

User's Guide for

Genetics Construction Kit

A BioQUEST Collection Simulation Module
(version 1.0.3)

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What is Genetics Construction Kit?

Genetics Construction Kit (GCK) is a simulation of a classical genetics laboratory. It provides you with a set of organisms with unknown patterns of inheritance, and gives you the tools to design and perform an experimental strategy to discover these inheritance patterns. You will be able to cross the unknown organisms and analyze your crosses in ways much like those used by practicing scientists. GCK is not meant to replace work with real organisms. But the constraints of time, space, money, and unskilled laboratory technique -- important parts of real scientific research -- make it practically impossible for most students to experience the excitement and challenge of a real research problem. GCK can give you the chance to work with problems that have the real surprise and real complexity that make scientific research a fascinating activity. We have tried in this program to let you tackle realistic problems in a way similar to that used in real scientific research. You or your instructor however, can set up GCK so you can start with a limited set of genetic phenomena and add new material as your understanding grows.

A Tour of Genetics Construction Kit

Starting the Program

To start the program, double click on the GCK program icon (see Figure 1).



Figure 1. The GCK Program Icon

The next thing you see will probably be a list of problems such as that shown in figure 2. The names of the problems will probably be different. If you don't see a list of problems, your copy of GCK only contains a single problem. It has started that problem, and you can skip the next section on how to choose a problem. If you do not see a display similar to that in Figure 2 or Figure 3, something is not working. Try looking at the end of this manual in **It Doesn't Work!** for some suggestions.

Choosing a Problem

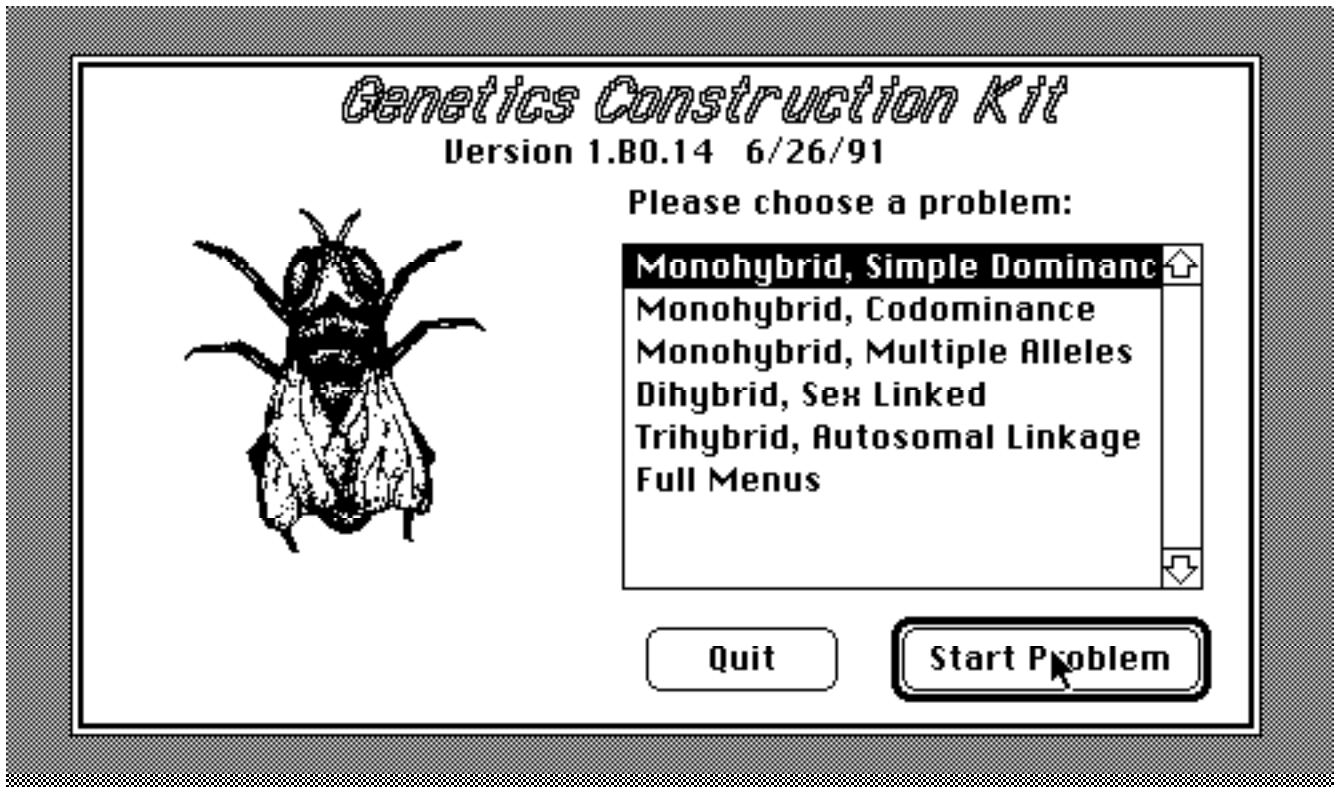


Figure 2. Selecting a GCK Problem¹

To choose a problem, click on it to highlight it in black (like **1 Trait, Simple Dominance** in Figure 2), then click on *Start Problem*.

If you click on the button labeled *Quit* instead of *Start Problem*, GCK will stop running.

¹If you don't see a picture of a fruit fly but have a set of buttons displayed instead, you have a customizable copy of the program that allows you to create your own problems. For the moment, ignore this difference and continue with the tutorial. The section of the manual entitled **Designing Your Own Problems** discusses how to customize the program.

Looking at the Field Population

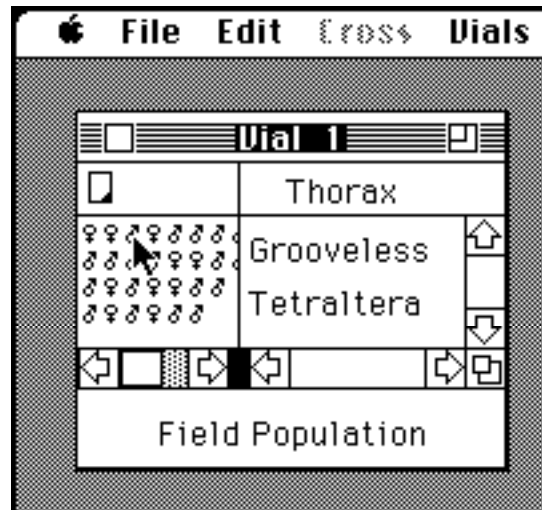


Figure 3. The initial display of a GCK problem

A GCK problem always starts like this (Figure 3), with a vial of organisms of unknown genetic constitution. The initial vial is labeled *Field Population* to remind you that these organisms may be considered to have been collected at random. They are not the result of a mating between two parents.

Your problem will not look exactly like this. This particular vial contains a number of organisms that differ in one trait, the thorax. Your problem may involve more than one trait, a different trait, or different variations.

Grooveless and tetralterra are the names of two thorax variations in real fruit flies. For our purposes right now, it does not matter what a tetralterra thorax actually looks like². Bear in mind, however, that although the names used here may be the names of the traits of a real organism, the way they are inherited will almost certainly be different. The genetics of the organisms used by GCK vary from problem to problem.

