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NIH NCHGR Genome Program Reorganizes

Changing Technology, Research Direction Require Flexibility

The rapid pace of today's technology revolution poses management challenges for any technology-based research organization. This is particularly true for genome research, in which specific goals are completed and new ones set. Now in its fifth research year, the NIH National Center for Human Genome Research (NCHGR) has reorganized its genome program administration to foster and stay abreast of new technology developments and remain flexible in responding to changes in research direction precipitated by those developments.

The new organization scheme acknowledges that large, multicomponent projects are central to all aspects of NCHGR-sponsored genome research. Spreading these larger components across the entire program will enable better advance planning and communication among the staff with respect to policy and administrative and management practices. This in turn will lead to more uniformity and consistency in decision making and interaction with grantees.

When NCHGR was established in 1989, the scientific component was organized according to the administrative mechanism by which grants were awarded. This plan distributed the workload and focused on getting the research program up and running as soon as possible. Projects funded by "R01" single-investigator grants were managed by the Research Grants Branch, whereas larger, multidisciplinary projects were funded and managed by the Centers Branch. The Ethical, Legal, and Social Implications (ELSI) Branch, begun as part of the Research Grants Branch, became a separate branch in 1992.

As goals of the first 5-year plan began to be met and new challenges presented themselves, NCHGR reorganized its research program to reflect new technology advances and prepare for future ones. "Genome science was evolving so rapidly," says Mark Guyer, NCHGR Assistant Director for Program Coordination, "we recognized it would be most efficient if the program were organized to be as flexible and responsive to technology developments as possible. It would not be surprising if further organizational changes were needed in 4 to 5 years."

In addition, he says, the new organization ensures that all program staff manage grant portfolios that include cutting-edge projects and allow the staff to gain experience with a variety of technologies and funding mechanisms. The program branches were reorganized and renamed to reflect most closely the way genome science is likely to develop over the next few years. Each branch will manage a set of large, multidisciplinary Genome Science and Technology Center projects (called GESTECS) and a set of regular research (R01) grants, pilot projects, conference grants, and other funding mechanisms in support of technology development in a particular research area.

The new branches are briefly described on the next page. The Sequencing Technology Branch is featured on p. 3; the other branches will be described in future issues.

Four Branches To Coordinate New Research Challenges

- Mapping Technology
- Mammalian Genomics
- ELSI
- Sequencing Technology

In This Issue. . .

Genome News

NCHGR Structure To Facilitate Planning, Communication, Consistency

Mapping Technology Branch (301/496-7531). *Bettie Graham, Chief; Elise Feingold, Program Director; Midge Bajefsky, Grants Technical Assistant:* Supports research with special emphasis on technology development to improve the efficient construction, annotation, resolution, information content, and usefulness of genetic and physical maps. Specific areas of interest include strategies for identifying genes, coding regions, and other functional elements in genomic DNA and techniques for high-throughput mapping and sequencing of cDNA. This branch is also the NCHGR focal point for training, career development, and special programs. Its staff plan and administer programs of individual pre- and postdoctoral fellowships, institutional training grants, career awards, minority scientist awards, international collaborations, short courses, and chromosome-specific workshops and other meetings.

Mammalian Genomics Branch (301/496-7531). *Jane Peterson, Chief; David Benton, Director, Genome Informatics Program; Jeffrey Schloss, Program Director; Molly Hilty, Grants Technical Assistant; Asli Yucel, Grants Technical Assistant:* Administers and supports research on the highly efficient construction of complete genetic and physical maps of mammalian chromosomes and genomes and on the sequencing of large (megabase) regions of mammalian DNA. The branch also serves as the focal point for development of the GESTEC program and supports research in genome informatics (including database research, development, and maintenance) and research into algorithms and techniques for genomic analysis.

ELSI Branch (301/402-4997). *Eric Juengst, Chief; Elizabeth Thomson, Genetic Services Research Coordinator; Wanda Seawright, Grants Technical Assistant:* Fosters public education and discussion of ELSI concerns and supports research to anticipate and resolve such issues arising from human genome research. Investigating ELSI issues concurrently with scientific advances is a novel approach prompted by concern about the responsible use of information generated by genome technologies. The ELSI program has defined three priority areas of research: (1) clinical practices to introduce new genetic services, (2) access to and use of personal genetic information by parties outside the clinical setting, and (3) public and professional understanding of concepts and issues surrounding human genetics.

Sequencing Technology Branch (301/496-7531). *Bob Strausberg, Chief; Carol Dahl, Program Director; Ommie Smith, Grants Technical Assistant:* See the article on page 3 for a detailed description of this branch.◊

Notes from HGMIS

DOE 1993 Program Report Available

The DOE *Human Genome 1993 Program Report* was published in March and is available to requesters. The report, a supplement to the red-covered 1991–92 report, contains information on DOE Human Genome Program management and centers as well as abstracts of DOE-funded research. Copies can be obtained from the Human Genome Management Information System (HGMIS) at the address on page 12.

Newsletter Receives Awards

HGMIS received awards for its publications in the 1994 competition sponsored by the Society for Technical Communication (STC). *Human Genome News* won an Award of Achievement, and the article "Researchers Report Mapping Progress" was given an Award of Merit at the presentation ceremony on February 23. STC chapters in North and South Carolina were responsible for judging the entries, which included 20 in the newsletter category and 116 overall.

HGN Conserving Resources

To save on distribution costs, *Human Genome News* is being sent by bulk mail to domestic and foreign subscribers. Beginning with the January issue, newsletters to foreign addresses are shipped by International Surface Air Lift (ISAL), in which bulk mail is flown from the United States for distribution overseas. ISAL promises reduced mailing costs and faster overseas delivery. Additional savings are realized by generating 9-digit zip codes from a U.S. Postal Service–approved database. HGMIS would like to be informed of undue delays or inconsistencies in newsletter delivery.

DOE Primer Available on WWW

The full text and graphics of the *Primer on Molecular Genetics* are now available to millions of Internet users via the World Wide Web (WWW) at *http://www.gdb.org/hopkins.html*, as well as by Gopher to the Johns Hopkins University Computational Biology system at *gopher.gdb.org* [see *HGN* 5(3), 8 (September 1993)]. DOE program reports and current and back issues of *Human Genome News* are also accessible at the Gopher address.

Over 27,000 paper copies of the primer, produced by HGMIS, have been distributed since 1992. The primer, which is being extensively revised and updated, has been requested by such groups as secondary and college teachers, genetics counselors, medical schools, educational organizations, genome centers, biotechnology companies, and attendees at professional meetings. In great demand for genetics courses, the primer is also being used by the Project on Court-Adjudicated and Court-Ordered Health Care as a basis for constructing a judicial reference book [see *HGN* 5(6), 1–3 (March 1994)].◊

☛ Video Available

A set of eight 60-min. videotapes is available for *The Secret of Life*, a series funded by NIH and DOE and shown last year on public television. The series explores how scientists' ability to decipher and manipulate genes will transform medicine and affect human lives. #3342. Tapes are also available separately. [Contact: Films for the Humanities & Sciences; P.O. Box 2053; Princeton, NJ 08543 (800/257-5126, Fax: 609/275-3767).]◊

Genome News

NCHGR Sequencing Branch States Goals

The philosophy and recent activities of the Sequencing Technology Branch, directed by Robert Strausberg and Carol Dahl, are highlighted in this article. Other NCHGR branches will be covered in future issues.

The NIH National Center for Human Genome Research (NCHGR) formed the Sequencing Technology Branch to support research toward several interrelated goals, including the following.

- Determine the complete genomic DNA sequence of several nonmammalian model organisms including *Caenorhabditis elegans, Drosophila melanogaster, Saccharomyces cerevisiae*, and *Escherichia coli.*
- Refine, fully automate, and integrate systems of current sequencing approaches to achieve tenfold improvements in sequencing capability.
- Develop novel methods, technologies, and instruments for fully integrated, innovative approaches to rapid, low-cost determination of DNA sequence. These new approaches are expected to offer 20- to 30-fold improvements in speed and cost.
- Serve as the NCHGR focal point for extramural technology transfer activities and promote collaborative multidisciplinary research with close integration among academic and industrial research laboratories.

Research Accomplishments and Challenges

Much effort and substantial resources will be needed to accomplish the ambitious sequencing technology goals of the Human Genome Project. However, encouraging progress and new ideas in sequencing technology development have come forth this year. Technological paths are now envisioned, say Dahl and Strausberg, for accomplishing and possibly exceeding the original sequencing goals of the project.

Recent advances in automating gel-based technology have resulted in significantly improved sequence throughput. These advances will require systems integration to match sample flow with data flow through all steps of the process. A particular need now is improved informatics, especially for the finishing stages of genomic sequencing. In addition, with the increase in DNA sequence throughput, better systems are needed to handle information output; these include improved data-management tools and analysis software.

Advances in capillary electrophoresis and ultrathin gel electrophoresis are projected to improve parallelization and speed of DNA analysis at least tenfold. In addition, new efforts are being undertaken to apply microfabrication and microelectromechanical systems technology to the sample preparation and separation steps and

(continued)

Projected Advances in Technology Development

- **Sequence Throughput**
- **DNA Analysis**
- **Sample Preparation, Separation**

NCHGR Sequencing Technology Development Plan

The following plan for sequencing technology development and transfer provides a philosophical framework for activities of the NCHGR Sequencing Technology Branch. The plan was prepared by Robert Strausberg and Carol Dahl.

Effective technology development and transfer are key to accomplishing the sequencing goals of the Human Genome Project. Technologies for rapid, cost-effective DNA sequencing and mapping will maximize the usefulness of the ultimate information and resource products of the Human Genome Project.

