A second enhancement of GSDB is the ability to store and represent sequence alignments. GSDB staff has been constructing alignments to several key sequences including the env and pol (reverse transcriptase) genes of the HIV genome, the complete chromosome VIII of Saccharomyces cerevisiae, and the complete genome of *Haemophilus influenzae*. These alignments are useful as possible sites of biological interest and for rapidly identifying differences between sequences.

A third key GSDB enhancement is the ability to represent known relationships of order and distance between separate individual pieces of sequence. These sets of sequences and their relative positions are grouped together as a single discontiguous sequence. Such a sequence may be as simple as two primers that define the ends of a sequence tagged site (STS), it may comprise all exons that are part of a single gene, or it may be as complex as the STS map for an entire chromosome.

GSDB staff has constructed discontiguous sequences for human chromosomes 1 through 22 and X that include markers from Massachusetts Institute of Technology–Whitehead Institute STS maps and from the Stanford Human Genome Center. The set of 2000 STS markers for chromosome X, which were mapped recently by Washington University at St. Louis, also have been added to chromosome X. About 50 genomic sequences have been added to the chromosome 22 map by determining their overlap with STS markers. Genomic sequences are being added to all the chromosomes as their overlap with the STS markers is determined. These discontiguous sequences can be retrieved easily and viewed via their sequence names using the GSDB Annotator. Sequence names follow the format of HUMCHR#MP, where # equals 1 through 22 or X.

GSDB staff also has utilized discontiguous sequences to construct maps for maize and rice. The maize discontiguous sequences were constructed using markers from the University of Missouri, Columbia. Markers for the rice discontiguous sequence were obtained from the Rice Genome Database at Cornell University and the Rice Genome Research Project in Japan.

New Tools

As a result of the major GSDB renovation, new tools were needed for submitting and accessing database data. Annotator was developed as a graphical interface that can be used to view, update, and submit sequence data (*http://www.ncgr.org/gsdb/beta.html*). Maestro, a Web-based interface, was developed to assist researchers in data retrieval (http://www.ncgr.org/gsdb/maestrobeta.html). Although both these tools currently are available to researchers, GSDB is continuing development to add increased capabilities.

Annotator displays a sequence and its associated biological information as an image, with the scale of the image adjustable by the user. Additional information about the sequence or an associate biological feature can be obtained in a pop-up window. Annotator also allows a user to retrieve a sequence for review, edit existing data, or add annotation to the record. Sequences can be created using Annotator, and any sequences created or edited can be saved either to a local file for later review and further editing or saved directly to the database.

Correct database structures are important for storing data and providing the research community with tools for searching and retrieving data. GSDB is making a concerted effort to expand and improve these services. The first generation of the Maestro query tool is available from the GSDB Web pages. Maestro allows researchers to perform queries on 18 different fields, some of which are queryable only through GSDB, for example, D segment numbers from the Genome Database at Johns Hopkins University in Baltimore.