On the left there is a set of male and female symbols. Remember that ♂ is the standard symbol for a male and ♀ is the standard female symbol. Each of these symbols represents a unique individual with its own, distinct genotype.

The first two rows of organisms in Figure 3 have a grooveless thorax and the second two rows have a tetralterra thorax. The arrow is shown over a male with

²If you are curious you might want to consult a drosophila manual. Most commercial suppliers of fruit flies have these.

a grooveless thorax. If you click on a trait variation name, a dotted line will be drawn around the organisms with that variation. Figure 4 is an example of this.

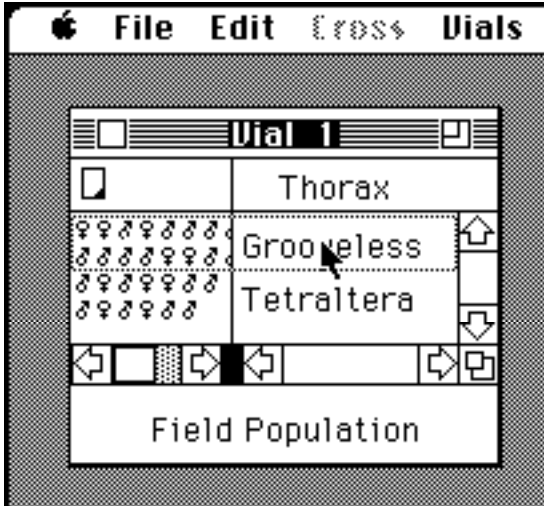


Figure 4. The dotted line shows that the first two rows of organisms are Grooveless

Doing a Cross

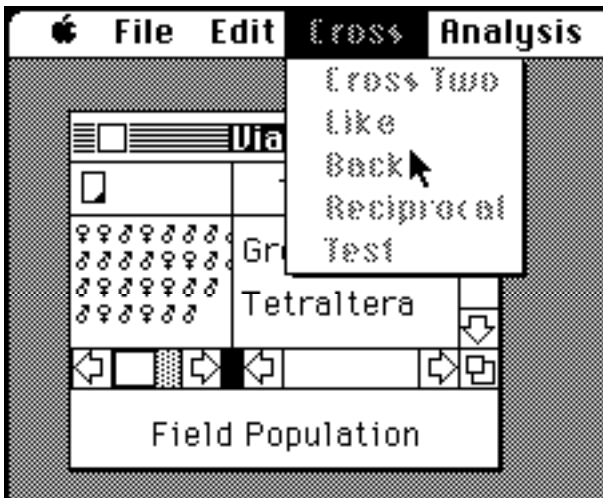


Figure 5. The GCK Cross menu

Get Some Help

In Figure 5 the **Cross** menu has been pulled down. You can see that the cross menu itself and all of the menu items are gray. A menu is gray if all of its items are gray, and a menu item is gray if it won't do anything. A gray menu or menu

item is usually called inactive. While the entire cross menu may not be gray in your problem, some of the individual items on the cross menu will be gray.

In GCK, if you try to choose an inactive menu item, you will be shown a short message explaining why the item is inactive and how to make it active.

To try this, pull-down the **Cross** menu and try to choose the *Cross Two* menu item.

When you release the button, a window like that in Figure 6 will appear. To see the remaining text, move the mouse pointer over the downward pointing arrow and click. To dismiss the help message, click in the window's close box.

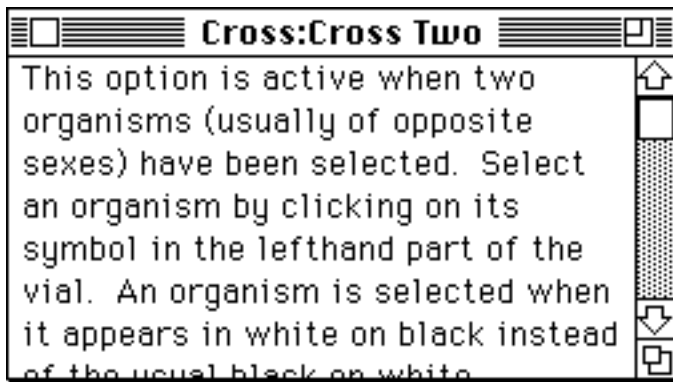


Figure 6. A message explaining why *Cross Two* is gray.

This message tells us that we need to select two organisms of opposite sexes before we can do a *Cross Two* cross .

Select the Organisms to Cross

To select the two organisms you want to cross, move the mouse pointer over an organism, and click. That organism will be selected. A selected organism is highlighted in black. In Figure 7, the third organism in the first row (a male) is selected. To select a second organism, you need to hold down the shift key on your keyboard while you click on the second organism.

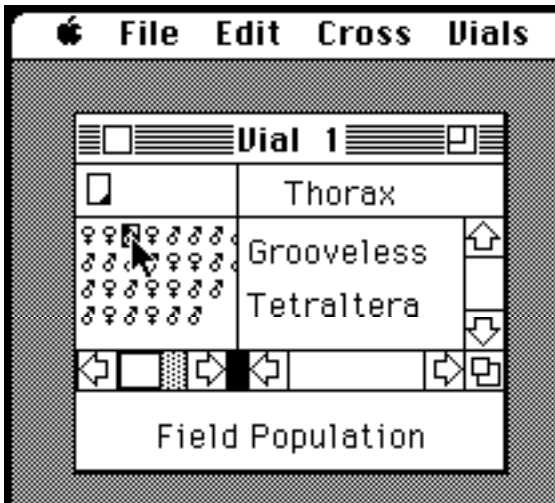


Figure 7. Selecting an organism

Choose *Cross Two*

After you have chosen and selected two individuals, pull-down the **Cross** menu and choose *Cross Two*. If you have selected two individuals of the same sex, or if you don't have two individuals selected, *Cross Two* will be gray to indicate that it is not possible. In this case, select two organisms of the opposite sex and try again.

Look at the Progeny

When you have crossed two individuals, a vial of progeny will be produced. This vial will be assigned the next number in the sequence of vials and placed in the next space on the screen. The sex and phenotype of the parents of each vial are recorded in a space at the bottom of every vial (note that vial 1 has no parents). Figure 8 shows vial 1 and vial 2. As you can see, the phenotypes of vial 2's parents are recorded at the bottom. The number preceding each parent is the number of the vial the parent came from. In this case both parents came from vial 1.

The two sex symbols that you see highlighted in Figure 8 represent the same individual, once in its home vial and once as a parent in vial 2. Clicking on either one will highlight them both. If the same organism is a parent in more than one vial it will be highlighted everywhere it appears. This is a convenient way to tell exactly which individuals have been used in which crosses.