These technologies, information, and resources will revolutionize biological and biomedical research, diagnostics, and therapeutic strategies. The way basic science research is conducted in both large and small laboratories will change profoundly. These changes, which may have their greatest impact in smaller laboratories, will provide the resources for creative new approaches to complex scientific concepts.

Strategies for technology development and transfer must ensure that genome products are rapidly introduced in the marketplace. These products will impact basic health care for the general public and find a wide variety of applications in the biotechnology, pharmaceutical, agricultural, chemical, and other industries.

Collaborative approaches among academic and industrial laboratories—with close integration at all stages of research, development, and implementation—often are the most effective for developing products best suited to the needs of the user community. No preconceived notions should determine which group will take the lead in the initial research stages. Instead, the focus should be on building the best team for the task.

Within the Sequencing Technology Branch, some projects are focused more on producing genomic sequence, while others are targeted toward developing new technologies. This programmatic balance is needed to ensure that technology development within the branch addresses the truly important issues.

Initial plans for developing new technology or instrumentation should consider how the technology will be made available to the community. This is important because emerging markets for critical technologies will be small in some cases, and the commercial incentive may not be apparent immediately.

In many cases, effective skills and resources are expected to come from industry-to-industry interactions. For example, startup Company A may have better skills in innovative research and no preconceived notions or products that limit creativity, whereas established Company B may have more skills in the finishing stages of product development, marketing, and sales. Similarly, two startup companies may have complementary basic skills and knowledge.

Also, with many government organizations having effective programs in technology development, coordination of those efforts is vital. Because the link between basic technology and application is sometimes not obvious, a general sense of other technology programs that currently seem far removed from the genome project is important.

Genome News

NCHGR Sequencing Branch Collaborating with NIST ATP To Enhance Technology Development

mass spectrometry to the separation step. These methods could afford a 100- to 1000-fold increase in speed and associated decreases in cost. Independent improvements must be made in methods for sample preparation, assay technology, detection systems, and data management and analysis. Ongoing efforts to develop fully automated and integrated modular systems based on current approaches are likely to benefit the development of newer miniaturized technologies under way in the NCHGR program and elsewhere.

The notion that new sequencing technologies would be an important product of the Human Genome Project was a common theme throughout the NIH-DOE planning process for the new 5-year plan (1994–98). Development of these technologies provides an unprecedented opportunity to interface technology development with biological research.

Sequencing Beyond the Reference Human Genome

The force driving sequencing-technology development for the Human Genome Project is the need for cost-effective methods to sequence the human and other genomes. Such technology should also serve as a platform for developing instrumentation for DNA sequence analysis in a wide variety of applications in the diagnostic, clinical, environmental, forensic, and agricultural markets. Successful implementation of these instruments will require substantial engineering design changes to address specialized needs. In medical diagnostic applications, for example, an ideal system might inject a biological sample into a cassette, automatically position the cassette in a reader, automatically and accurately determine the results, display them on a computer screen, and immediately transfer the results to the patient's record. For environmental or agricultural uses, readily transportable, miniaturized, handheld devices would be desirable. Others outside the Human Genome Project who are studying the effects of environmental mutagens will require sequencing instruments with a very high degree of sensitivity. Goals will include searching for rare genetic changes in cell populations.

Agencies Cooperating To Develop New Sequencing Technology Applications

NIH and DOE can interface effectively with other federal agencies to facilitate further development and application of genome technologies in the marketplace. Toward that end, Strausberg and Dahl have developed extensive collaborations with the staff of the Advanced Technology Program (ATP) of the National Institute of Standards and Technology (NIST) within the U.S. Department of Commerce.

The mission of ATP is to stimulate economic growth in the United States through technology development and deployment to the marketplace. Projects selected for support by ATP have the potential for broad-based economic impact but a relatively high technical risk and a long time horizon. Funding is through cooperative agreements with companies or industrial consortia. The ATP mission is well suited to advancing DNA sequence-based technologies to serve the needs of many markets. [See *HGN* 5(5), 5 (January 1994).]

NCHGR sequencing technology staff and Stanley Abramowitz, manager of the ATP Biotechnology Program, organized a workshop on ATP funding at "The Human Genome Project: Commercial Implications" meeting this spring in San Francisco. The workshop emphasized ATP interest in biotechnology and pointed to projects already supported by ATP for developing transgenic animals and oligonucleotide array hybridization.

Dahl and Strausberg, who are formally detailed part-time to NIST, will continue to work with ATP managers. Other federal agencies have also been identified as having technology-development programs that could interface well with the Human Genome Project. Through such interagency collaboration, products of the Human Genome Project will be positioned more effectively to impact biology, medicine, and many other areas of opportunity.◊

Broido Joins DOE OHER

Michelle S. Broido recently joined the Health Effects and Life Sciences Research Division of the DOE Office of Health and Environmental Research (OHER) in Germantown, Maryland. Her responsibilities as Structural Biologist will involve a range of activities supported by the three OHER divisions. As a member of the Structural Biology Task Group and the Human Genome Task Group, Broido is expected to focus on technological developments in nuclear magnetic resonance (NMR), genome instrumentation, the problem of protein folding, the use of structural biology databases such as Protein Data Bank, and other issues in computational biology.

Broido comes to OHER from the NIH National Institute of General Medical Sciences, where she served for 4 years as a program administrator in the Biophysics and Physiological Sciences Program. Her research grant portfolio included nucleic acid biophysics; protein biophysics, including protein folding; and NMR spectroscopy. She was also responsible for management and oversight of institutional structural biology predoctoral training grants and for administration of the individual minority predoctoral fellowship program. This program was established to help support the graduate education of students from minority groups underrepresented in the biomedical sciences.

Broido obtained her Ph.D. in chemistry at the University of California, San Diego. Her research there concentrated on NMR applications for determining the dynamics and three-dimensional structure of nucleic acid oligomers. As an NIH postdoctoral fellow, she spent 2 years at the Weizmann Institute of Science in Rehovot, Israel, where her studies centered on the use of electron paramagnetic resonance to probe the dynamics of fatty acids in model membrane systems. Upon completion of her postdoctoral training, Broido was a tenured faculty member at Hunter College and the Graduate School of the City University of New York.◊

ELSI Group Lists Health-Care Reform Basics

As the Human Genome Project uncovers more disease genes, "it is likely in the next few years that every one of us will have a preexisting condition and be uninsurable," said Hillary Rodham Clinton in a speech last September to the audience at the Lasker Awards. The First Lady has cited the Human Genome Project several times recently as one more reason for health-care reform.

In mid-February, the DOE-NIH Joint Working Group on the Ethical, Legal, and Social Implications (ELSI) of Human Genome Research, chaired by Nancy Wexler (Columbia University), met in Washington, D.C., to discuss the implications of health-care reform for people with or at risk for genetic disease. In a report on genetic information and health insurance released last May [*HGN* 5(2), 1–2 (July 1993)], the working group concluded that ensuring fair and affordable health insurance would require modification of the current health-care system. The report called for universal access to a broad array of services and contained several recommendations to the President's Task Force on Health Reform about how to achieve that goal.

At the February workshop, experts on health policy, law, ethics, and genetic diseases gathered to evaluate how each of the half-dozen major proposals for health-care reform would affect people with or at risk for genetic disease. The bills vary greatly in detail and are likely to change substantially as they wend their way through congressional committees. Even so, workshop participants identified several features to be included in any health-care-reform package:

- universal access to a comprehensive set of benefits, including genetic services;
- protection against arbitrary denial of affordable health insurance due to genetic conditions; and
- safeguards to protect the confidentiality of genetic health information about individuals and families.

Universal Coverage

Participants agreed that any reform bill must provide universal access to health care. If not, inequities in the existing health-care system—in which some 39 million Americans may be uninsured—will only be exacerbated. "Discrimination is common today in our employment-based system for health-care coverage," noted Kay Johnson (March of Dimes). "Health status discrimination among individuals has long been legally, ethically, and socially acceptable. Only some specific forms of discrimination based on race, color, religion, gender, national origin, and disability are illegal." Without reform, she warned, genetic knowledge can become a new tool for excluding people from the health-care system.

All major bills either prohibit or restrict exclusions based on preexisting conditions, but such protections alone are not enough to ensure universal access to affordable health insurance, attendees agreed. In fact, only two bills would actually deliver such access, said Peter Budetti (Director, Center for Health Policy Research, George Washington University); these are the Clinton bill or Health Security Act of 1994 and the "single-payer plan" introduced by Sen. Paul Wellstone (D-Minn.) and Rep. Jim McDermott (D-Wash.).

"Universal" coverage means something different in each bill, explained Robert Griss (Center on Disability and Health). In the "Managed Competition Act" introduced by Rep. Jim Cooper (D-Tenn.), for instance, employers must offer workers the opportunity to buy into a plan but have no obligation to pay for it. According to a recent analysis by the Congressional Budget Office, Griss said, 25 million Americans would remain uninsured.

(continued)

Copies of the May 1993 Report of the Task Force on Genetic Information and Insurance are available from

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Narla Named Acting Director of LBL Center

Mohandas Narla, head of the Department of Cell and Molecular Biology at Lawrence Berkeley Laboratory (LBL), has been named Acting Director of the LBL Human Genome Center. He succeeds geneticist Jasper Rine, who has returned to full-time research as a faculty member at the University of California, Berkeley (UCB).

Mohandas Narla

Narla, a native of Madras, India, has been a senior staff scientist in the LBL Life Sciences Division since 1989 and has served on the staff of the University of California, San Francisco, since 1976. He received his bachelor's degree from the University of Madras and master's degree from the Indian Institute of Technology, Kanpur. He was awarded the Doctor of Science degree from Washington University in St. Louis in 1971.

