- Implementation of a new database to support sequencing and mapping work on multiple chromosomes and species. Web-based automated tools were developed to facilitate construction of this database, the loading of over 100 million bytes of chromosome 19 data from the existing LLNL database, and automated generation of Web-based input interfaces.
- Significant enhancement of the LLNL Genome Graphical Database Browser software to display and link information obtained at a subcosmid resolution from both restriction map hybridization and sequence feature data. Features, such as genes linked to diseases, allow tracking to fragments as small as 500 base pairs of DNA.
- Development of advanced microfabrication technologies to produce electrophoresis microchannels in large glass substrates for use in DNA sequencing.
- Installation of a new filter-spotting robot that routinely produces $6 \times 6 \times 384$ filters. A $16 \times 16 \times 384$ pattern has been achieved.
- Upgrade of the Lawrence Berkeley National Laboratory colony picker using a second computer so that imaging and picking can occur simultaneously.

Future Plans

Genomic sequencing currently is the dominant function of Livermore's Human Genome Center. The physical mapping effort will ensure an ample supply of sequence-ready clones. For sequencing targets on chromosome 19, this includes ensuring that the most stable clones (cosmids, BACs, and PACs) are available for sequencing and that regions with such known physical landmarks as STSs and expressed sequenced tags (ESTs) are annotated to facilitate sequence assembly and analysis. The following targets are emphasized for DNA sequencing:

- Regions of high gene density, including regions containing gene families.
- Chromosome 19, of which at least 42 million bases are sequence ready.
- Selected BAC and PAC clones representing regions of about 0.2 million to 1 million bases throughout the human genome; clones would be selected based on such high-priority biological targets as genes involved in DNA repair, replication, recombination, xenobiotic metabolism, cell-cycle checkpoints, or other specific targets of interest.
- Selected BAC and PAC clones from mouse regions syntenic with the genes indicated above.
- Full-insert cDNAs corresponding to the genomic DNA being sequenced.

The informatics team is continuing to deploy broader-based supporting databases for both mapping and sequencing. Where appropriate, Web- and Java-based tools are being developed to enable biologists to interact with data. Recent reorganization within this group enables better direct support to the sequencing group, including evaluating and interfacing sequence-assembly algorithms and analysis tools, data and process tracking, and other informatics functions that will streamline the sequencing process.

The instrumentation effort has three major thrusts: (1) continued development or implementation of laboratory automation to support high-throughput sequencing; (2) development of the next-generation DNA sequencer; and (3) development of robotics to support high-density BAC clone screening. The last two goals warrant further explanation.

The new DNA sequencer being developed under a grant from the National Institutes of Health, with minor support