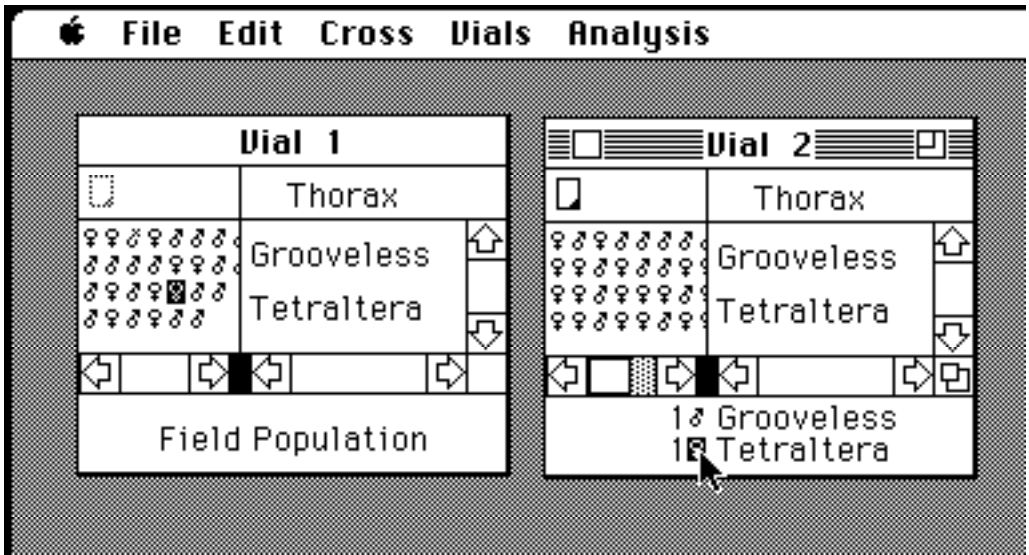


Figure 8. The results of the cross. The female parent of vial 2 has been selected.

Look at All the Progeny

If you click in a vial's zoom box, in the upper righthand corner, the vial will expand so as to display all of the organisms it contains. Figure 9 shows vial 2 after it has been zoomed in this way. To return the vial to its former size, click in the zoom box a second time.

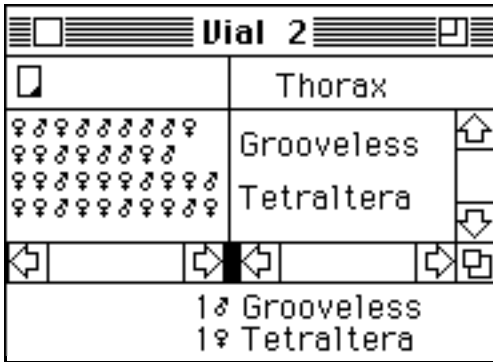


Figure 9. Vial 2 zoomed so that all progeny are visible.

Summarizing the Vial

Instead of counting each of the symbols in vial 2 to find the ratio of Tetraltera to Grooveless organisms, you can have the computer do the counting for you. Select the vial you want to summarize (in this case, vial 2) by clicking once on the vial title. The title will be displayed on a black background when a vial is selected. Then, choose the *Summary Chart* option from the **Analysis** menu. A window similar to that shown in Figure 10 will appear.

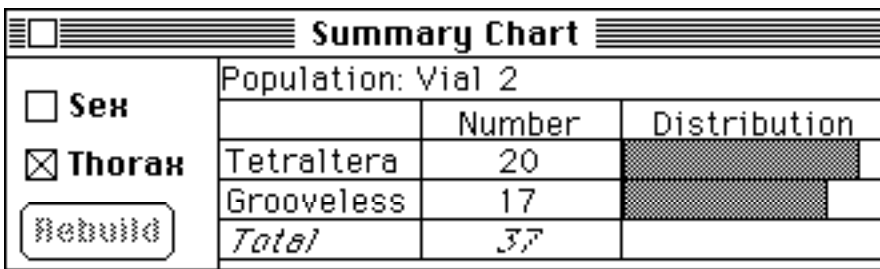


Figure 10. A vial summary for the Thorax trait

This summary shows the ratio between Tetraltera and Grooveless, two variations of the Thorax trait. If you want to look at the ratio between the sexes instead, click in the box to the left of *Sex* to mark it, click in the box to the left of *Thorax* to unmark it, and click on the *Rebuild* button to rebuild the summary chart to show the ratio between the sexes. At least one box must always be marked, so you cannot remove the mark on *Thorax* before you mark *Sex*.

Quitting

This is the end of the tour of Genetics Construction Kit. If you want to quit at this point, you can do so by choosing the *Quit* item from the **File** menu. If you have done any crossing, you will be asked if you want to save your work. If you decide not to quit after all, click on the *Cancel* button. If you save your work, the section in the reference section entitled **Opening a Saved Problem** will tell you how to restore the problem to where you left it.

If you want to look at Genetics Construction Kit in more detail, read the **Reference** section.

Reference

Controlling Vials

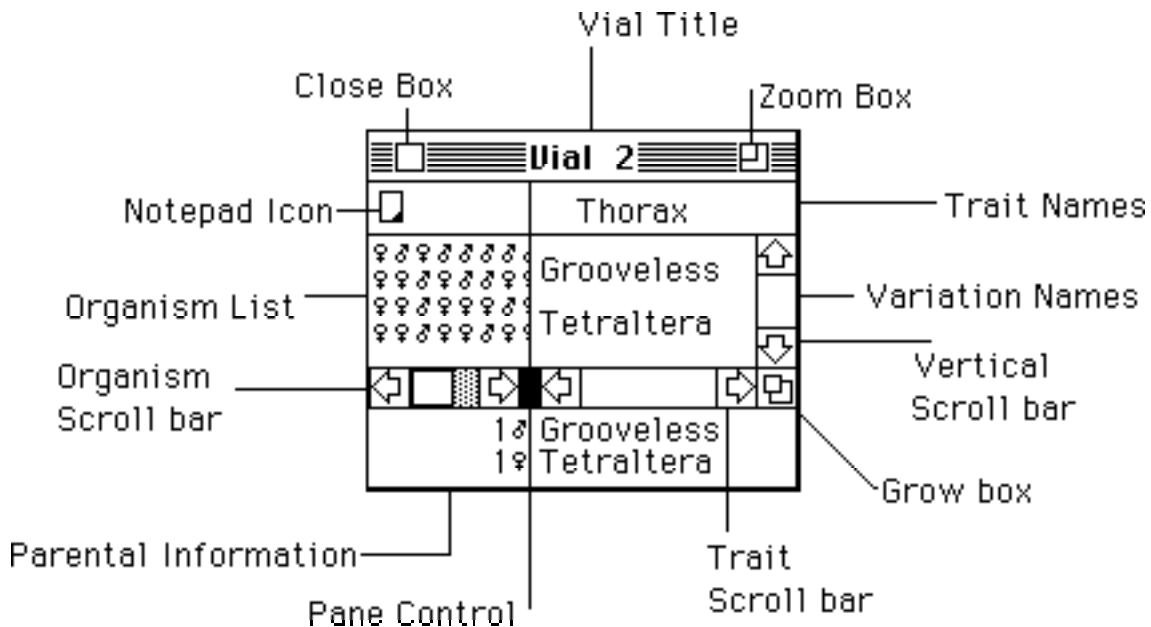


Figure 11. The parts of a vial

Selecting a Vial

Before you can perform an operation on the contents of a vial or a series of vials, you need to select it. Selection is necessary if you want, for example, to destroy vials, summarize them, or perform a chi squared test on their population.

Note that a selected vial may or may not be the frontmost or active vial. There is always only one frontmost window, but there may be one or many selected vials.

The easiest way to select a vial is to click once on its title. Clicking a second time will unselect the vial. A selected vial's title is printed on a black background. An unselected vial's title is printed on a white background. The vial shown in Figure 12 is selected.