Narla's research involves biophysical, biomechanical, and molecular biological approaches to understanding the red blood cell membrane assembly. Also, in collaboration with Eddy Rubin (LBL), Narla is exploring transgenic mouse systems and homologous recombination methods in developing animal models of sickle cell disease and thalessemias. He is a member of the American Society of Hematology and the American Society of Cell Biology.

Under Narla's direction, the genome center is expected to undertake large-scale sequencing of the human and *Drosophila* genomes. The center has been studying the fruit fly in collaboration with a team headed by Gerald Rubin (UCB), principal investigator for an NIH center whose goal is to complete the mapping of the *Drosophila* genome. Mina Bissell, Director of the LBL Life Sciences Division, says that LBL hopes to be a major participant in this effort.◊

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Privacy Issue Being Addressed Separately from Health Care

Access to What?

Even for those bills that do provide universal access, the key question is, Access to what services and treatments? Clearly, with concerns about cost containment high, not all genetic services would be covered in the various basic plans, but the proposed legislation gives only general guidance about what might be included. In the Clinton proposal, for example, consumers would choose from various plans administered by insurance-purchasing pools or alliances. Each plan would offer at least a basic set of benefits. A national health board and Congress would decide what belongs in the basic minimum benefit package. As written, the Clinton package includes "preventive family planning" and "pregnancy-related" and "diagnostic" services—presumably, genetic testing could fall under those categories. Similarly, the Cooper bill states that the basic benefits package shall include a full range of diagnostic services, including "appropriate screening."

A crucial question relevant to all the bills is who decides what is in the basic package, said Budetti. Specifically, he asked, how much should be spelled out in legislation and how much should be left up to a national board? Would the genetics community (which the group understood to be both providers and receivers of genetic services) be served best by specific or generic language in the bills? Concerning the "clinical preventive services" in the Clinton basic plan, Budetti asked, "Do you want them vague or more defined than this? We can't anticipate all preventive services. There is a danger in being too specific in the statute, in being locked into 1994 science."

Access to genetic services will hinge on several other features of any health-care proposal, participants noted. One is whether the various proposals cover experimental therapies, as many genetic services are likely to be classified. Similarly, coverage of long-term and rehabilitative treatment of congenital health problems will be critical to those with genetic disorders. Will people have access to specialists and academic health centers, where much of genetic testing and other advanced services are done today?

Privacy of Genetic Information

Any health-reform measure must establish rigorous procedures to ensure the confidentiality of health and genetic data. "If you look closely at the current situation for the legal protection of privacy," said Lawrence Gostin (Georgetown University Law Center), who chaired the privacy committee of the President's Task Force on Health Care Reform, "you will find it is highly limited and inadequate. State laws are inadequate and variable." What's more, as the Human Genome Project advances, "the health data that could be generated could provide a complete profile of patients. It warrants our serious attention," said Gostin.

At a minimum, Gostin called for preemptive federal legislation to guarantee the privacy of genetic and other health information and to establish a data-protection board. Individuals should have the right to review and correct personal data, and the data should be used only for the purposes authorized. All the major bills recognize the need to ensure the privacy of health data, including genetic data, although only three describe it in detail.

NIH NACHGR Issues Statement on Use of DNA Testing for Presymptomatic Identification of Cancer Risk

The following statement was adopted by the NIH National Advisory Council for Human Genome Research (NACHGR) at its scheduled January meeting in Washington, D.C., and endorsed by the DOE-NIH Ethical, Legal, and Social Implications Working Group. [Reprinted from JAMA 1994; 271: 785]

Recent advances in the genetics of cancer have raised the possibility of widespread DNA testing for the detection of predisposition to cancer. This may allow individuals at high risk to avail themselves of preventive measures and potentially avoid early death. At least one company has already announced plans to begin offering testing for genetic cancer risk. While much alleviation of human suffering may eventually result [from] these advances in cancer genetics, a number of important questions must be addressed before widespread testing of this sort can be recommended.

Two relatively common heritable cancer risk genes have recently been located. Among people with colon cancer, it appears that as many as 10% carry an altered germline copy of a gene called *MSH2*.[1-3] Individuals with an altered *MSH2* gene face an approximately 80% risk of colon cancer; women also have an elevated risk of endometrial and ovarian cancer. Intense medical surveillance may be beneficial in preventing cancer deaths in this high-risk group.[4]

Similarly, approximately 5% of women with breast cancer have inherited an altered copy of the *BRCA1* gene, which has been pinpointed to a small region of chromosome 17.[5] As the gene itself has not yet been identified, *BRCA1* mutation carriers currently can only be identified by linkage analysis, which requires DNA samples from several affected relatives. A woman with an inherited *BRCA1* mutation faces an approximately 85% lifetime risk of breast cancer and an elevated risk of ovarian cancer. Medical or surgical interventions may be effective in reducing the risk of cancer death for these women, but their effectiveness has not been fully evaluated.[6,7]

Despite the promise of these discoveries for benefiting humankind, it is premature to offer testing of either high-risk families or the general population as part of general medical practice until a series of crucial questions has been addressed. These questions include, but are not limited to, the following:

- How many different mutations of *MSH2* and *BRCA1* will be found, what are their actual frequencies, and what is the risk of cancer associated with each?
- What are the technical and laboratory issues associated with detection of mutations in these genes, what frequency of false-positive and false-negative results will occur, and how can quality control of testing be assured?
- How effective are interventions to prevent cancer morbidity and mortality in high-risk families and in the general population?
- How can education about the complexities of DNA testing be provided to large numbers of potentially at-risk individuals, how can informed consent be ensured, and how can effective, culturally sensitive, nondirective genetic counseling be offered about such profoundly wrenching issues?

In addition, members discussed the Fair Health Information Practices Act of 1994, introduced in March by Rep. Gary Condit (D-Calif.), that addresses many concerns about genetic privacy. This bill establishes safeguards for information arising from either medical treatment or payment, explained Robert Gellman (general counsel to the House Committee on Government Operations). Under the proposed system, information would be protected wherever it may be, Gellman said, in contrast to the current situation in which information is protected only in a doctor's office. Other participants worried that this legislation does not go far enough. It will not, for example, protect data that emerge from such other sources as DNA fingerprinting and genetic counseling or are generated by health research.

Special Treatment?

Participants grappled repeatedly with the question of whether the genetics community should seek "special treatment" in health-care reform by specifying which genetic technologies would be covered and asking for protection of genetic information. "The [ELSI] health insurance task force labored for a year to make a case that genetic risks are different," noted ethicist Tom Murray (Case Western Reserve University). "We had to abandon it. I think that all health risks ought to be covered equally."

Marsha Saxton (The Project on Women and Disability) stated that individuals with or at risk for genetic disease will simply encounter discrimination before the rest of society does. In this regard, they might be compared with canaries in a mine.

While analyzing any of the proposals in terms of how well they deal with issues raised by genetic advances, one overriding point should be kept in mind, Budetti cautioned. "The heart of the political question is not a choice between a good bill and a perfect bill but a pretty good bill and phony reform. We can say what's missing from this particular bill, but . . . what will happen to the current system without reform?"◊

☛ NIGMS Repository Resources

The NIH National Institute of General Medical Sciences (NIGMS) Human Genetic Mutant Cell Repository is distributing the following resources:

REGIONAL MAPPING PANELS (cell cultures or DNA). Panels consisting of human-rodent somatic cell hybrids with deletion or derivative human chromosomes are available now for chromosomes 11, 15, 17, and 18 and will be obtainable soon for other human chromosomes. Panels have been characterized by (1) G-banded chromosome analysis, (2) in situ hybridization using biotinylated total human DNA, and (3) Southern blot hybridization.

ONLINE CATALOG. This first-generation catalog contains all the textual material in the printed catalog as well as additional information for each listing. Cultures are cross-referenced to allow users to search by disease category for all fibroblast and lymphoblast cell lines and related DNA samples in the repository's collection.

[Information or catalog: NIGMS Human Genetic Mutant Cell Repository; Coriell Cell Repositories; Coriell Institute for Medical Research; 401 Haddon Ave.; Camden, NJ 08103 (800/752-3805 or 609/757-4848, Fax: -9737). Catalog access via Internet: telnet to *coriell.umdnj.edu* (at login prompt, type *online*). Access via modem: 609/757-9728 (long distance telephone charges apply, but no additional charge for connect time).] ◊

- Finally, how will the possibility of genetic discrimination against those found to be at high risk be avoided?

Gathering the information and establishing the protocols that will be needed to safely integrate genetic testing and counseling for cancer risk into clinical practice can best be accomplished through a coordinated set of clinical research studies. An initiative to sponsor such studies is currently being launched by the National Center for Human Genome Research, the National Cancer Institute, the National Institute of Mental Health, and the National Institute for Nursing Research. Such studies should be widely available, prepared to handle the magnitude of requests for testing, and should provide as complete information about the tests and their limitations as possible. Until more information is available to address these critical issues, it is premature to offer DNA testing or screening for cancer predisposition outside a carefully monitored research environment.

1. R. Fishel, M. K. Lescoe, M. R. S. Rao, et al., "The Human Mutator Gene Homolog *MSH2* and Its Association with Hereditary Nonpolyposis Colon Cancer," *Cell* 75, 1027–38 (1993).

2. F. S. Leach, N. C. Nicolaides, N. Papadopoulos, et al., "Mutations of a *Mutʃ* Homolog in Hereditary Non-Polyposis Colorectal Cancer," *Cell* 75, 1215–25 (1993).

