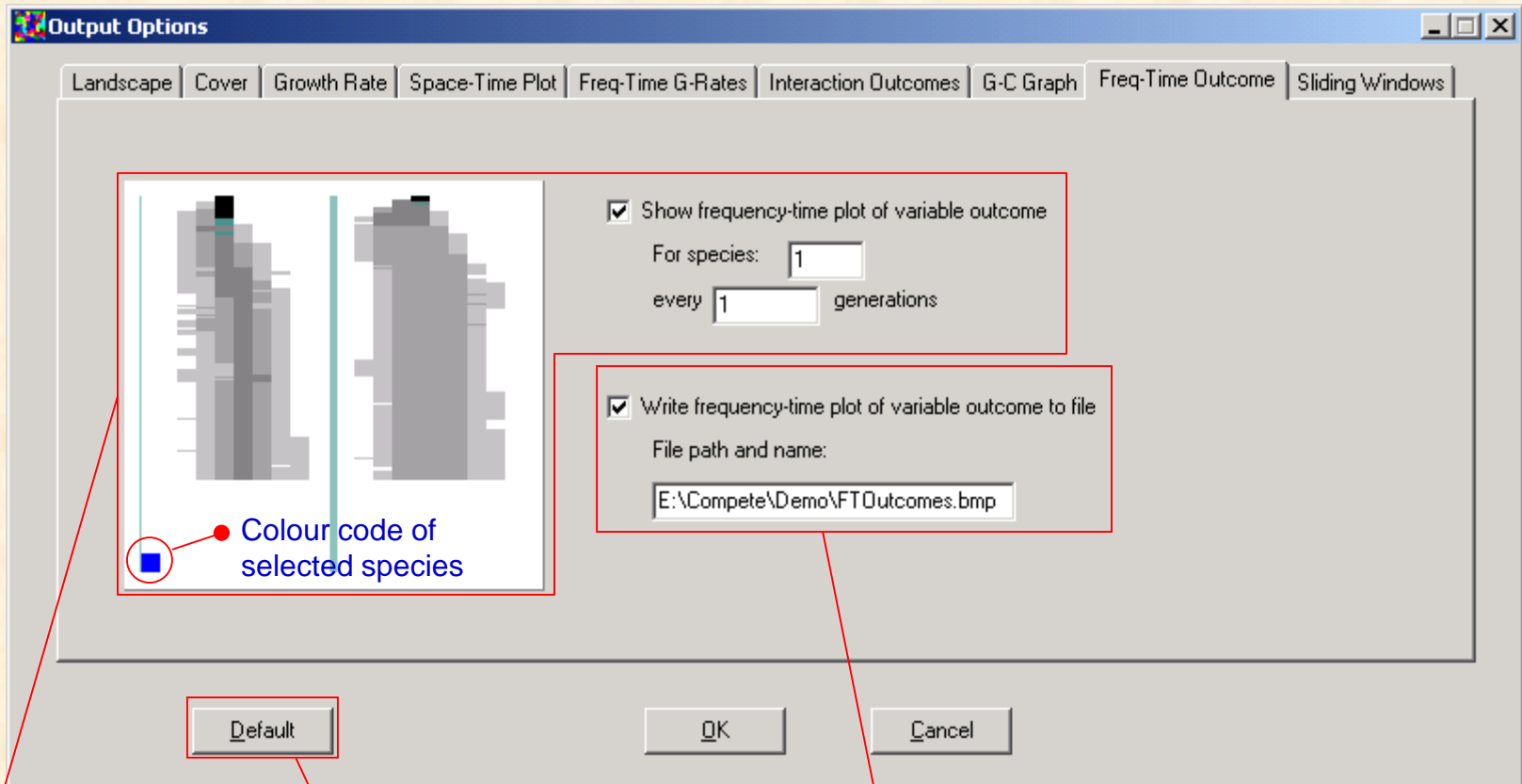
Data. In this example, at generation = 0 there is one cell on the landscape with growth = 0 and probability of winning against the nominated competitor = 0.42 (first line); and there are 2 cells on the landscape with growth = 1 and probability of winning against the nominated competitor = 0.42 (last line shown in this example).

Column headings indicating that the 3 columns record the growth genotype (col 1), competitiveness genotype (= probability of winning over the nominated competitive species) (col 2), and the frequency of this particular genotype combination on the landscape at the designated timestep (col 3).

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Frequency-Time plot of outcome genotypes: Output options

This plot shows temporal changes in the frequency of 'outcome' genotypes for a selected species. The probability of winning against all other species for whom the interaction outcome is 'variable' is shown on the x-axis (0-100 in 10 class intervals) and time on the y-axis. Frequency is indicated by the intensity of the grey-scale (white = 0; black = 100). The left graph depicts absolute frequencies of 'win' genotypes of all individuals on the landscape. The right graph depicts the 'binary' frequency of genotypes, i.e. it scores the occurrence of a genotype but ignores the total number of individuals with that genotype.



