

Blue Genes Program

The Blue Genes program solves most of the difficulties that general graphic programs available on the Macintosh have in making genetic maps. The greatest weakness arises from an insufficient support for drawing arcs and rings. BlueGenes has the capacity to draw such objects and directly produce high level representations of these objects in Postscript®.

Furthermore, since BlueGenes is specialized for drawing genetic maps, it can scale map segments according to a user defined map length and search for sites according to a user defined sequence. In most other respects BlueGenes is very similar to other Macintosh drawing programs. Objects are defined and moved by using the mouse. Changes to objects are performed by selecting the object and then selecting a menu choice. Most operations can be undone. BlueGenes exports to other programs using the standard PICT format. In addition, most of the objects are exported in a form that can be conveniently edited using other drawing programs .

Distribution of the program.

BlueGenes is being distributed in two versions: a demo version and a full version. The latest demo version is available through CompuServe for a nominal fee of US. \$40.00. This software has been registered in the CompuServe shareware data base. Its registration ID is 648. It is located in the Science and Engineering library of the Macintosh Applications Forum (Go Macapp) and named BlueGe.sea.

The demo version is a useful program. The principal differences between the demo version and the full version are the ability to store in the native BlueGenes file format and draw restriction sites according to a sequence.. Sites may be produced using the mouse in the demo version and for a limited number of restriction enzymes sites automatically and manually using the mouse. Rotated text can be associated with arcs and circles only in the full version. The full version also includes technical support and one free update to the next major version. Licenses for the full version are \$100.00. Purchasers of the demo version are entitled to a \$40.00 discount on the full version.

To order and obtain information about the program you can send messages to a CompuServe mailbox using either the Internet or CompuServe directly:

Internet: 71011.1377@CompuServe.com
CompuServe: 71011,1377

Or by traditional mail:

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User Manual

Creation of objects

The mouse is used to create all of the graphic objects. A tool must be selected from the tear-off tool menu for this purpose. Two tools are used to establish the origin and scale of the maps. One of these tools must be used before the other tools can be used. They are located in the top row. One establishes a circular map and the other a linear one. Each use of either of these two tools creates a new coordinate system that is used by subsequently selected tools. To return to the coordinate system of an object created earlier, that object and only that object should be activated using the selection tool. The icon on the tool palette indicates what kind of the tool will create. The location of the mouse relative to this coordinate system appears next to the mouse when any of the other tools except for the text tool are used. Pressing the mouse button starts object creation. Dragging and mouse release determine the size of the object. Rapid clicking and short mouse drags are sometimes difficult to interpret when creating objects. If the clicks or drags are not long enough, BlueGenes will ignore these events a couple of times before complaining about them. When creating an arc with an arrow at its tip, you need to make the arc large enough to contain the arrow, otherwise it is interpreted as a large arc with an arrow pointed in the other direction.

Defining Sequences

The length of the map can be established directly using the Define Sequence command or indirectly from sequence file using the Get Sequence command. The name and length of the current sequence appear in the small pane in the bottom left corner of the window. Double clicking on this pane produces a dialog box that can be used to define a sequence. All currently defined sequences are located in the Sequences menu.

BlueGenes can also use flat text files to define a sequence. Use the Get Sequence command for this purpose. BlueGenes ignores characters that are not accepted abbreviations for nucleotide bases. This means that spaces, tabs, returns and other characters are not counted in determining the sequence length. For example, because numerical characters are ignored, a text file containing a sequence with numerical positions before each sequence line is compatible with BlueGenes. After a sequence file has been opened, BlueGenes will remember its location by storing its location in the current BlueGenes FIND file. Upon restarting the program the names of these sequences will automatically be loaded into the Sequences menu.

Pattern and Size of Map Objects

The pattern and width of the objects are determined by setting them using either the pattern palette or the items in the Draw menu. They can be changed by activating the objects by using the select tool and then using the appropriate menu item. The patterns at the far left in the pattern are special. They are converted into gray scale values on Postscript devices.

Alignment of objects to one another

Object creation by subsequent uses of the same or uses of other tools can be aligned to the last created object by holding the shift key down. Whether the shift key is down or not is determined at the start of mouse dragging so it really only needs to be held down at this time. Although this is not intuitive, it is the method used by many other Macintosh programs for this purpose. The same function can be performed by selecting the Draw Together menu choice in the Drawing menu. To create a circular or linear map with several aligned segments but different widths and patterns, use this technique.

A second way to align objects is to use a grid. The grid is created by using items in the Draw menu.

A simple rectangular grid is created. Selection of the grid menu item is also useful in other situations such as when a few bits get left behind from an operation since it forces a complete redraw of the window.

Arrows

The end of the object at which the arrow appears is determined by the dragging direction. The arrow appears at "the end of the mouse drag" end of the object.

Marking sites

Two tools can be used to mark restriction enzyme cutting sites or other landmarks on objects. The two tools differ only in the line segments that are created. One creates a single line and the other a jointed line to mark the site. In order to add sites to an object first select that object by clicking on it. The ticks connected to only one shape can be edited at a time. The cursor will change its shape to a pencil over the currently selected shape. Immediately after selecting a shape with several ticks or sites, all of them will be activated and you can make changes in all of them or delete all of them at this time. Immediately after creating a new tick, it is active and other changes such as dragging, changing its text or the thickness of its line segments can be performed at that time.