3. R. Parsons, G. M. Li, M. J. Longley, et al., "Hypermutability and Mismatch Repair Deficiency in *RerI*⁺ Tumor Cells," *Cell* 75, 1227–36 (1993).

4. H. T. Lynch, T. C. Smyrk, P. Watson, et al., "Genetics Natural History, Tumor Spectrum, and Pathology of Hereditary Nonpolyposis Colorectal Cancer: An Updated Review," *Gastroenterology* 104, 1535–49 (1993).

5. D. F. Easton, D. T. Bishop, D. Ford, et al., "Genetic Linkage Analysis in Familial Breast and Ovarian Cancer: Results from 214 Families," *Am. J. Hum. Genet.* 52, 678–701 (1993).

6. B. B. Biesecker, M. Boehnke, K. Calzone, et al., "Genetic Counseling for Families with Inherited Susceptibility to Breast and Ovarian Cancer," *JAMA* 269, 1970–74 (1993).

7. M. C. King, S. Rowell, S. Love, "Inherited Breast and Ovarian Cancer: What are the Risks? What are the Choices?" *JAMA* 269, 1975–80 (1993).◊

National Advisory Council for Human Genome Research

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Genome News

Discussion Topics

- Databases
- ELSI
- Intellectual Property Rights
- Material Sharing

Article adapted from the *HUGO Genome Digest*.

HUGO Hosts First Genome Summit

The first HUGO International Genome Summit Meeting, hosted by the Human Genome Organisation (HUGO) and organized by HUGO President C. Thomas Caskey, was held in January in Houston. HUGO convened the meeting to identify common areas of interest and joint activities among various national and regional genome programs. Scientific and administrative delegates from 13 genome programs also defined areas where future international collaboration would be beneficial.

To set the scene for later discussions, the summit opened with overview presentations from four genome scientists. Kay Davies (University of Oxford, U.K.) outlined the development and future directions of the Human Genome Project, with Eric Lander (Whitehead Institute) discussing the importance of such model systems as the mouse. The current state of sequencing technology was summarized by Leroy Hood (University of Washington, Seattle), and John Sulston (Sanger Center, U.K.) discussed the international collaborative efforts to sequence the *Caenorhabditis elegans* genome.

Individual delegates presented brief summaries of their own genome programs and the contributions they could make to the international project. Countries and organizations represented were Australia; Canada; Commission of the European Union; France; Italy; Japan; Latin America; Netherlands; Russia; United Nations Educational, Scientific, and Cultural Organization; United Kingdom; United States; and the World Health Organization.

The presentations showed the many different efforts and initiatives that are moving the Human Genome Project forward. In addition to obvious differences in the size of individual national and regional programs, great variation in content, structure, and priorities also became apparent. Nevertheless, numerous common problems or concerns began to emerge, and these concerns were explored in more detail on the second day of the summit. Discussions were held under four broad headings: Databases; Ethical, Legal, and Social Issues (ELSI); Intellectual Property Rights; and Material Sharing.

Databases. Dialogues focused on the kind and quality of data currently being stored; the need for analyzing stored data in an increasing number of different ways (e.g., searching sequence data for biological motifs as well as for coding, noncoding, and regulatory regions); and on the growing likelihood that a single monolithic database will not be able to meet all future needs. An alternative possibility is to develop a federated system of databases, each transparently connected to the others. Scientists addressing biological questions to the database network would gain access to information stored in various formats in different databases; this information could then be integrated into a more meaningful whole. These summit considerations will provide invaluable input to HUGO scientists who formulate principles and policies for recommendation to the wider scientific community.

ELSI. Some participants pointed out that the promise of the Human Genome Project is accompanied by certain perils, pitfalls, and problems that no single approach can tackle. Multiple approaches are needed to develop international "best practices" in at least five key areas: counseling, choice, consent, control, and confidentiality. HUGO clearly has a coordinating role in this area and through its Ethics Committee will continue to address these challenges.

Intellectual Property Rights. On the question of patenting DNA, delegates expressed a lack of support for patenting full-length or partial sequences of undetermined function. This unanimous view was passed on to NIH Director Harold Varmus in hopes of aiding the decision about appealing the Patent and Trademark Office ruling. On February 11, NIH withdrew the applications from the appeals process. On February 12, the Medical Research Council followed suit. [For more information, see *HGN* 5(6), 6–7, 12 (March 1994).]

Material Sharing. Discussions centered largely on current arrangements for screening and distributing libraries. HUGO's coordination of data about the availability of libraries and screening facilities in all parts of the world has been hampered by only partial response from users, but the need for such coordination was reaffirmed.

Special Lectures. During the summit, Nancy Wexler (Columbia University) delivered the 1994 Jeanette Oshman Efron lecture. Her topic was the search for the Huntington's disease gene locus and implications for the public of the availability of personal genetic data. James A. Baker, III, former U.S. Secretary of State, presented a special lecture in which he used the development of foreign affairs policies to illustrate the importance of international collaboration for the Human Genome Project.◊

☛ Chromosome 4 Networking

An e-mail message may be sent to everyone on the Stanford University Human Genome Mapping Center (HGMC) chromosome 4 mailing list by ftp at the address *chrom4@toolik.stanford.edu*. To see the mailing list, log on by anonymous ftp and retrieve the file *chrom4_ftp_list* from the directory *pub/hgmc/misc*.

Primer pairs are obtainable from Research Genetics for 935 HGMC sequence tagged sites (STSs) on human chromosome 4 [see *Human Molecular Genetics* 2(8), 1271–88 (1993)]. Details of all the STSs—including names, Genome Data Base locus names, GenBank® accession numbers, primer sequences, polymerase chain reaction fragment size, and bin number—are available on the anonymous ftp server (*toolik.stanford.edu*) in the *pub/hgmc/sts_data* directory. Requests to Research Genetics should state that the STSs are from HGMC and should include locus name and STS name. [Research Genetics; 2130 Memorial Parkway SW; Huntsville, AL 35801 (800/533-4363 or 205/533-4363, Fax: /536-9016; United Kingdom, 800/89-1393)].◊

Genome News

Computational Molecular Biology Workshop

The third international workshop on Open Problems of Computational Molecular Biology was held July 11–25, 1993, in Telluride, Colorado. The meeting was organized by Andrzej Konopka (BioLingua Research) and Peter Salamon (San Diego State University), with Danielle Konings (University of Colorado, Boulder) as meeting coordinator. The workshop was sponsored by the DOE Human Genome Program, Convex Computer Corporation, and BioLingua Research. Presentations and discussions focused on the four topics highlighted below.

Foundational Issues. Participants identified two logical problems with modeling techniques used in molecular biology. These problems result from lack of methods to (1) judge the formal correctness of sentences that contain ill-defined terms and (2) determine the degree to which a given model corresponds to the modeled phenomenon. This degree of correspondence is generally similar to what logicians call "material adequacy" of a model or definition.

Discussion revealed that the problem of formal correctness is solvable, at least in principle, by employing new mathematical methods (e.g., fuzzy logic) known from the fields of artificial intelligence, system theory, and pattern recognition. Participants were pessimistic, however, about inventing a general methodology for determining material adequacy. Some attendees pointed out that methods of addressing this problem on a case-by-case basis can and should be developed. Others suggested that such techniques should explore situation logic rather than classical, sentence-based logic. Another strategy would require creation of a new information theory based on language pragmatics instead of syntax. How much the two approaches overlap has been hotly debated, but conclusions have not been reached thus far.

Mathematical Modeling. Several discussions and presentations focused on (1) statistical approaches to determine biological significance of sequence and structural patterns in biopolymers, (2) new results concerning local compositional complexity of nucleotide and protein sequences, and (3) new mathematical models of molecular evolution, including classification of evolutionary landscapes and design of algorithms for traversing them.

Computational Issues. A number of new algorithms for sequence analysis, physical mapping of chromosomes, and sequencing by hybridization (SBH) were presented and discussed to facilitate the following.

- Estimation of protein-coding density in unannotated nucleotide sequences.
- Technique for determining coordinated changes in protein multiple-sequence alignments.
- Method to determine distant repeats in protein sequences.
- Software library for physical mapping of chimeric clones.
- Vocabulary of elementary RNA structures.
- Design of a low-redundancy SBH chip that can be miniaturized without sacrificing resolving power.

Structure Predictions. Methods were discussed for predicting protein folding pathways using hydrogen-exchange nuclear magnetic resonance experiments. A new protocol for configuring protein side chains in homology modeling also attracted considerable attention.

Collaborations. As in previous years, the workshop promoted collaborations among scientists from different fields and geographical locations. Topics include local compositional complexity of nucleotide and protein sequences, evolving rugged landscapes, mapping the space of RNA sequences into the space of secondary structures, and correlating surface contraction and expansion waves with differentiation in embryos of some species. *[Andrzej K. Konopka (BioLingua Research) and Peter Salamon (San Diego State University)]* ◊

Completed work initiated during the workshop and invited papers have undergone extensive peer review and will be published in the third special issue of *Computers and Chemistry* [18(3), 1994] devoted to computational molecular biology.

☛ Newsletter on Software for Technology Transfer

A quarterly newsletter describes U.S. government software available for commercialization and use from DOE and the National Aeronautics and Space Administration (NASA). *Software Technology Transfer* abstracts new and updated software packages and includes articles about companies and people who have made successful use of federally developed software. A bulletin board announces upcoming related events. The newsletter is published by COSMIC, the NASA Software Technology Transfer Center; the Energy Science and Technology Software Center (ESTSC); and the National Technical Information Service (NTIS) of the Department of Commerce.

COSMIC, the central repository for software developed under NASA funding, offers the following services:

- Annual printed catalog.
- Free subscription to *Software Technology Transfer* (available in United States only).
- Custom inventory search based on requester's key words.
- Periodic e-mail press releases about new and updated programs.
- E-mail user group conferences for computer programs CLIPS, TAE+, NETS, FEAT, and NQS.