To select more than one vial, hold down the shift key while clicking on subsequent vials. This is useful when you want to clump the populations of several vials together and summarize them, or to do a chi squared test.

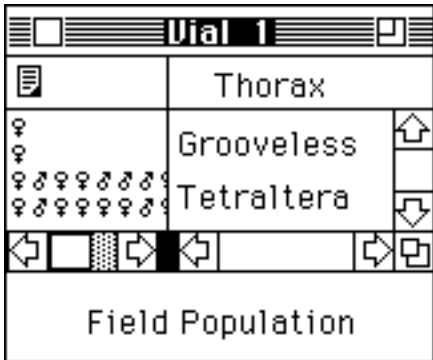


Figure 12. A selected vial

Changing Vial Size and Shape

Closing a Vial

When you have many vials on the screen, it is convenient to reduce some of them to miniature form so that you can put them out of the way. If you move the mouse pointer over the *close box*, in the upper left corner (see Figure 11), and click, the vial will shrink down to icon form. Figure 13 is a picture of a vial in icon form. When you want to re-open a vial in icon form, click twice in quick succession on the icon.

Note that it is not necessary for a vial to be open for you to select it. Select a vial in icon form by clicking anywhere on the icon.



Figure 13. A vial in icon form

Zooming a Vial

If you click in the zoom box, in the upper right corner (see figure 11), the vial will enlarge to display its entire contents. Clicking in the same place again will shrink it back to its former size and position.

Resizing a Vial

To change the size or shape of a vial, press the mouse pointer over the *grow box*, in the lower right corner (see Figure 11) and, while holding the mouse button down, move the mouse. Move the mouse down to make the vial taller, and move it to the right to make the vial wider. When you release the mouse button, the vial will be redisplayed with the new size and shape. Figure 14 is a picture of a vial that has been widened so that all of the traits are visible.

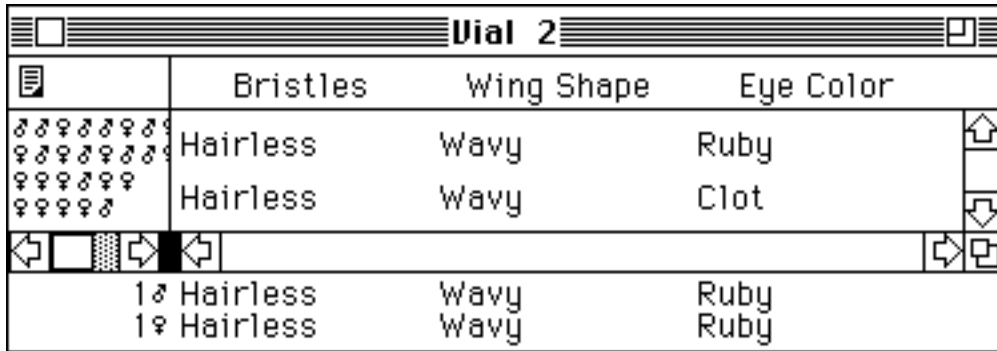


Figure 14. A resized vial.

Scrolling Vials

Many vials hold considerably more information than they have room to display. The three scroll bars (see Figure 15) allow you to see information that was not originally visible. The organism scroll bar scrolls horizontally through the organism symbols, the trait scroll bar scrolls horizontally through the traits, and the vertical scroll bar scrolls vertically through the phenotype descriptions and associated organism symbols.

Every scroll bar is either active or inactive. An active scroll bar has a gray background, which indicates that there is invisible material. An inactive scroll bar is all white, indicating that all available material is already visible. In Figure 15, both horizontal scroll bars are active and the vertical scroll bar is inactive. This means that that there are only two phenotype classes in this vial. If there were more than two, the vertical scroll bar would be active. Similarly, there is at least one trait other than Wing Shape. To see what it is, we can click once in the trait scroll bar's right arrow. The result is illustrated in Figure 16.

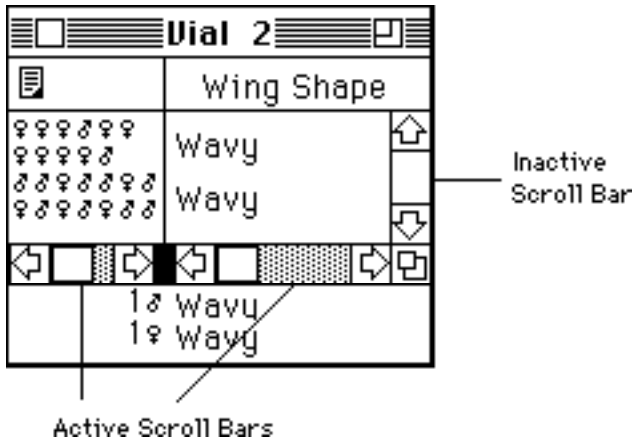


Figure 15. Both horizontal scroll bars are active, the vertical is inactive.

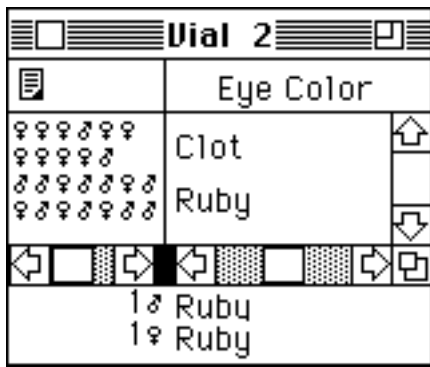


Figure 16. The trait scroll bar has been scrolled to the right once.

Notice that the white box (the scroll box) in the trait scroll bar now appears in the center of the scroll bar. This indicates that there is additional information both to the right and to the left of the Eye Color trait. There are at least three traits in this problem.

Adjusting the Window Pane

Vials are divided into two window panes. The left hand pane holds the organism sex symbols, and the right hand pane holds phenotype descriptions. You can change the allocation of space between the two panes by clicking in the black rectangle at the base of the line separating the two panes (the pane control) and dragging it to the right or left.

Figure 17 shows the same vial as in Figure 14 but the pane control has been dragged to the right so that all the organism symbols are visible. The mouse pointer is over the pane control.

Changing Row Order

Just as you can rearrange the horizontal order in which traits are displayed, you can rearrange the vertical order of the phenotype classes. This allows you to cluster organisms with interesting phenotypes near the top of the vial.

To drag a vial row, click somewhere over the phenotype description part of the row (in this example, over one of the words 'Wavy', 'Ruby', or 'Clot'), and drag up or down.

Figure 19 shows the same vial as Figure 18, but with the order of the two phenotypes reversed.

	Wing Shape	Eye Color	
♀♀♂♂♀♀ ♀♀♂♂♂	Wavy	Clot	↑
♂♂♀♀♂♂♀♀♂♂♂♂♂♂♀♀♀♀♂♂♂♂ ♀♀♀♀♂♂♂♀♀♀♀♂♂♂♂♀♀♀♀♂♂♂♂	Wavy	Ruby	↓
←	→ ←		→
	1 ♂ Wavy	Ruby	H
	1 ♀ Wavy	Ruby	H

Figure 19. The order of the two phenotype classes is reversed.

