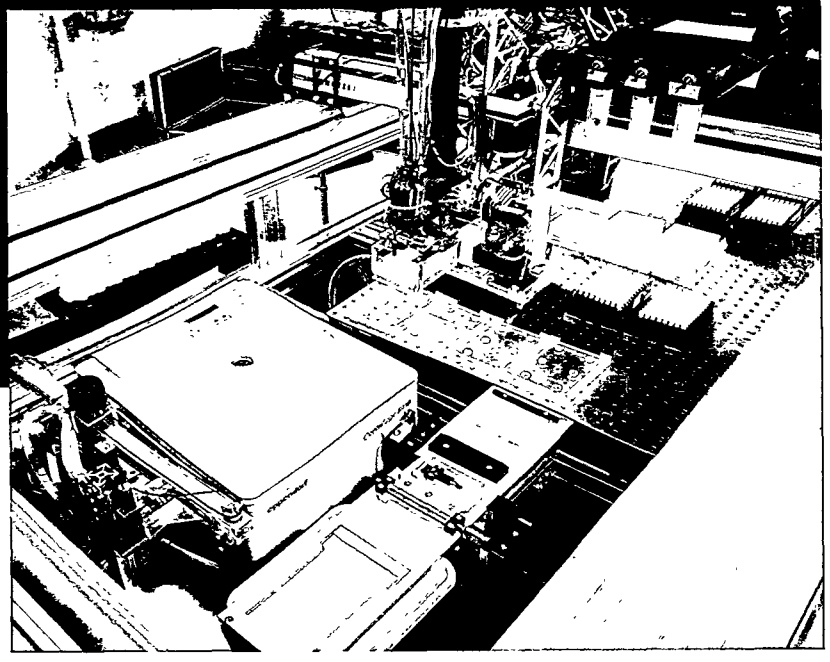

DNA Prep Machine. *The DNA Prep machine (above) was designed by Berkeley Lab's Martin Pollard to perform plasmid preparation on 192 samples (2 microtiter plates) in about 2.5 to 4 hours, depending on the protocol. Controlled by a personal computer running a Visual Basic Control program, the instrument includes a gantry robot equipped with pipettors, reagent dispensers, hot and cold temperature stations, and a pneumatic gripper.* [Source: LBNL]

fluorescence-assay methods, including DNA sequence analysis and mass spectrometry for molecular sizing.

Recent advances in the instrumentation group include DNA Prep machine and Prep Track. These instruments are designed to automate completely the highly repetitive and labor-intensive DNA-preparation procedure to provide higher daily throughput and DNA of consistent quality for sequencing (see photos, p. 43, and Web pages: *http://hgighub.lbl.gov/esd/DNAPrep/TitlePage.html* and *http://hgighub.lbl.gov/esd/prepTrackWebpage/preptrack.htm*).

Berkeley Lab's near-term needs are for 960 samples per day of DNA extracted from overnight bacteria growths. The DNA protocol is a modified boil prep prepared in a 96-well format. Overnight bacteria growths are lysed, and samples are separated from cell debris by centrifugation. The DNA is recovered by ethanol precipitation.

Informatics

The informatics group is focused on hardware and software support and system administration, software development for end sequencing, transposon mapping and sequence template selection, data-flow automation, gene finding, and sequence analysis. Data-flow automation is the main emphasis. Six key steps have been identified in this process, and software is being written and tested to automate all six. The first step involves controlling gel quality, trimming vector sequence, and storing the sequences in a database. A program module called Move-Track-Trim, which is now used in production, was written to handle these steps. The second through fourth steps in this process involve assembling, editing, and reconstructing P1 clones of 80,000 base pairs from 400-base traces. The fifth step is sequence annotation, and the sixth is data submission.

Annotation can greatly enhance the biological value of these sequences. Useful annotations include homologies to known genes, possible gene locations, and gene signals such as promoters. LBNL is developing a workbench for automatic sequence annotation and annotation viewing and editing. The goal is to run a series of sequence-analysis tools and display the results to compare the various predictions. Researchers then will be able to examine all the annotations (for example, genes predicted by various gene-finding methods) and select the ones that look best.

Nomi Harris developed Genotator, an annotation workbench consisting of a stand-alone annotation browser and several sequence-analysis functions. The back end runs several gene finders, homology searches (using BLAST), and signal searches and saves the results in ".ace" format. Genotator thus automates the tedious process of operating a dozen different sequence-analysis programs with many different input and output formats. Genotator can function via command-line arguments or with the graphical user interface (*http://www-hgc.lbl.gov/inf/annotation.html*).