Contact: COSMIC Product Information; University of Georgia; 382 East Broad Street; Athens, GA 30602-4272 (706/542-3265, Fax: -4807; Internet: *service@cosmic.uga.edu*).

ESTSC is the centralized management facility for software packages sponsored by DOE or the Nuclear Regulatory Commission (NRC). The center has about 200 NRC and 500 DOE technical and scientific packages ready for purchase and several hundred that can be made ready on request.

Contact: ESTSC; P.O. Box 1020; Oak Ridge, TN 37831-1020 (615/576-2606, Fax: -2865, Internet: *estsc@adonis.osti.gov*).

NTIS, the leading U.S. government agency in technical information exchange, uses the following methods to inform audiences about its services:

- Announces and provides technical reports of R&D and engineering activities sponsored by the United States and foreign governments.
- Manages the Federal Computer Products Center, which provides access to software, data files, and databases produced by federal agencies.
- Manages the Center for the Utilization of Federal Technology (CUFT), which runs the most active invention-licensing program in the U.S. government. CUFT also links U.S. firms to federal laboratory contacts and technologies with its directories and catalogs.
- Announces new R&D efforts from such leading industrialized nations as Japan, Germany, United Kingdom, and France.

Contact: NTIS; U.S. Department of Commerce; 5285 Port Royal Road; Springfield, VA 22161 (703/487-4807, Fax: 321-8547).◊

Genome News

Genome Informatics Minitrack at Hawaii Conference

To request a free copy of the published papers, send e-mail to *shin@cse.uconn.edu.*

For the second year, a Genome Informatics Minitrack was included in the Biotechnology Computing Track of the Hawaii International Conference on System Sciences (HICSS). More than 70 biologists, computational biologists, and computer scientists from the United States, Japan, France, and Switzerland attended the 27th meeting, which was held January 4–7 in Maui, Hawaii.

The minitrack was organized by Dong-Guk Shin (University of Connecticut) and Francois Rechenmann (National Institute of Informative and Automatic Research, France). Support was provided jointly by the National Science Foundation, NIH, and DOE. The minitrack included ten rigorously reviewed full papers and four extended abstracts in the following five research subareas of genome informatics.

Data Modeling and Management: modeling biological data and querying; requirements for a high-level database tool; unified way of modeling heterogeneous genomic databases using the Entity-Relationship data model; and adaptability of an interactive query system.

Sequence Analysis: tree data structure and its associated operations that reduce the cost of sequence comparison; approximate string search problem with an external search structure; and method of automating similarity search of expressed sequence tags.

Graphical User Interface: visualizing density and sequence maps; cross-referencing between Genome Data Base (GDB) and GenBank® sequence and map links; querying by form-based windows; aligning visually between genetic and sequence maps; supporting a high degree of interface portability; and graphically superimposing GDB locus data on corresponding information from a mouse chromosome.

Interoperation in Heterogeneous Computing Environment: way of making interoperation feasible between two heterogeneous genome databases by using ASN.1 as the common data-exchange language; and strategy that promotes open-system architecture and distributed computing environment for the biology community.

System Integration in Knowledge-Based Approach: method of modeling analysis tasks into knowledge-based objects; software tool designed to automate pre- and post-BLAST search activities using rules elicited from human experts; and deductive object-oriented language to streamline data-retrieval activities.

In addition to the presentation of formal papers, activity reports were presented from the Human Genome Mapping Center at Stanford University by Sidney Cowles and from the *Drosophila* Genome Center at the University of California, Berkeley, by Suzanna Lewis [Lawrence Berkeley Laboratory (LBL)]. The minitrack also included informal round-table discussion sessions moderated by Shin. Discussion leaders were Mary Berlyn (Yale University), Nathan Goodman (Whitehead Institute–Massachusetts Institute of Technology), Dick Douthart (Pacific Northwest Laboratory), and Manfred Zorn (LBL). Topics discussed in the open forum included standardization for genome database interoperability, relational vs object-oriented modeling of genome data, and use of Mosaic and World Wide Web for data integration across databases.

Plans are being made to include a minitrack on genome informatics at the next HICSS (for details, send an e-mail message to Larry Hunter at *hunter@ncbi.nlm.nih.gov*).

[Dong-Guk Shin, University of Connecticut] ◊

GDB Forum: Restructuring OMIM

To incorporate new information and integrate OMIM text with the resources of GDB and other databases, OMIM staff, assisted by an editorial board to provide expertise in specific areas, are restructuring OMIM entries. Defined sections of OMIM will permit links within entries and to other databases, and subject-area editors will be able to work simultaneously on different parts of the same entry.

Some entries may be split; this will permit database links between genes and disease phenotypes in cases of (1) multigene mutations that have the same phenotype or (2) multiple phenotypes that derive from different mutations in the same gene. All entries will eventually be restructured, with the most commonly used ones first, and become available online as they are completed.

The restructured OMIM documents are in Standard Generalized Markup Language (SGML) format, which allows easy conversion of documents for World Wide Web access, IRX generation, CD-ROM, and book production. Errors within documents can also be noted and corrected immediately.

Sections and Abbreviations of New OMIM Entry Structure*

- MIM Number [no]
- Title [ti]
- Description [id]
- Nomenclature [nm]
- Phenotype (contains Clinical Features, Biochemical Features) [pt]
- Genotype (contains Mapping Information, Molecular Genetics, Mode of Inheritance, Cytogenetics) [gt]
- Pathogenesis/Pathophysiology [pa]
- Diagnosis [dg]
- Clinical Management [tr]
- Population Genetics [pg]
- Evolution [ev]
- Animal Models [am]
- Historical Information [hi]
- Allelic Variants [av]
- References [rf]
- Clinical Synopsis [cs]
- Old MIM Number (if applicable)
- Edit Dates (with editor name) [ed]

*Only sections and subsections with information available will appear in the documents.

GDB Adds Nodes in Israel, Japan, and France

To increase GDB accessibility worldwide, additional nodes have been added in Israel, Japan, and France. These nodes offer database and user support services equivalent to those at GDB in Baltimore. To register for an account at any of the nodes, see contact information at right.

ISRAEL. The GDB Israel node is located at the Bioinformatics Unit of the Weizmann Institute of Science in Rehovot. The main objective of this site is to serve molecular biology needs in the scientific community, with emphasis on Human Genome Project research.

In addition to GDB and OMIM applications, data can be accessed through client software communicating with the following servers:

1. GDB/Accessor at Weizmann Institute
   Server: *inherit1.weizmann.ac.il*
2. World Wide Web server
   URL: *http://bioinformatics.weizmann.ac.il:70*
3. Gopher server: Bioinformatics (Weizmann Institute)
   Host: *bioinformatics.weizmann.ac.il* Port: 70
4. Anonymous ftp server: *bioinformatics.weizmann.ac.il*
   Address: 132.76.55.12

JAPAN. The GDB Japan node is run by the Japan Information Center of Science and Technology (JICST) in cooperation with the Institute of Physical and Chemical Research (RIKEN). Located in Tsukuba City, the node is supported financially by the Science and Technology Agency. Access to this node from Japan and other Asian countries is available via Internet and direct modem connection. A brochure in Japanese describes the GDB and OMIM databases, and user documentation is available in both Japanese and English.

FRANCE. The GDB French Node is run by the Bioinformatics Center at Villejuif, a joint service of the National Scientific Research Center (CNRS) and the National Institute of Health and Medical Research (INSERM), with financial support from the French National Genome Program. The center is also the new French EMBnet node responsible for maintaining additional genetic databases, molecular sequence databases, and computational analysis tools for the research community.◊

GDB, OMIM on WWW

GDB and OMIM data are available via several WWW searching methods through the JHU computer in Baltimore. From a GDB/OMIM login account, at the Main Menu select Local Databases, then Internet WWW Access.

"GDB Browser" and "OMIM Using HTML+Query Forms" require a WWW client that supports HTML+ forms. Users accessing WWW via X Windows through the JHU computer in Baltimore automatically use Xmosaic2.x, and those with character-based terminals use Lynx2.x. Any WWW client can be used to access the other databases and resources, including GDB WAIS (Wide Area Information Servers), OMIM, GDB anonymous ftp, JHU Gopher, and a variety of biological information worldwide. Users with a WWW client can access the GDB Home Page directly via the URL (Uniform Resource Locator) *http://gdbwww. gdb.org/.*◊

GDB USER SUPPORT, REGISTRATION

To become a registered user of GDB and OMIM, contact one of the User Support offices listed below (a user may register to access both Baltimore and a remote node). Questions, problems, or user-registration requests may be sent by telephone, fax, or e-mail. User-registration requests should include name, institutional affiliation, and title (if applicable), street address (no P.O. box numbers), telephone and fax numbers, and e-mail address.

The Help Line in Baltimore is staffed from 9 a.m. to 5 p.m. EST for information on accounts and training courses, technical support, and data questions. Calls received after hours will be forwarded to the appropriate voice mail and returned as soon as possible. To obtain a user's local SprintNet (Telenet) number for locations within the United States: 800/736-1130.

GDB, OMIM Training Schedule

"GDB/OMIM and Genomic Data on the Internet" classes will be held in Baltimore on June 13–14, Sept. 19–20, and Nov. 14–15. Contact the U.S. GDB User Support Office.