- Select (✓) to display the **Freq-Time Outcome** plot, and specify the species and frequency of plotting.

• Saves settings as **Default**.

- Select (✓) to record **Freq-Time Outcome** plot to file as a bitmap. Specify the location to save the file (clicking this area will trigger appearance of a 'browse' box').

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'Sliding Windows': Output options

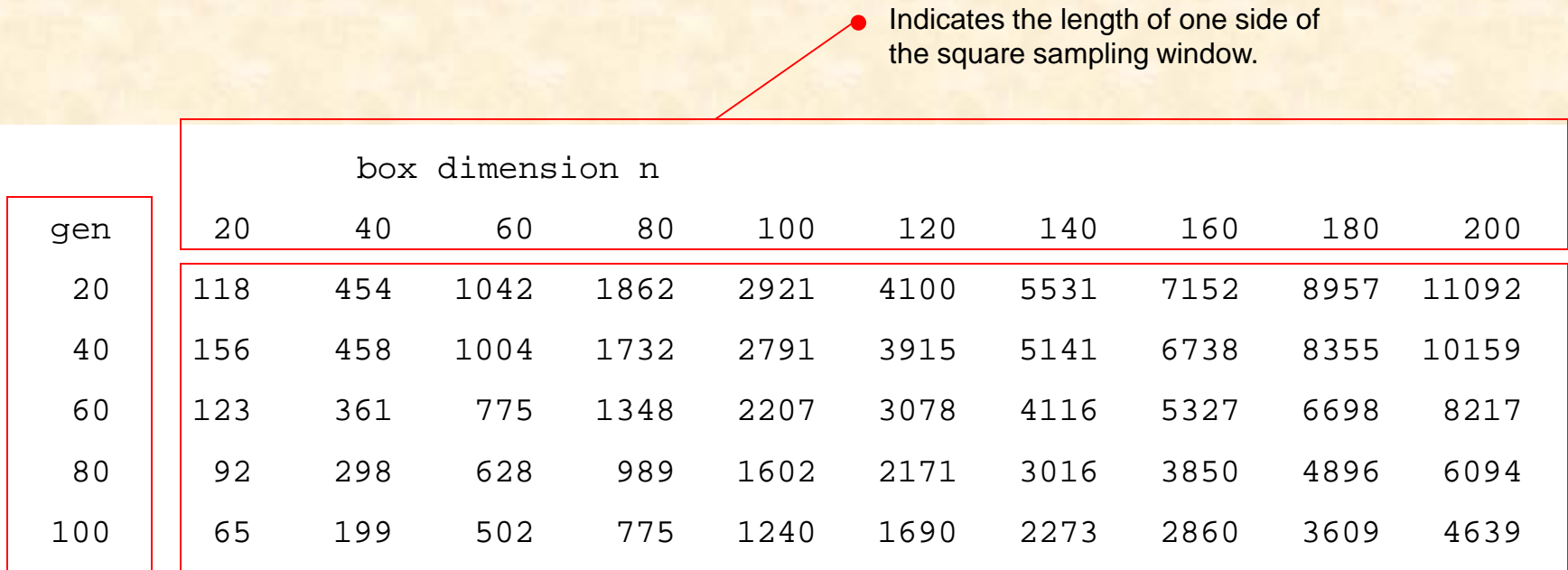
'Sliding Windows' enables sampling any species through time using square 'windows' of a range of sizes. It is a useful feature to produce a range of scale-dependent variance spectra. One corner of the sampling window is always in the top left corner of the landscape, and the steps in window size (= length increment of one side of the window) are determined by the user.

- Select (✓) to write results of 'Sliding Windows' sampling to file. Specify the sampling frequency (A), sampling interval (B), length increment of the sampling window (C), and location to save the file (D) (clicking this area will trigger appearance of a 'browse' box'). A separate file is created for each species selected ([click here for example](#)).

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'Sliding Windows': Example of output file

A separate output file is created for each species selected (or for unoccupied space, if this option is selected). For each selected species, the file presents a count of the total population of that species in specified 'window' sizes at specified generations:



gen	box dimension n									
	20	40	60	80	100	120	140	160	180	200
20	118	454	1042	1862	2921	4100	5531	7152	8957	11092
40	156	458	1004	1732	2791	3915	5141	6738	8355	10159
60	123	361	775	1348	2207	3078	4116	5327	6698	8217
80	92	298	628	989	1602	2171	3016	3850	4896	6094
100	65	199	502	775	1240	1690	2273	2860	3609	4639

Indicates the generation (timestep) at which census of selected species is taken.