The maximum length of the text in a single tick is limited to 15 characters. Each tick can have a different font, face and text size. To change these properties select the appropriate menu choice while the tick(s) is selected. In order to draw labels that require larger text segments, such as polylinkers, use the general text tool to list all of the sites in the polylinker and use two ticks with an empty space to indicate the polylinker site. The text attached to the marks is initially established by the entering the text in a dialog window that is brought up by selecting the Set Tick Text command. This dialog will appear automatically if you have not previously entered any text or if the text you have entered is a single '?'. The same dialog window can be used to change the text associated with the tick. Double-clicking on the current text of the site, or selecting the Set Tick Text command from the Drawing menu when a tick is active will bring up the dialog to allow you to change the text.

A simple trick allows you to create a label that is associated with a shape without having any lines associated: after creating a tick select a zero width for the lines. One use of this trick is to attach the name to a plasmid map.

Text

The text tool is used to create and edit text boxes. Multiple text styles, fonts and sizes may appear in a single text box. The size and position of a text object can be changed by selecting the object using the select tool. A selected text object has a grab box in the lower right hand corner which can be dragged to change its size. Text lines wrap at the right border of the box.

Text Boxes

Text boxes are anchored to a beginning and ending character. This is what one usually desires for sequence comparisons. Selecting the starting and ending characters is not as intuitive as it could be. This is because the starting and ending character are determined by a normal text selection. The text box does not necessarily enclose all of the selected text. i.e. it encloses the starting and ending characters of the selection range. The text box is created by selecting text and then the Box Text menu item in the Text menu. The boxes can be quirky when multiple font sizes are used.

Saving and Opening Blue Gene Files

In the full version of the BlueGenes program files can be saved either as PICT or in a native format. The demo version only saves in the PICT format. The native format preserves all information about the objects in a compact format that includes the sequence dependent information. PICT files are generally much larger and do not preserve sequence information. They can be used by other drawing programs. BlueGenes cannot open PICT files.

Printing

Apple's suggestions for creating device-independent printing were followed. However, the variety of printers currently available for Macintoshes make it difficult to test whether the program functions with all of them. If you have problems with your printer and you have purchased the full version of the program we will attempt to correct any printing problems. Since rings and arcs can be rendered better by Postscript than by the Macintosh Quickdraw system, most of the objects are rendered by program-created Postscript when sent to a Postscript device. I have relied on the Laser Writer Driver to set up the coordinate system and to make text objects. BlueGenes has tested on the latest laserwriter drivers (Laserwriter 7.0). All Postscript created is currently Level 1 and is therefore compatible with both Level 1 and Level 2 Postscript devices.

Restriction sites

BlueGenes will automatically find restriction sites or other sites when the sequence is defined by a text file. BlueGenes will prompt for a text file containing the sequence if one is not currently associated with the sequence shown in the box in the lower left corner of the screen. The program will ignore Genetics Computer Group comments at the beginning of text files by default. The comments are at the beginning of a sequence file and are ended with a double period (..). If for some reason you wish to turn this off uncheck the appropriate menu choice in the Sequence menu. The program also ignores characters other than those commonly used to symbolise bases (i.e. numbers if present).

To see a complete listing of the sites use the Restriction Sites... menu selection in the Sequence menu. It will display a window that has a pane on the left side with the names of all of the restriction enzymes in the EMBO restriction enzyme data bank (REBASE).

The recognition site will appear in the center of the window when you select one of the enzymes with the mouse. To quickly find a site in the rather long list, enter the first two to three letters of the restriction enzyme name. BlueGenes will scroll to the nearest selection that matches the letters in much the same way that the file finding dialog in System 7 works.

In order to perform a restriction enzyme site search, BlueGenes invokes a special compiler that creates a very efficient program for finding that site. The program is stored in a special FIND file that is initially named "Restriction Sites". In order to draw the sites on a graphic object you need to add the site to the menu by pressing the appropriate button. New sites cannot be added to the menu in the shareware version of the program. After adding a site to the menu, BlueGenes will also store the search program for this site in the current BlueGenes sites file and will automatically be available when you restart BlueGenes. BlueGenes will not load these programs into memory until you do a search so there is little penalty for having many sites in the menu.

To add the sites to an object you must select one of the "tick making tools". Then you must select the object just as you would to draw sites manually. When an object is selected to which sites can be added, the items in the sites menu will become enabled. The mouse cursor should appear as a pencil when it is moved over the selected object. Selecting the appropriate site from the sites menu will tell BlueGenes to find the sites and draw them.

The restriction enzyme list also includes several enzymes for which only the methylase has been characterized. They are followed by: (M). In addition, there are several asymmetric restriction enzymes that have two recognition sites. The second site is listed under the first and its name is followed by : "~". To find all of the sites with one of these enzymes you need to load both sites into the menu. For completeness, enzymes for which the recognition sites are unknown were also included. Their sites, as in the REBASE database, are indicated by a question mark. Of course no program can be created for these sites.

Exporting to other programs

Data can be exported in PICT format to other programs by storing the data as a PICT file or by copying and cutting to the clipboard. The Copy All selection in the exit menu copies the current window to the clipboard in PICT format. A program which handles objects i.e. Aldus Superpaint or MacDraw is better than one which handles bitmaps (MacPaint). Most objects were rendered as polygons. Since rings cannot currently be rendered as polygons by Quickdraw, they are exported as bitmap objects. They behave differently from the other objects exported by Blue Genes. However, they can be manipulated by most recent versions of Macintosh drawing programs to achieve the same effect. The Postscript version for most objects is included in the PICT files. However, most currently available programs will not be able to take advantage of this after you have made any changes in the file.