User Support Offices

UNITED STATES
GDB User Support
Genome Data Base
Johns Hopkins University
2024 E. Monument Street
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Internet: *help@gdb.embnet.se*

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+ 44/81-869-3446
Fax: -3807
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WORLD WIDE WEB. WWW (also called the Web) is designed to facilitate access to Internet resources by transmitting hypertext data, which contain words linked to other items including documents, photographs and other graphics, ftp archives, Gopher servers, and other Web servers. Documents and graphics can be viewed full screen and, with the appropriate software, just as they would appear on the printed page.

Basic requirements for using WWW are a computer on the Internet and software for information viewing. A common client program for those with direct Internet access is NCSA Mosaic, which is available for different computer platforms by anonymous ftp from *ftp.ncsa.uiuc.edu* in the *Mosaic* directory. Additional viewers needed for graphic and sound files are generally found in the same area as the Mosaic program.

Modem users who dial into a central computer for e-mail and Internet access can use WWW through Lynx, which is available by anonymous ftp from *ftp2.cc.ukans.edu* in the */pub/lynx* directory. Users should consult their system administrator to determine how they can best access WWW.◊

Resources

Human Genome news

National Center for Human Genome Research

This newsletter is intended to facilitate communication among genome researchers and to inform persons interested in genome research. Suggestions are invited.

Human Genome Management Information System

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☛ Software, Services, Electronic Data Access

UT, Memphis, Offers Mouse Resources

Mouse Gene Loci Data Files. A group of servers has been set up at the University of Tennessee (UT), Memphis, from which data files on mouse loci, many from the 1992 and 1993 Chromosome Committee reports, can be downloaded (see addresses below). New data include map position information for Massachusetts Institute of Technology loci released in April. Chromosome-specific files can be downloaded in generic text format or as Excel or FileMaker Pro files.

The World Wide Web (WWW) server, accessible using Mosaic (from the National Center for Supercomputing Applications at the University of Illinois), is a repository of Map Manager files. These include data sets on the new Birkenmeier loci [Lucy Rowe and Ed Birkenmeier (Jackson Laboratory)], the Shionogi loci from the National Center for Cardiovascular Research, Japan [Ken Manly and Verne Chapman [Roswell Park Memorial Institute (RPMI)], Rosemary Elliott's (RPMI) new recombinant inbred data files in Map Manager format, and updates of the Portable Dictionary files.

All these servers require an Internet-connected computer. The WWW Mosaic program is the only known client for downloading Map Manager files. Map Manager, a Macintosh-only program written and supported by Manly, is accessible via ftp at *mcbio.med.buffalo.edu*. Users who have Map Manager data sets to make available over the Internet should e-mail the Map Manager files to *rwilliam@nb.utmem.edu*. All collaborators should agree to making files public before data are sent.

Server Addresses

- WWW/Mosaic: *http://mickey.utmem.edu/front.html*
- Gopher: *mickey.utmem.edu* or *anat4.utmem.edu*
- Ftp: *ncbi.nlm.nih.gov* in the directory */repository/genedict* or *nb.utmem.edu* in the directory */pub/genedict*

Portable Dictionary of the Mouse Genome. The Portable Dictionary of the Mouse Genome, a compact database for use on personal computers, contains information on over 12,000 mouse loci and on homologs in several other mammalian species, including human, rat, cat, cow, and pig. Key features are its compact size (less than 10 MB), network independence, and ability to convert to formats suitable for a wide variety of common programs. The dictionary includes DNA sequence accession numbers for over 1200 genes. Loci can be resorted rapidly by chromosomal position, type, human homology, or gene effect. The accessible, easily manipulated set of data has many uses, from a quick review of loci and gene nomenclature to the design of experiments and analysis of results. Updated versions of the Portable Dictionary of the Mouse Genome can be downloaded from the addresses above. The dictionary is also available on the January NCBI Data Repository CD-Rom disk.

[Contact for comments, corrections, and additions: Robert Williams; Department of Anatomy and Neurobiology; University of Tennessee; 875 Monroe Ave.; Memphis, TN 38163 (901/448-7018, Fax: -7193, Internet: *rwilliam@nb.utmem.edu*).] ◊

LBL Develops Automatic Submissions to Genome Databases

SubmitData is a newly developed software program that allows fast and easy submissions to a particular database by merging a list of data records with a predefined template. SubmitData, which was developed in Smalltalk-80™, generates appropriate forms from individual database protocol definitions and checks data values for conformance to the protocol. This capability makes the program readily adaptable to new or changing definitions.

SubmitData combines three functions: (1) template creation and editing, (2) data merging, and (3) data submission. The template editor presents a number of forms showing required and optional fields for constructing a valid data submission. The editor allows the user to choose from a controlled vocabulary when appropriate, checks entered values for agreement with type and range specifications, inserts default values, revises dates if necessary, and generates error messages. Column and reference variables can also be defined in the template (a column variable is a placeholder for the value in a column of the data record, and a reference variable allows references to other template fields). A finished template can be saved, printed, and modified to fit future submissions.

Another editor is used to specify the merging operation, and each variable in the submission template is associated with a column in a tab-delimited input file. Merging can be tested for accuracy and completeness. The final step names the input data file and merges each data record with the template. A dialogue at the end confirms the automatic transfer to a particular database. Once a template and merging operation have been defined, new data can be submitted in a single step.

The first version of SubmitData constructs submissions for GenBank® using the same protocol as AUTHORIN, which can be edited and used for automatic bulk submissions. Submission to Genome Data Base is under development and will be available soon. For more information, contact Manfred Zorn (Lawrence Berkeley Laboratory, 510/486-5041, Internet: *mdzorn@lbl.gov* or BITNET: *mdzorn@lbl*).◊

☛ *HGN* Reprinting Encouraged

Numerous *HGN* articles are being reprinted in other publications, including the newsletters of various universities and disease-gene groups. HGMIS encourages readers to duplicate and reprint any part of *HGN*. Contacting HGMIS is not necessary, permission is not required, and no charge is made. When reprinting an article, please add a credit such as "Reprinted from the U.S. DOE-NIH newsletter *Human Genome News*. For a free subscription to *HGN*, contact Betty Mansfield at 615/576-6669 or *bkq@ornl.gov*." Send us a copy of the publication, if possible.◊

Resources

EMBL Data Library

The following three products of the European Molecular Biology Laboratory (EMBL) Data Library are freely available by ftp (*ftp.embl-heidelberg.de*), Gopher (*gopher. embl-heidelberg.de*), and WWW (*www. embl-heidelberg. de*). [Contact: EMBL Data Library; Postfach 10.2209; 69012 Heidelberg, Germany (Fax: +49/6221-387-519, Internet: *datalib@ embl-heidelberg.de*).]

MacPattern Fast Pattern and Block Searching: A computer program that helps researchers find putative biological functions for new protein sequences through a combination of algorithms. Fast and user friendly, MacPattern supports protein pattern searches using the PROSITE database, protein block searches with the BLOCKS database, and identification of statistically significant protein segments. It allows batch processing of sequences and automatic translation of nucleotide sequence data. Already in use by various genome projects worldwide, MacPattern is particularly suited for genome analysis and cDNA sequencing projects.

EMBL-Search: A database query-and-retrieval program for Macintosh systems. It enables easy construction of complex queries on EMBL, SWISS-PROT, PROSITE, EPD, and ENZYME databases as supplied on the EMBL CD-ROM, which also includes EMBL-Search. Full utilization of database cross-reference information allows easy movement between databases and exploration of related information. EMBL-Search can be particularly cost-effective because of its ability to run on a local computer network accessing a shared database CD-ROM [Internet: *datalib@embl-heidelberg.de*].

Mail Server Utility (MSU): Simplifies the use of electronic mail servers for sequence analysis by helping users produce properly formatted requests with a simple menu interface. Service descriptions are defined in external control files, which can be changed with a normal text editor without affecting the main program. MSU, which runs on UNIX and OpenVMS platforms, is a highly flexible tool that allows easy modification, extension, and customization to suit individual requirements. *[Rainer Fuchs, EMBL Data Library]* ◊

¶ AAAS Publishes ELSI Reports

The following books are available from the American Association for the Advancement of Science (AAAS):

The Genetic Frontier: Ethics, Law, and Policy (catalog no. 93-27S), based on an invitational conference, consists of 15 original essays by experts in genetics, ethics, law, philosophy, and social science. Topics include privacy and confidentiality issues, genetic testing, property rights, family relationships, and social policies. [AAAS Press Books: P.O. Box 521; Dept. D3GT; Annapolis Junction, MD 20701 (800/222-7809, Fax: 301/206-9789).]

Ethical and Legal Issues in Pedigree Research reports on an invitational conference at which participants, including researchers studying five different genetic disorders, discussed such issues as informed consent, subject recruitment and withdrawal, privacy and the control of genetic information, children as research subjects, the role of researchers and provision of clinical care, and publication practices. [Contact for ordering: Kamla Butaney; AAAS Directorate for Science and Policy Programs; 1333 H Street NW; Washington, DC 20005 (202/326-6792, Fax: /289-4950).] ◊

Whitehead/MIT Announces Release Six of Mouse Genetic Map

Release Six of the Whitehead Institute–Massachusetts Institute of Technology Genome Center Genetic Map of the Mouse is now available. The map consists of randomly chosen simple sequence length polymorphisms (microsatellites) that can be analyzed using the polymerase chain reaction, as described in W. Dietrich et al., *Genetics* **131**, 423–47 (1992).

Release Six contains 3752 markers that fall into 20 linkage groups spanning about 1400 cM with an average spacing of less than 0.5 cM. The map can be accessed via the following:

- Internet e-mail: For a copy of the most-current e-mail query forms, send a message to *genome_database@genome.wi.mit.edu* with *help* in either the subject line or body text. Instructions and a query form will be returned by e-mail. The filled-out form should be sent to *genome_database@genome.wi.mit.edu*, and the query answer will be mailed back automatically.
- Anonymous ftp to *genome.wi.mit.edu* in directory */distribution/mouse_ssip_release/apr94/* (log in as *anonymous* with user's e-mail address as password). The file README describes the file format and gives other information about the map.
- WWW browser (client such as NCSA Mosaic is required). Point the client at *http://www-genome.wi.mit.edu/*.

