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 on GDB's representation of genetic variation, which is being enhanced to model mutations and polymorphisms at the sequence level. These modifications will allow GDB to act as a repository for single-nucleotide polymorphisms, which are expected to be a major source of information on human genetic variation in the near future.

Mouse Synteny

Genomic relationships between mouse and man provide important clues regarding gene location, phenotype, and function. One of GDB's goals is to enable direct comparisons between these two organisms, in collaboration with the Mouse Genome Database at Jackson Laboratory. GDB is making additions to its schema to represent this information so that it can be displayed graphically with Mapview. In addition, algorithmic work is under way to use mapping data to automatically identify regions of conserved synteny between mouse and man. These algorithms will allow the synteny maps to be updated regularly. An important application of comparative mapping is the ability to predict the existence and location of unknown human homologs of known, mapped mouse genes. A set of such predictions is available in a report at the GDB Web site, and similar data will be available in the database itself in the spring of 1998.

Collaborations

GDB is a participant in the Genome Annotation Consortium (GAC) project, whose goal is to produce high-quality, automatic annotation of genomic sequences (*http://compbio.ornl.gov/CoLab*). Currently, GDB is developing a prototype mechanism to transition from GDB's Mapview display to the GAC sequence-level browser over common genome regions. GAC also will establish a human genome reference sequence that will be the base against which GDB will refer all polymorphisms and mutations. Ultimately, every genomic object in GDB should be related to an appropriate region of the reference sequence.

Sequencing Progress

The sequencing status of genomic regions now can be recorded in GDB. Based on submissions to sequence databases, GAC will determine genomic regions that have been completed. GDB also will be collaborating with the European Bioinformatics Institute, in conjunction with the international Human Genome Organisation (HUGO), to maintain a single shared Human Sequence Index that will record commitments and status for sequencing clones or regions. As a result, the sequencing status of any region can be displayed alongside other GDB mapping data.

Outreach

The Genome Database continues to seek direct community feedback and interact with the broader science community via various sources:

- International Scientific Advisory Committee meets annually to offer input and advice.
- Quarterly Review Committee confers frequently with the staff to track GDB progress and suggest change.
- HUGO nomenclature, chromosome, and other editorial committees have specialized functions within GDB, providing official names and consensus maps and ensuring the high quality of GDB's content.

Copies of GDB are available worldwide from ten mirror sites (nodes), and GDB staff members meet annually with node managers.