Reading the Parental Information


Information about the breeding pair that produced a vial is displayed at the bottom of the vial. The initial number is the number of the vial that contains the parent. In figure 19, both parents are from vial 1.

If you click on a parent's symbol, the parent will be highlighted not only where you have clicked, but also in its home vial. This allows you to identify which particular individual was used in the cross. It is also useful when you want to do another cross using the same parent, select it here and do the cross.

Opening a Notepad

Clicking on the notepad icon (📄, upper left corner of every vial), will open a window which can be used for taking notes. You can type into this notepad,

paste pictures from other GCK windows into it, print it, or copy it out into a word processor to help when you prepare your lab report.

When you have written into a notepad, the icon changes to indicate that the notepad is no longer blank (.

For more information about using notepads, see the sections below entitled **Taking Notes** and **Communicating With Other Programs**.

Destroying a Vial

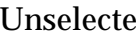

To destroy a set of vials, select them and then choose *Destroy Vials* from the **Utilities** menu. If you destroy a vial, it cannot be recovered.

Since destroying a vial is a somewhat dangerous action, you will be asked to confirm if this is really what you want to do. The original vial (the field population) cannot be destroyed.

There are really only two reasons to destroy a vial. If you have reason to believe that you are running out of computer memory, destroying vials will give you more space. Or you may find that the computer display is becoming too cluttered, and that destroying a few uninteresting vials will make it easier to find things.

Selecting Organisms

In order to do anything with an organism, such as breed it with another organism, you need to select it. To select an organism, move the mouse pointer over the symbol that represents the organism and click the mouse button once.

Unselected organisms look like this: ; selected organisms look like this: .

To select a second organism, you have to press the shift key on the keyboard while you click on the second organism. The second organism need not be from the same vial as the first. If you click on a third organism while still pressing the shift key, the first organism you selected will be unselected.

Organisms that have participated in one or more crosses appear slightly dimmed. In some problems, where an organism is only permitted to mate once, these organisms may not participate in a cross.

Doing Crosses

Genetics Construction Kit allows you to perform several kinds of crosses. Any particular problem may only support some subset of the available crosses. To find out what crosses are supported, look at the list under the **Cross** menu.

Cross Two This is the most general type of cross, it allows you to choose any two individuals and cross them (provided, of course that they are of opposite sexes if the organisms are dioecious).

To cross two organisms, select them both (remember to press the shift key while selecting the second one), and choose *Cross Two* from the **Cross** menu.

There is a shortcut method of crossing two organisms. If you shift double click on the second organism, the cross will be performed automatically.

Like Cross A like cross is between parents with the same phenotype. To perform a like cross, select an individual and choose *Like* from the **Cross** menu.

If no organism of opposite sex and the same phenotype exists, no cross will be performed. If more than one such organism exists, one will be chosen at random.

With monoecious organisms, *Like* will be replaced by *Self* and will cross an organism with itself.

Back Cross A back cross is a cross between an organism and its parent of the opposite sex. To perform a back cross, select an organism and choose *Back* from the **Cross** menu.

Since the parents of organisms in the field population are not known, you cannot back cross an individual in vial 1.

Reciprocal Cross A reciprocal cross is a cross between parents that have the opposite combination of sex and phenotype than the parents that produced the offspring in the selected vial. For example: if a vial has a female parent with Rosy eyes and a male parent with Carmine eyes, a reciprocal cross would be one between a female with Carmine eyes and a male with Rosy eyes.

To perform a reciprocal cross, select a vial and choose *Reciprocal* from the **Cross** menu.

Parents used for a reciprocal cross will be taken from the same vials as the selected vial's parents. If no such parents exist, the cross will not be performed. If there is more than one possible parent, one will be chosen at random from those available.

Test Cross A test cross is usually defined as a cross with a homozygous recessive individual. GCK allows you to choose up to two organisms (one of each sex) to be your test organisms. Once you have chosen test organism(s), you can perform test crosses by selecting a single organism and choosing *Test* from the **Cross** menu.

To choose test organism(s), select the organism(s) and choose *Set Test Organism(s)* from the **Cross** menu. If you only set one test organism you will only be able to do test crosses with organisms of the opposite sex.

GCK will not check to that the organisms you choose as test organisms are really homozygous recessive organisms. This is your responsibility.

To see the current set of test organisms, select the *Show Test Organism(s)* option from the **Cross** menu (see Figure 20). The number in front of the organism symbol is the number of the vial containing the test organism. To identify the particular organism, click on the sex symbol and it will be selected everywhere it occurs, including in its original vial.

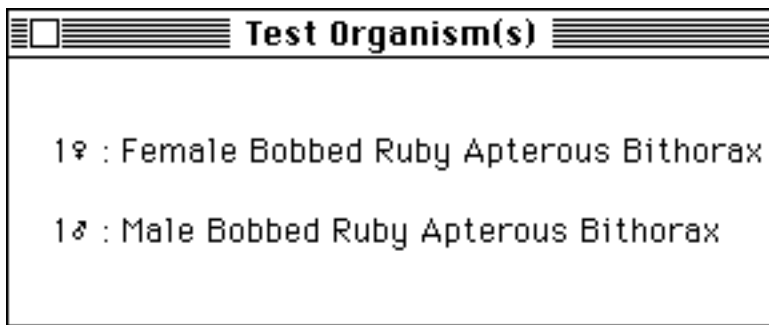


Figure 20. The current set of test organisms.

Analyzing and Organizing Your Data

Abbreviating Names

In order to display more information in the same space you may abbreviate the names of traits and variations. To do this, choose *Abbreviate Names* from the **Utilities** menu. To reverse the abbreviation, choose *Abbreviate Names* a second time.

Vial Summary Chart

To summarize the contents of a vial or set of vials, select the set of vials you want to summarize (remember to hold down the shift key if you want to select more than one), and choose *Summary Chart* from the **Analysis** menu. A window similar to that shown in Figure 21 will open.

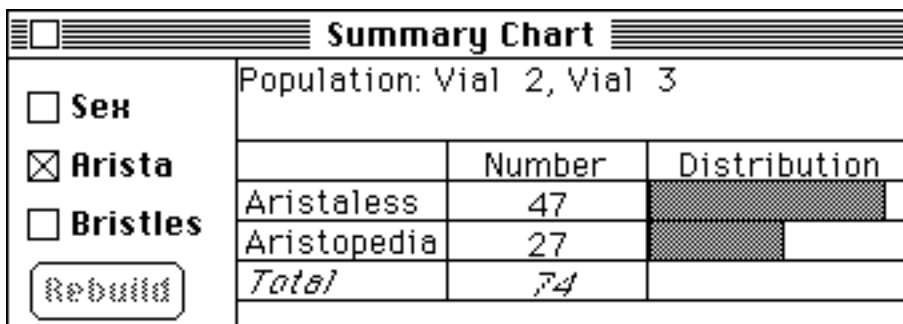


Figure 21. A vial summary chart for vials 2 and 3.

The control panel to the left of the summary chart controls which traits are summarized. To change the summary, click in the boxes to toggle the traits on and off and then click the *Rebuild* button. At least one trait be marked at all times. Turn on a trait before turning off the old one if you are looking at only a single trait.

The population box on top of the summary chart lists the vials that have been clumped together for this summary.