This project is ongoing, and new markers will be released at the beginning of each quarter. [Contact for questions and comments: Ert Dredge; Whitehead Institute Center for Genome Research; One Kendall Square; Bldg. 300, 5th Floor; Cambridge, MA 02139 (617/252-1922, Fax: -1902; Internet: *ert@genome.wi.mit.edu*).] ◊

Mouse Map-Drawing Resource

A mouse genetic linkage map file can be generated via e-mail using a new map-drawing resource from the Mouse Genome Informatics Project at Jackson Laboratory. After a text file is e-mailed to the service, a postscript file is returned by e-mail. When sent to a postscript printer, this file will print a mouse genetic linkage map displaying loci at their relative positions along a chromosome.

Access to the program is accomplished in three steps:

- Address e-mail to *services@beadle.informatics.jax.org*.
- In the subject or first line of the message body, enter the request in the following form: *map [options] filename*. [Options] refers to optional variations, and filename is the name of a user-specified file or (for local users) a printer designation.
- Attach a text document containing the data for executing the service.

The return e-mail message will be either a postscript file for printing the linkage map or a report of errors detected in the map request. Maps can be customized in a number of ways, and several variations in the data file can be used to create maps for different purposes.

A manuscript describing this service has been submitted to *Mammalian Genome*. For a copy of the paper, including example figures showing the file sent and the resulting map, contact Michelle Stanley (207/288-3371, ext 1421, Fax: -2516, Internet: *mls@informatics.jax.org*). *[Janan T. Epping and Michael Kosowsky, Jackson Laboratory]* ◊

☛ Resources?

***HGMIS* would like to be informed about informatics and educational resources freely available for use by genomics researchers and educators.** **See address, p. 12.**

Find Errors in *HGN*?

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Internet:
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✓ Correction

The fax number for George Kutukdjian at UNESCO is +33/1-4306-0772.

This newsletter is prepared at the request of the DOE Office of Health and Environmental Research and the NIH National Center for Human Genome Research by the Biomedical and Environmental Information Analysis Section of the Health Sciences Research Division at Oak Ridge National Laboratory, which is managed by Martin Marietta Energy Systems, Inc., for the U.S. Department of Energy, under Contract DE-AC05-84OR21400. ◊

Calendar of Genome-Related Events* (acronyms, p. 16)

July

6–10. SINEs, LINEs, and Retrotransposable Elements: Functional Implications; Davis, CA [M. Batzer, 510/423-3637, Fax: -3608, Internet: *batzer2@llnl.gov*]

10–24. **Open Probl. in Computational Mol. Biol.: 4th Intl. Workshop; Telluride, CO [A. Konopka, 301/663-1206, Internet: *akonopka@lifsci.sdsu.edu*]

16–21. Sorting and Intracellular Transport of RNA; Santa Cruz, CA [FASEB, 301/530-7095, Fax: /571-0650]

21–22. **NIH-DOE Joint Working Group Meet. on ELSI of HGP; Washington, DC [D. Drell, 301/903-4742, Fax: -8521, Internet: *daniel.drell@mailgw.er.doe.gov*]

23–28. Yeast Chromosome Struct., Replication, and Segregation; FASEB, Santa Cruz, CA [see contact: July 16–21]

28–29. DNA Sequencing, Mapping, & Bioinformatics; San Francisco [IBC Conf., 508/481-6400, Fax: -7911]

28–Aug. 5. Hum. Genome Anal.: From YAC to Gene; London (reg. deadline: Mar. 31) [WLMG, P. Falk, +44-71/403-6998, Fax: /407-5281]

August

8–9. 2nd Ann. Conf. on Transcriptional Regul.: Adv. in Drug Discovery and Dev.; IBC, San Francisco [see contact: July 28–29]

9–12. Interconnection of Mol. Biol. Databases; Stanford, CA [P. Karp, 415/859-6375, Fax: -3735, Internet: *pkarp@ai.sri.com*]

10–11. High Throughput Screening for Drug Discovery; IBC, San Francisco [see contact: July 28–29]

11–12. Combinatorial Libr. for Mol. Diversity; IBC, San Francisco [see contact: July 28–29]

13–18. Transcriptional Regul. During Cell Growth, Differ., and Dev.; FASEB, Santa Cruz, CA [see contact: July 16–21]

14–17. 2nd Intl. Conf. on ISMB; Stanford, CA [R. Altman, 415/723-6979, Fax: /725-7944, Internet: *ismb@camis.stanford.edu*]

14–19. Mol. Genet. Basis of Cell and Tissue Struct. and Funct.; FASEB, Copper Mountain, CO [see contact: July 16–21]

28–Sept. 1. 10th World Cong. on Med. Law; Jerusalem [A. Carmi, +972-3/751-6422, Fax: -6635]

31. Chromosome 14 Assoc. Neurol. Dis.; Antwerp, BG [C. van Broeckhoven, +32-3/820-2301, Fax: -2541]

31–Sept. 2. **Autom. in Mapp. and DNA Sequencing; Hinxton, UK [Sanger Center, D. Cooper, +44-22/349-4957, Fax: -4919, Abs. submiss.: *denise@sanger.ac.uk*]

31–Sept. 4. Mouse Mol. Genet.; Cold Spring Harbor, NY [CSHL, 516/367-8346]

September

1–3. **2nd Intl. Chromosome 14 Workshop; Oxford, UK [J. H. Edwards or S. Craig, +44-86/527-5314, Fax: -5318, Internet: *c14@bioch.ox.ac.uk*]

3–5. 4th Nordic Genome Workshop; Helsinki, FN [L. Peltonen, Fax: +358-0/474-4480, Internet: *lpalotie@ktl.fi*]

16–18. 2nd Intl. Chromosome 8 Workshop; Oxford, UK [N. Spurr, +44-71/269-3846, Fax: -3802, Internet: *nspurr@mahler.dh.lc-net.uk* or R. Leach, 210/567-6947, Fax: -6781]

17–21. Intl. Genome Sequencing and Anal. Conf. VI; Hilton Head, SC (abs. deadline: June 29) [D. Hawkins, 301/869-9056, Fax: /977-7233, Internet: *seqconf@tigr.org*]

22–23. **NIH Natl. Advis. Council for Hum. Genome Res.; Washington, DC [J. Ades, 301/402-2205, Fax: -2218]

21–25. Gene Therapy; CSHL [see contact: Aug. 31–Sept. 4]

21–25. **Workshop in Mouse Mol. Neurogenet.; Bar Harbor, ME (reg. deadline: June 15) [Jackson Lab., 207/288-3371, Fax: -8254, Abs. submiss.: *wmmn94@aretha.jax.org*]

23–25. 1st Intl. Swine Chromosome 6 Workshop; St. Paul, MN [C. Louis, Fax: 612/624-7284, Internet: *pazek001@maroon.tc.umn.edu*]

25–28. 4th Chromosome 11 Workshop; Oxford, UK [V. van Heyningen, Fax: +44-31/343-2620, Internet: *vervan@mrcvax.ed.ac.uk* or G. Evans, 619/453-4100 ext. 279, Fax: /559-9513, Internet: *gevans@salk-sc2.sdsc.edu*]

26–28. Chromatin Struct. & Gene Expression; Madrid [CIMB, González, +34-1/435-4240, Fax: /576-3420]

October

2–5. Hum. Genome 94: The Genes and Beyond; Washington, DC (abs. deadline: July 1) [G. Griffin, 703/671-1400, Fax: -7695]

14–17. 2nd Intl. Workshop on Hum. Chromosome 7; Toronto [L.-C. Tsui, 416/813-6015, Fax: -4931, Internet: *cfdata@sickkids.on.ca*]

15–18. 13th Annu. NSGC Edu. Conf.; Montreal [B. Leopold, 610/872-7608, Fax: -1192]

16–18. 4th Intl. Id. of Transcribed Sequences Workshop; Montreal (abs. deadline: August 15) [ERI, N. Matthews, 303/333-4515, Fax: -8423]

20–23. 8th Annu. North American CF Conf.; Orlando, FL [CFF, C. McPherson, 301/951-4422, Fax: -6378]

November

4–9. 3rd Intl. *E. Coli* Genome Meet.; Woods Hole, MA [MBL, M. Riley, 508/548-3705, Fax: /540-6902, Internet: *mriley@hoh.mbl.edu*]

5–9. 18th Annu. Symp. on Comput. Appl. in Med. Care; Washington, DC [AMIA, G. Mutnik, 301/657-1291, Fax: -1296, Internet: *amia@camis.stanford.edu*]

6–10. 8th Intl. Mouse Genome Conf.; London [S. Brown, +44-71/723-1252, Fax: /706-3272]

9–11. 5th Intl. Workshop on Chromosome 21; Tsukuba-city, JP [N. Shimizu, Tel/Fax: +81/3/3351-2370, Internet: *shimizu@dmb.med.kelo.ac.jp*]

13–17. **4th DOE Genome Contractor-Grantee Workshop; Santa Fe, NM [S. Spengler, 510/486-4879, Fax: -5717, Internet: *sylvia@ux5.lbl.gov*]

14–16. Computational Approaches in the Anal. and Eng. of Proteins; CIMB, Madrid [see contact: Sept. 26–28]

