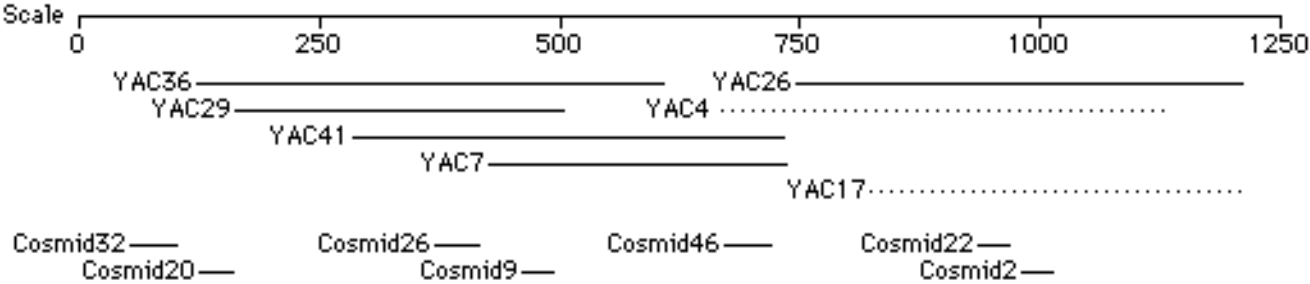


1991 February 12

DESCRIPTION:

This stack was designed as an interim solution to store and assimilate a variety of physical mapping data generated for the Human Genome Project. It stores detailed information regarding YACs, cosmids, PFGE, and annotations to contigs, including sequences and digitized gel images. Each type of information can be localized to a specific region of a contig, and contigs may be drawn (automatically) which incorporate all information into a single view. For example:



WARNING: THIS STACK HAS NOT BEEN THOROUGHLY TESTED. AS SUCH, IT MAY CONTAIN BUGS WHICH CAUSE DATA LOSS OR OTHER ERRATIC BEHAVIOR. IN ADDITION, DATA STORED HERE MAY NOT BE COMPATIBLE WITH FUTURE VERSIONS OF THE STACK.

SYSTEM REQUIREMENTS:

This stack should run on any Macintosh, although a Macintosh II series computer with a hard disk, >30 cm (12 inch) monitor and 2+Mb RAM are recommended. HyperCard 2.0 and System 6.0.5 (or later versions) are required; System 7 compatible. Some stack operations require more memory than is allocated to HyperCard by default; it is suggested that HyperCard's memory allocation be increased to 1200K (from 1000K) in the "Get Info..." window to prevent "out of memory" errors.

As you will notice -- and hopefully expected -- the system is still rough around some edges, but has no known bugs. I expect that some bugs will show up somewhere, and that users will have some suggestions which will make the interface more approachable; I am very interested in hearing of both. (If you have an extended keyboard, clicking the "F12" key will take you to a scratchpad for suggestions which you can print and send to me.)

Update Note (91 October 23)

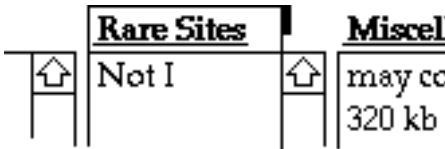
Since the writing of the above documentation, I have moved to Saint Louis to attend Washington University and do not intend to make improvements to this stack; however, Glen Evans (at the Molecular Genetics Laboratory, Salk Institute and by whom this project was originally supported) will continue to use and improve this stack. I will still be interested to hear of suggestions, bug reports, and other comments.

Reece Hart

internet: reece@informatics.wustl.edu

Although the framework for a help system exists, very little help text has been entered. Therefore, the following tips may provide a quick jump start:

1) Pull down menus are indicated by a black tab to the right of the identifier for a field. For example, depressing the mouse button on "Rare Sites" displays a pop up of rare sites, and when a site is selected it is added to the list.



2) If a reference to another card is shown, as in clone overlaps, clicking on the name of an overlap will take

you to that card. This is true of the "Contig" field in clone cards, and the lists of clones on contig cards.

3) A card is automatically locked when it is left to go to a new card. This lock may be toggled manually by clicking the picture of the lock in the bottom right of each card. Cards must be unlocked to enter or change data.

4) Finally, **the best way to learn is by fooling around with the test data. Don't be afraid to click buttons:** deleting cards and other unrecoverable actions require verification and aren't likely to occur accidentally.