You can change the order of the phenotypes in the summary chart by dragging the variation names up or down. Large summary charts have a grow box and a vertical scroll bar so that they can be resized and scrolled.

There are three ways you can copy the information in a summary chart to store it in a notepad or to export it to another program. When a summary chart is the frontmost window, the *Copy Window*, *Copy Window Data*, and *Copy Window Graph* options on the **Edit** menu will be active.

Copy Window will put an exact replica of the entire summary window on the clipboard.

Copy Window Data will put a textual version of the data on the clipboard that can be easily exported to a word processor, spreadsheet, or data analysis program. Figure 22 shows the textual form of the summary chart in Figure 21.

Population: Vial 2, Vial 3
 Phenotype Number
 Aristaless 47
 Aristopedia 27
 Total 74

Figure 22. The textual form of a vial summary created by **Copy Window Data**.

Copy Window Graph will put a picture of the summary chart proper on the clipboard. From the clipboard it can be pasted into a notepad, a word processing program, or a painting program.

Aristaless	47	
Aristopedia	27	
Total	74	

Figure 23. The picture created by **Copy Window Graph** from a vial summary.

Chi Squared Analysis

The chi squared worksheet allows you to test how closely an observed ratio matches the ratios you expect under a given hypothesis. A chi squared worksheet may be configured to refer to any subset of the possible traits.

Chi Squared					
Population: Vial 2, Vial 3					
<input type="checkbox"/> Sex		Expected Ratio	Observed Numbers	Expected Numbers	(O - E) ² / E
<input checked="" type="checkbox"/> Arista	Aristaless	2	47	49.3	0.11
<input type="checkbox"/> Bristles	Aristopedia	1	27	24.7	0.22
<input type="button" value="Rebuild"/>	Other	0			
<input type="button" value="Calculate"/>	1 degree of freedom.		Chi squared value:		0.33
			P-value is:		0.5650

Figure 24. A Chi Squared Worksheet. The hypothesis tested predicts a ratio of 2:1 for Aristaless and Aristopedia. The p value is .5650.

The control panel is the lefthand part of the chi squared worksheet. It consists of a check box for every trait in the problem, a check box for sex, if appropriate, and *Rebuild* and *Calculate* buttons. You select the subset of traits you want in the chi squared worksheet by clicking in the check boxes and click on the *Rebuild* button to redraw the worksheet. Click on the *Calculate* button when you have changed the expected ratio to recalculate the chi squared values. Pressing the Return key is equivalent to clicking on the *Calculate* button.

You cannot specify an empty chi squared worksheet (one with no traits). If you try to uncheck the last checked trait, nothing will happen.

If you believe that one or more classes of phenotype are missing, enter the component of the ratio represented by them in the row marked Other. The Other row is not used unless the expected ratio is non-zero.


Any category can be removed from the analysis by setting its expected ratio to zero.

The p value (lower righthand corner) is the probability of obtaining the observed ratio if the expected ratio is the true ratio. By convention, if it is less than 0.05 you may safely reject the hypothesis that predicted the expected ratio.

If there are more than four rows of phenotypes, there will be a scroll bar and a grow box so that you can make the chi squared analysis window smaller and still access all the phenotypes.

You can reorder the phenotype rows by dragging the phenotype names up and down.

The names of traits and phenotypes can be abbreviated by choosing the *Abbreviate Names* option from the **Utilities** menu.

Under some circumstances, a caution symbol, , may appear on your chi squared worksheet. If this occurs, click on it for a warning message about the statistical validity of the particular test you have made.

To perform a test:

- Select the vial or vials that contain the population of interest.
- Choose *Chi Squared Test* from the **Analysis** menu.

- Click in the check boxes to set the traits you need.
- Click the *Rebuild* button to set up these traits.
- Enter the phenotype ratios you expect in the first column.
- Press Return, or click on the *Calculate* button to recalculate.

The Cross Matrix

The cross matrix is a record of the crosses you have made so far; it is also an index of the vials generated by these crosses. As a record, you can use it to think about the kinds of crosses you have made and the kinds of crosses that you need to make in the future. As an index, it is a useful way to find that pesky little vial you shrank to an icon a while ago but can't find anymore.

A Record of Crosses

To open the cross matrix, choose *Cross Matrix* from the **Data Analysis** menu. You don't need to select anything first (there is only one cross matrix). Figure 25 is a cross matrix from a problem with two traits.

		Female		
		Garnet	Ruby	Purple
Male	Garnet			
	Ruby	3		
	Purple	4	2	

Figure 25 A cross matrix for a two-trait problem. It is set up to look only at the Eye Color trait.

The cross matrix in figure 25 tells us that we have crossed a Ruby male and a female Garnet and that vial 3 contains the result of this cross. Similarly, vial 4 contains a Purple x Garnet cross and vial 2 contains a Purple x Ruby cross. The blank positions in the matrix make clear which crosses have not been made.



An Index into Vials

To retrieve a vial shown in a cross matrix, double click on the vial number. The vial will be enlarged if it is in icon form, brought to the front and selected.

The vial shown in the cross matrix is the vial produced by the *latest* cross of the indicated phenotypes. If you hold down the option key while double clicking on a cross matrix cell, all vials produced by the corresponding cross will be brought forward and selected.

Taking Notes

Using Notepads

Every vial has an associated notepad; to open it, click on the notepad icon ( or ) in the upper right corner. The notepad stays in existence as long as you do not destroy its associated vial. You can close it temporarily by clicking in its close box, and when you re-open it, any notes you typed will still be there.

A blank notepad icon indicates that the corresponding notepad is currently empty.

Use the notepad just as you would any other Macintosh word processor. You can type into it, paste pictures into it, select parts of it to cut or copy into the clipboard, and print it.

If you are not familiar with standard Macintosh word processing methods you should consult your Macintosh Owner's Guide for a description.

Printing Notepads

To print a notepad, make sure that it is the frontmost window (clicking somewhere in the window will make it frontmost). The frontmost window is the only window which has a set of parallel horizontal lines around its title. Then choose *Print Notepad* from the **Edit** menu.

For more information on notepad use, see the section on **Communicating With Other Programs**.

Cleaning Up the Benchtop

After you have been working for a while, your lab bench (the computer screen) is likely to get quite messy. The **Clean Up** option on the **Utilities** menu will straighten things up by putting things in their original places and closing certain windows.

Changing the Cleanup Process

The standard Clean Up process places vials and other windows on your screen in a way appropriate for the standard Macintosh 9-inch screen. If you have a larger screen or if you do not like the way clean up works, you can change it. To do this, choose the *Clean Up Options* option on the **Utilities** menu. The window shown in Figure 26 will open.

The check boxes at the bottom of the window allow you to specify which windows should be automatically closed or (for vials) collapsed to icon form during a clean up operation.

The box in the upper part of the window shows where each of the different kinds of windows created by GCK will be placed when it is first created and when you ask for a clean up. In Figure 26, the six black rectangles represent the placement of the first six vials (later vials will be placed on top of the first six, offset a little). You can change the number of rows and columns of vials, and the spacing between them, by adjusting the large rectangle with the little grow box in the lower right corner. You can change the placement of the group of all vials by dragging the big rectangle around the screen.

To change the placement of other kinds of windows, click on the *Next* button to bring the next set of windows to the top, or click directly on the gray boxes representing the window you want to change.