Population size of selected species in sampling window (box) of specified dimensions at specified generation.

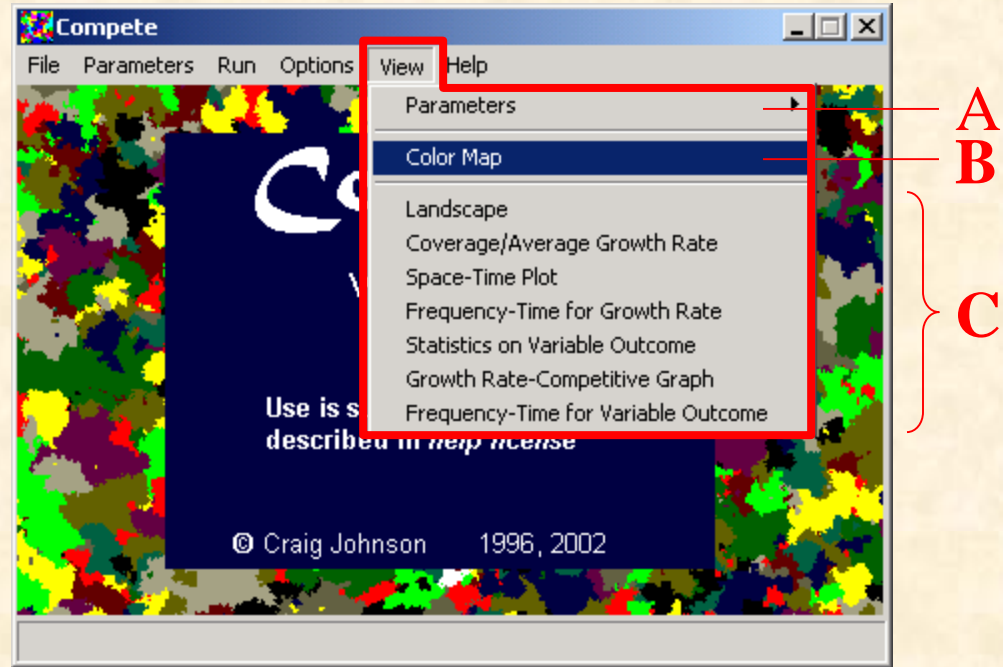
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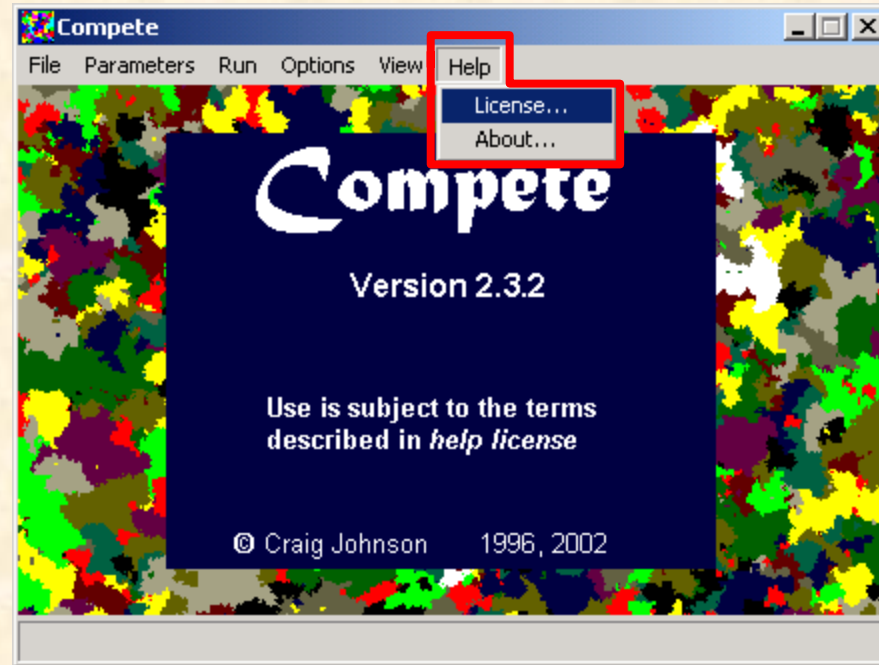
View Menu



The View Menu enables:

- A. Viewing any of the parameter settings during a run.
- B. Displaying a 'colour map' depicting the colour code of each species.
- C. Bringing to the 'front' any output window that has been activated under the output options, or reactivating an output window that was originally activated under output options but then closed.

Help



The Help Menu displays the License Agreement (under *License ...*), and the version number and contact details of the author (under *About ...*).