

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://compmio.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) that make the data more easily accessible to the international research community. GDB staff meet annually with node managers to facilitate interaction and to benefit from other user perspectives.