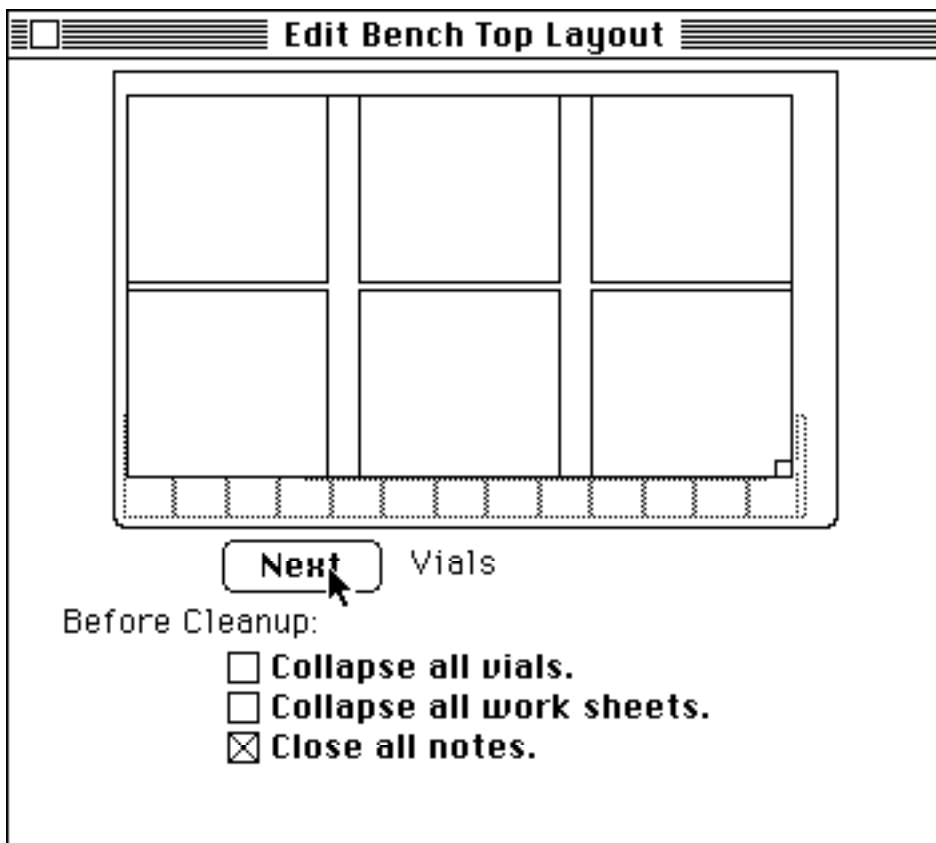


Figure 26. The **Clean Up Options** window.

Communicating With Other Programs

All communication between GCK and other programs takes place via the Macintosh Clipboard. Think of the clipboard as a place you can temporarily store a piece of text or a picture from one program, and then retrieve it from another program. You proceed by Copying material from one program into the clipboard, switching to the other program, and then Pasting the clipboard into the second program.

This can be quite clumsy if you need to move several different things between the same two programs, since the clipboard can only hold one thing at a time. In this situation you may want to look into using the Macintosh Scrapbook (see your Macintosh Owner's Guide) which can hold more than one thing at a time.

Cut, Copy, Paste, and Clear

You can use *Cut*, *Copy*, and *Paste* to move text and pictures between GCK notepads and other programs. Unfortunately, however, it is not possible to copy and paste mixed text and pictures at one time.

To copy a notepad that contains both text and pictures you need to do the following:

- Select the entire content of the notepad. You can do this by clicking before the first word and dragging to the end, or by clicking once before the first word, scrolling to the end, and shift-clicking after the last character.
- Choose *Copy* from the **Edit** menu.
- *Paste* the result into an external word processor. Where pictures exist in the original notepad you will see a little box (□).
- For each picture in the notepad:
 - Select the picture. It is critical that you select only the picture and no surrounding blank space.
 - Choose *Copy* to put a copy of the picture on the clipboard.
 - *Paste* the picture into your word processor.

Copy Window

The *Copy Window* option on the Edit menu is active as long as there is at least one window open. It will put a picture of the current frontmost window on the clipboard. Once it is on the clipboard it can be pasted into a notepad or into another Macintosh program.

The picture of the window looks exactly like the window. This is potentially confusing because it is not a window any more, but just a picture of one. This means that the close box and other controls will not work.

Copy Window Data

The *Copy Window Data* option on the **Edit** menu will put a copy of the data a window contains on the clipboard in a form that is usable (not only displayable) by other programs. The data is in tab delimited text format that is usable by many word processors, spreadsheets, data base managers, and graphing programs.

Tab delimited text is text arranged in columns with each column separated by a tab. If you paste this into a word processor you will need to set the tab stops to line up the columns.

Vials, Summary Charts, and Chi Square Worksheets are the GCK windows that export their data in this way. The data stored in the frontmost window will be exported.

Copy Window Graph

The *Copy Window Graph* option on the **Edit** menu will put a copy of the graph in a Summary chart on the clipboard. This option is only available if the frontmost window is a Summary Chart window.

Printing a Window

You can always print the frontmost window, if you have a printer attached to your computer, by holding down three keys simultaneously. The three keys are the shift key, the command key(⌘), and the "4" key. If you also press the caps lock key, the entire computer screen will be printed. These procedures are not only part of GCK , but are characteristic of every Macintosh program.

Getting Help

There are several ways to ask for help from GCK or any other BioQUEST program.

Why Can't I Use This Menu Item?

At any one time several menu items will be gray, indicating that they are inactive and therefore cannot be used. Active menu items appear in black. It is not always obvious why a menu item is inactive, or how to make it active. In GCK, if you try to choose an inactive menu item, you will get a short message explaining what to do in order to enable it (see Figure 27). Usually this means selecting an object.

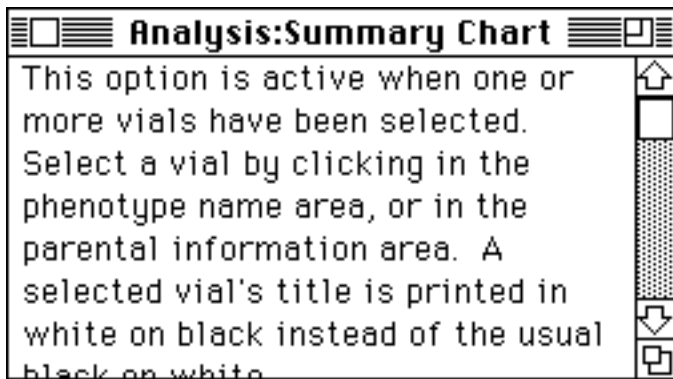



Figure 27. A Help message explaining why the Vial Summary item is inactive.

Use the scroll bar on the right to see text that is not immediately visible. When you have finished reading the help message, you can dismiss it by clicking in the window close box.

What Is This Thing For?

To find out what something is or does, you need to be in help mode. To enter help mode, press the command key () while simultaneously pressing the question mark (?) key. On some keyboards there is a key labeled help. If your keyboard has a help key, it will do the same thing.

When you are in help mode, the mouse cursor will look like this , instead of the usual arrow shape. In help mode, all menu items are always active.

