Querying by Region of Interest

A region of interest can be specified using a pair of flanking markers, which can be cytogenetic bands, genes, amplimers (sequence tagged sites), or any other mapped objects. Given a region of interest, the comprehensive maps are searched to find all loci that fall within them. These loci can be displayed in a table, graphically as a slice through a comprehensive map, or as slices through a chosen set of primary maps. A comprehensive map slice shows all loci in the region, including genes, expressed sequence tags (ESTs), amplimers, and clones. A region also can be specified as a neighborhood around a single marker of interest.

Results of queries for genes, amplimers, ESTs, or clones can be displayed on a GDB comprehensive map. Results are spread across several chromosomes displayed in Mapview (see figure, p. 52). A query for all the PAX genes (specified as symbol = PAX* on the gene query form) retrieves genes on multiple chromosomes. Double-clicking on one of these genes brings up detailed gene information via the Web browser.

Querying by Polymorphism

GDB contains a large number of polymorphisms associated with genes and other markers. Queries can be constructed for a particular type of marker (e.g., gene, amplimer, clone), polymorphism (i.e., dinucleotide repeat), or level of heterozygosity. These queries can be combined with positional queries to find, for example, polymorphic amplimers in a region bounded by flanking markers or in a particular chromosomal band. If desired, the retrieved markers can be viewed on a comprehensive map.

Work in Progress

Mapview 2.3

Mapview 2.1, the next generation of the GDB map viewer, was released in March 1997. The latest version, Mapview 2.3, is available in all common computing environments because it is written in the Java programming language. Most important, the new viewer can display multiple aligned maps side by side in the window, with alignment lines indicating common markers in neighboring maps. As before, users can select individual markers to retrieve more information about them from the database.

GDB developers have entered into a collaborative relationship with other members of the bioWidget Consortium so the Java-based alignment viewer will become part of a collection of freely available software tools for displaying biological data (*http://goodman.jax.org/projects/biowidgets/consortium*).

Future plans for Mapview include providing or enhancing the ability to generate manuscript-ready Postscript map images, highlight or modify the display of particular classes of map objects based on attribute values, and requery for additional information.

Variation

Since its inception, GDB has been a repository for polymorphism data, with more than 18,000 polymorphisms now in GDB. A collaboration has been initiated with the Human Gene Mutation Database (HGMD) based in Cardiff, Wales, and headed by David Cooper and Michael Krawczak. HGMD's extensive collection of human mutation data, covering many disease-causing loci, includes sequence-level mutation characterizations. This data set will be included in GDB and updated from HGMD on an ongoing basis. The HGMD team also will provide advice