analytical genomics team provides statistical and advanced algorithmic expertise. Tasks include development of model-based methods for data capture, signal processing, and feature extraction for DNA sequence and fingerprinting data and analysis of the effectiveness of newly proposed methods for sequencing and mapping.

Instrumentation

The instrumentation group also has multiple components. Group members provide expertise in instrumentation and automation in high-throughput electrophoresis, preparation of high-density replicate DNA and colony filters, fluorescence labeling technologies, and automated sample handling for DNA sequencing. To facilitate seamless integration of new technologies into production use, this group is coupled tightly to the biologist user groups and the informatics group.

Collaborations

The center interacts extensively with other efforts within the LLNL Biology and Biotechnology Research Program and with other programs at LLNL, the academic community, other research institutes, and industry. More than 250 collaborations range from simple probe and clone sharing to detailed gene family studies. The following list reflects some major collaborations.

- Integration of the genetic map of human chromosome 19 with corresponding mouse chromosomes (ORNL).
- Miniaturized polymerase chain reaction instrumentation (LLNL).
- Sequencing of IMAGE Consortium cDNA clones (Washington University, St. Louis).
- Mapping and sequencing of a gene associated with Finnish congenital nephrotic syndrome (University of Oulu, Finland).

Accomplishments

The LLNL Human Genome Center has excelled in several areas, including comparative genomic sequencing of DNA repair genes in human and rodent species, construction of a metric physical map of human chromosome 19, and development and application of new biochemical and mathematical approaches for constructing ordered clone maps. These and other major accomplishments are highlighted below.

- Completion of highly accurate sequencing totaling 1.6 million bases of DNA, including regions spanning human DNA repair genes, the candidate region for a congenital kidney disease gene, and other regions of biological interest on chromosome 19.
- Completion of comparative sequence analysis of 107,500 bases of genomic DNA encompassing the human DNA repair gene *ERCC*2 and the corresponding regions in mouse and hamster (p. 32). In addition to *ERCC*2, analysis revealed the presence of two previously undescribed genes in all three species. One of these genes is a new member of the kinesin motor protein family. These proteins play a wide variety of roles in the cell, including movement of chromosomes before cell division.
- Complete sequencing of human genomic regions containing two additional DNA repair genes. One of these, *XRCC*3, maps to human chromosome 14 and encodes a protein that may be required for chromosome stability. Analysis of the genomic sequence identified another kinesin motor protein gene physically linked to *XRCC*3. The second human repair gene, *HHR*23A, maps to 19p13.2. Sequence analysis of 110,000 bases containing *HHR*23A identified six other genes, five of which are new genes with similarity