

laboratories own the data they submit to GDB and that other researchers cannot modify it. However, others should be able to add information and comments, so an additional feature is the community's ability to conduct electronic online public discussions by annotating the database submissions of fellow researchers. GDB is the first database of its kind to offer this feature, and the number of third-party annotations is increasing in the form of editorial commentary, links to literature citations, and links to other databases external to GDB. These links are an important part of the curatorial process because they make other data collections available to GDB users in an appropriate context.

Improved Map Representation and Querying

Accompanying the release of GDB 6.0, the program Mapview creates graphical displays of maps. Mapview was developed at GDB to display a number of map types (cytogenetic, radiation hybrid, contig, and linkage) using common graphical conventions found in the literature. Mapview is designed to stand alone or to be used in conjunction with a Web browser such as Netscape, thereby creating an interactive graphical display system. When used with Netscape, Mapview allows the user to retrieve details about any displayed map object.

Maps are accessed through the query form for genomic segment and its subclasses via a special program that allows the user to select whole maps or slices of maps from specific regions of interest and to query by map type. The ability to browse maps stored in GDB or download them in the background was also incorporated into GDB 6.0.

GDB stores many maps of each chromosome, generated by a variety of mapping methods. Users who are interested

in a region, such as the neighborhood of a gene or marker, will be able to see all maps that have data in that region, whether or not they contain the desired marker. To support database querying by region of interest, integrated maps have been developed that combine data from all the maps for each chromosome. These are called *Comprehensive Maps*.

Queries for all loci in a region of interest are processed against the comprehensive maps, thereby searching all relevant maps. Comprehensive maps are also useful for display purposes because they organize the content of a region by class of locus (e.g., gene, marker, clone) rather than by data source. This approach yields a much less complex presentation than an alignment of numerous primary maps. Because such information as detailed orders, order discrepancies between maps, and nonlinear metric relations between maps is not always captured in the comprehensive maps, GDB continues to provide access to aligned displays of primary maps.

A Variety of Searching Strategies

Recognizing the eclectic user community's need to search data and formulate queries, GDB offers a spectrum of simple to complex search strategies. In addition, direct programming access is available using either GDB's object query language to the Object Broker software layer or standard query language to the underlying Sybase relational database.

Querying by Object Directly from GDB's Home Page

The simplest methods search for objects according to known GDB accession numbers; sequence database-accession numbers; specified names, including wildcard symbols that will automatically match synonyms and primary names; and keywords contained anywhere in the text.