14–18. Supercomput. 94: Conf. on High Performance Comput. and Commun.; Washington, DC (poster deadline: Aug. 1) [Supercomput. 94, 515/294-0673, Fax: -0888, Internet: *info@sc94.ameslab.gov*]

17–20. 1994 Miami Bio/Technol. European Symp. on Adv. in Gene Technol.: Mol. Biol. and Hum. Genet. Dis.; Monaco [P. Burnett, +44-71/836-6633, Fax: /379-5417]

Training Calendar*

June

27–July 1. In Situ Hybridization Tech.; CATCMB/CUA, Washington, DC [M. Miller, 202/319-6161, Fax: -4467]

27–July 1. Recombinant DNA Tech. I; Germantown, MD [LTI, 800/952-9166, Fax: 301/258-8212]

July

4–9. Recombinant DNA Tech. II; LTI, Germantown, MD [see contact: June 27–July 1]

4–24. *Arabidopsis* Mol. Genet.; Cold Spring Harbor, NY [CSHL, 516/367-8346]

4–24. Mol. Cloning of Neural Genes; CSHL [see contact: July 4–24]

5–29. Summer Program on Mol. Biol.; Minneapolis (reg. deadline: May 6) [IMA, A. Friedman, 612/624-6066, Fax: /626-7370]

6. Intro. to PCR; Hartford, CT [BTP, S. Chance, 800/821-4861, Fax: 603/659-4708]

7–8. Clin. Appl. of PCR; BTP, Hartford, CT [see contact: July 6]

7–8. Metaphase and Interphase Chromosome Anal.; Gaithersburg, MD [Oncor, Inc., 800/776-6267, Fax: 301/926-6129]

*Dates and meeting status may change; courses may also be offered at other times and places; check with contact person.
**Attendance is either limited or restricted.

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11–15. Recombinant DNA Methodol.; Columbia, MD [Exon-Intron, Inc., 410/730-3984, Fax: -3983]

12–13. Quantitative RNA-PCR; BTP, Hartford, CT [see contact: July 6]

14–15. Basic Cloning & Hybridization Tech.; BTP, Hartford, CT [see contact: July 6]

14–15. DNA Sequencing Without Radioact.; BTP, Hartford, CT [see contact: July 6]

15–21. Genet.-Epidemiol. Studies of Complex Dis.; CSHL, [see contact: July 4–24]

18–22. PCR Methodol.; Exon-Intron, Inc., Columbia, MD [see contact: July 11–15]

18–29. Recombinant DNA Methodol. and Appl.; Baltimore, MD [UMBC, B. Bartholomay, 410/455-2336, Fax: -1074]

18–29. 35th Annu. Short Course in Med. & Exp. Mamm. Genet.; Bar Harbor, ME [Jackson Lab., 207/288-3371 ext. 1253]

20–25. **Practical Course on Restriction Landmark Genomic Scanning Method; Tsukuba, JP (appl. deadline: June 25) [RIKEN Tsukuba Life Sci. Ctr., +81/298-36-9136, Fax: -9100]

26–Aug. 15. Adv. Mol. Cloning and Expression of Eukaryotic Genes; CSHL [see contact: July 4–24]

26–Aug. 15. Yeast Genet.; CSHL [see contact: July 4–24]

31–Aug. 6. Short Course on Mol. Diagn., Counseling, and HGP; Ann Arbor, MI [L. Hallett, 313/764-8050, Fax: -4133]

August

1–12. Genethics: Hum. Genet. and Bioethics; Medford, MA [R. Yashon, 617/628-5000 ext. 5395, Fax: /627-3995, Internet: *ryashon@pearl.tufts.edu*]

1–14. Adv. *Drosophila* Genet.; CSHL [see contact: July 4–24]

7–19. Mol. Evol.; Woods Hole, MA (appl. deadline: June 1) [MBL, D. Chrysler, 508/548-3705 ext. 401]

8–12. Tissue Culture/Baculovirus Expression Syst.; Exon-Intron, Inc., Columbia, MD [see contact: July 11–15]

8–12. PCR Tech.; LTI, Germantown, MD [see contact: June 27–July 1]

11–12. Tissue In Situ Hybridization; Oncor, Inc., Gaithersburg, MD [see contact: July 7–8]

16–19. Plant Biotechnol. Methods; Univ. Park, PA [Penn. State Univ., P. Phillips, 800/833-5533, Fax: 814/863-1357]

18–20. Recombinant DNA for Chemists; Washington, DC [ACS, 800/227-5558, Fax: 202/872-6336]

20. Intro. to Computational Chem. and Mol. Model.; ACS, Washington, DC [see contact: Aug. 18–20]

21–Sept. 1. **Exp. Genet. of Lab. Mouse; Bar Harbor, ME [Jackson Lab., P. Mobraaten, 207/288-3371 ext. 1376, Fax: -5079, Internet: *pam@aretha.jax.org*]

29–Sept. 3. Anal. of Gene Expression; LTI, Germantown, MD [see contact: June 27–July 1]

September

12–16. DNA Protein Interactions; LTI, Germantown, MD [see contact: June 27–July 1]

21–23. Probe Labeling; Oncor, Inc., Gaithersburg, MD [see contact: July 7–8]

October

3–7. RNA Isol. and Charact.; Exon-Intron, Inc., Columbia, MD [see contact: Aug. 8–12]

13–26. Anal. and Genet. Manipulation of YACs; CSHL [see contact: July 4–24]

18–31. Adv. In Situ Hybridization and Immunocytochem.; CSHL [see contact: July 4–24] ◊

An extended calendar is available from HGMIS. See p. 12 for contact information.

For Your Information

U.S. Genome Research Funding Guidelines

Note: Investigators wishing to apply for funding are urged to discuss their projects with appropriate agency staff before submitting proposals.

NIH National Center for Human Genome Research (NCHGR)

Application receipt dates:

- R01, P01, R21, R29, P30, P50, K01,* and R13 grants – February 1, June 1, and October 1.
- Individual postdoctoral fellowships – April 5, August 5, and December 5.
- Institutional training grants – January 10, May 10, and September 10.
- Small Business Innovation Research Grants (SBIR: firms with 500 or fewer employees) – April 15, August 15, and December 15.
- Research supplements for underrepresented minorities – applications are accepted on a continuing basis.
- Requests for Applications (RFAs) – receipt dates are independent of the above dates. Notices will appear in *HGN* and other publications.

*Expedited review possible. Check with NCHGR during application development phases.

Program announcements are listed in the weekly *NIH Guide for Grants and Contracts*,* which is available electronically through one of the following methods.

- Gopher (*gopher.nih.gov*).
- Institutional Hubs. A designee receives automatic updates and distributes them locally to researchers. Send a message naming the responsible person to BITNET: *q2c@nihcu* or Internet: *q2c@cu.nih.gov*.
- NIH Grant Line (also known as DRGLINE): Electronic bulletin board updated weekly. Connection is through a modem (301/402-2221), and files can be transmitted rapidly via BITNET or Internet. The Grant Line is also accessible by Telnet to *wylbur.cu.nih.gov*. When connection is open, type *VT100*. At the INITIALS? prompt, type *BB5* and at the ACCOUNT? prompt, type *CCS2*. For more information, contact John James (301/594-7270, Fax: -7384).

Full text of RFAs listed in the NIH grants guide may also be obtained from NIH NCHGR in Bethesda, Maryland (301/496-0844).

DOE Human Genome Program

Solicitations for proposals were announced in the *Federal Register* (February 18), *Science*, and other publications. Proposals for FY 1995 are due July 14.

For funding information or general inquiries, contact the program office via

- 301/903-6488 or Internet: *genome@er.doe.gov*. Relevant documents are available by ftp to *oerhp01.er.doe.gov* in directory */genome*.

SBIR Grants

DOE and NIH invite small business firms to submit grant applications addressing the human genome topic of SBIR programs, which are designed to strengthen innovative firms in research and development and contribute to the growth and strength of the nation's economy. For more information on human genome SBIR grants, contact

- Kay Etzler; c/o SBIR Program Manager, ER-16; DOE; Washington, DC 20585 (301/903-5867, Fax: -5488).
- Bettie Graham; Bldg. 38A, Rm. 610; NIH; 9000 Rockville Pike; Bethesda, MD 20892 (301/496-7531, Fax: /480-2770).

National SBIR conferences: Washington, DC (October 12–14); San Jose, CA (November 14–16); Chicago, IL (April 26–28, 1995). Conference Hotline: 407/791-0720.◊

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4. ___ *Meeting Report: DOE Informatics Summit*—DRAFT (April 26–27, 1993, Baltimore, Maryland)

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SELECTED ACRONYMS

ACS Am. Chem. Soc.
AMIA Am. Med. Informatics Assoc.
BTP Biotechnol. Train. Programs
CATCMB/CUA Ctr. for Adv. Train. in Cell and Mol. Biol./Cathol. Univ. Am.
CFF Cystic Fibrosis Found.
CIMB Ctr. for Intl. Meet. on Biol.
CSHL Cold Spring Harbor Lab.
DOE Dept. of Energy
ELSI Ethical, Legal, & Social Issues
ERI Eleanor Roosevelt Inst.
FASEB Fed. of Am. Soc. for Exp. Biol.
HGP Hum. Genome Proj.
IBC Intl. Bus. Comm.
IMA Inst. for Math. and Appl.
ISMB Intelligent Syst. for Mol. Biol.
LTI Life Technologies, Inc.
MBL Marine Biological Lab.
NCSA Natl. Ctr. for Supercomput. Appl.
NIH Natl. Inst. of Health
NSGC Natl. Soc. of Genet. Counselors
WLMG Wellcome Lab. for Mol. Genet.
UMBC Univ. of Md. Baltimore County

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