Selecting a menu item will give you a short description of what the menu item does (see Figure 28).

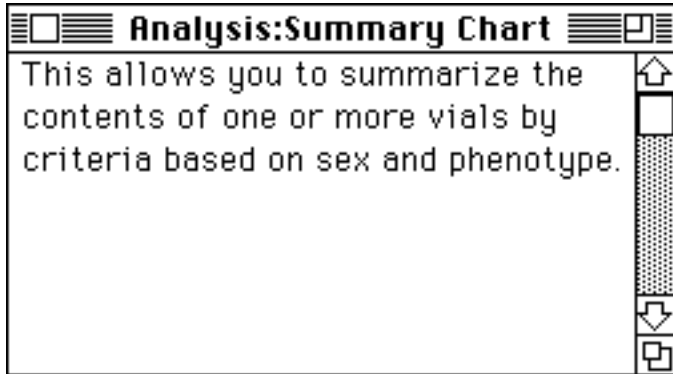


Figure 28. An Explanation of the Vial:Summarize menu item

Besides menus, you can click on just about anything and get some information about it.

Usually, you automatically drop out of help mode after you get help once. Sometimes you want to ask for help on several things and it is useful to stay in help mode. If you hold down the option key while clicking, you will stay in help mode.

What About the Big Picture?

The general help system is accessible from the *Help With GCK* option under the **Apple** () menu. If you choose this option you will be given a list of topics from which to choose the subject of interest (see figure 29). To open a topic, click on it and click the *Open* button at the bottom of the help window, or double click on the topic line. When you open a topic you will either see a list of sub-topics or a discussion of the subject.

At the bottom there will often be a *Back* button. Pressing it will return you to the topic list that led you to the current window. Sometimes there will be other buttons that should be labeled so as to be self explanatory.

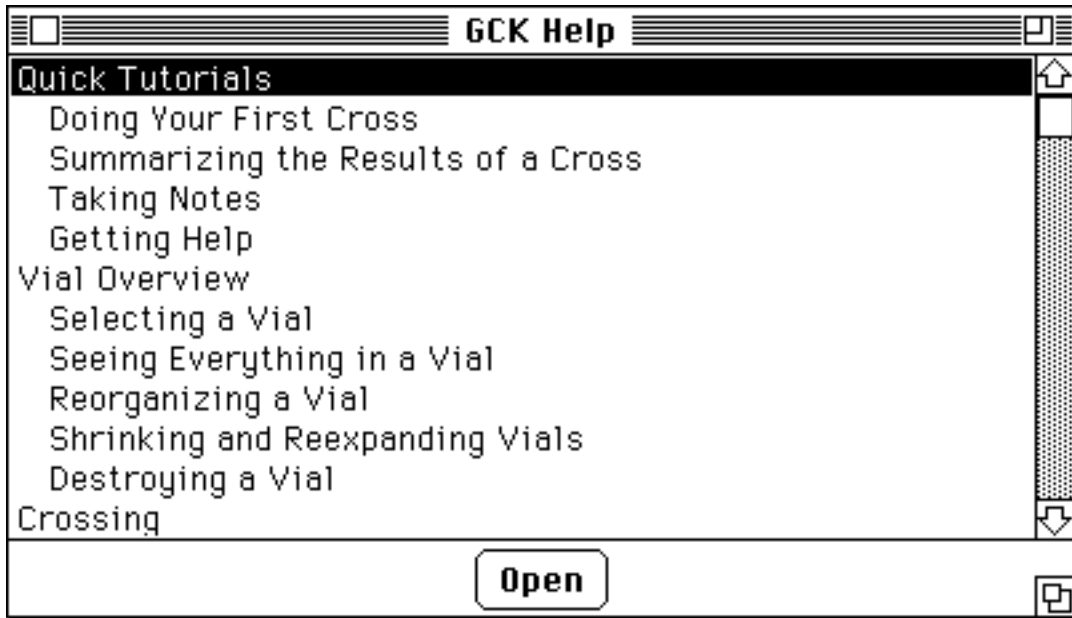


Figure 29. The **Help with GCK** topic list. Clicking **Open** will lead to information about Quick Tutorials.

Saving and Opening a Problem

Saving a Problem

You can save the state of the problem you are working on at any point by choosing the *Save* option from the **File** menu. This saves everything so that you can later come back to the problem in the same state it was in when you left it.

There are a number of reasons you may want to save a problem. The simplest is that you may want to take a break and come back to a problem later. Another reason is to keep all of your original research data. If someone then challenges your conclusions, you can go back to the original organisms with new questions. Or you may want to save a copy of a problem before you do any work at all so that another research team can work on exactly the same problem and you can pool, and argue over, your results.

You may also want to save against the possibility of catastrophe in the form of as power failure or an problem with the program that causes it to stop working suddenly.

When you choose *Save* the first time, you will be asked to give the problem a name (see Figure 30). If the process of giving a file a name is unfamiliar to you, please refer to **BioQUEST: Macintosh Basics**.

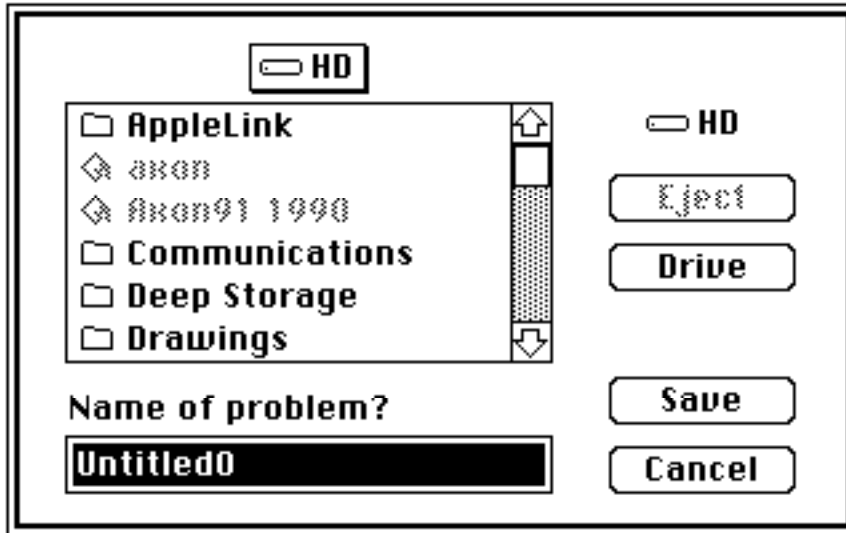


Figure 30. A Save Problem dialog box. By default, the problem will be saved under the name 'Untitled0'.

When you are ready, click the *Save* button to save the problem, or click the *Cancel* button if you decide not to save.

The second time you choose *Save*, your problem will automatically be re-saved under the same name you used the first time.

If you want two different copies, use the *Save As* option instead of *Save*. This will ask you for another name.

Opening a Saved Problem

There are two ways to open a previously saved problem. The simplest way is to double click on the saved problem's icon from the Finder (see Figure 31).



My Problem

Figure 31. A saved problem icon.

Alternatively, if you are already running GCK, you can choose *Open* from the **File** menu and choose your problem from the list presented there.

Note that you can only have one problem open at a time. If you try to open a second problem, you will first be asked if you want to save the current problem.

