BIOLOGY CHEMISTRY PHYSICS ENGINEERING MATHEMATICS

Human Genome news

Sponsored by the U.S. Department of Energy and the National Institutes of Health

ISSN: 1050-6101

Vol. 4, No. 1, May 1992

Successful Worm Studies Yield Much Data

An international research team has deposited the first 121,298 bp of finished DNA sequence data from the roundworm genome into public databases, and researchers say another 250 kb will be ready for inclusion soon. Christened an "honorary human" by Human Genome Project researchers, the worm whose scientific name is *Caenorhabditis elegans* has become an important testing ground for efforts to make large-scale DNA sequencing faster and more economical.

C. elegans is only a millimeter long, but it is extremely well studied by scientists seeking to understand how genes control growth and development. Cell division has been traced from fertilization to each of the adult worm's 959 body cells, and the wiring of its nervous system has been completely diagrammed. More than 95% of the worm's DNA along its six chromosomes has been physically mapped using cosmid and yeast artificial chromosome clones. The entire *C. elegans* genome, which is slightly smaller than one average human chromosome, is estimated to contain about 100 Mb.

"Honorary human" is important testing ground.

In a recent issue of *Nature* [Vol. 356 (March 5, 1992)], Robert Waterston (Washington University, St. Louis) and John Sulston [U.K. Medical Research Council (MRC)] and their coworkers reported significant progress in their large-scale sequencing effort. Having sequenced more than 350,000 bp of the worm's DNA, the researchers plan to complete over 3 Mb in the next 2 years. The team has also uncovered a number of completely new genes, including genes not previously known to occur in *C. elegans*.

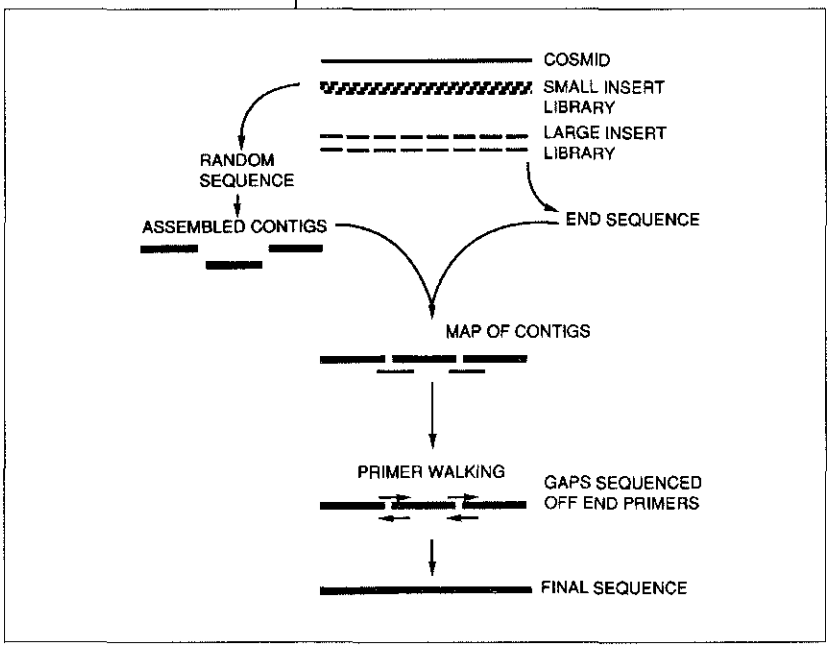
In addition to their achievements in sequencing and in discovering new genes, the team reported that they expect to lower the cost of DNA sequencing to $1 per base by applying their strategy to production-scale sequencing, according to the *Nature* report. With further refinements in technique, "a reduction in costs to $0.50 per base seems realistic," the authors said. When the Human Genome Project began, the cost of sequencing was estimated to be $2 to $5 per base.

⇒

Cost-Effective, Faster Sequencing Technologies To Result

In This Issue...

Genome News



Strategy for Sequencing the *C. elegans* Genome Starting from Mapped Cosmid Clones. Thick lines represent DNA sequence, thin lines cloned DNA. Sequence represented as an arrow is the product of primer walking.
(Reprinted with permission from **Nature**, Vol. 356, p. 14, copyright©1992 Macmillan Magazines Ltd.)

Computer Programs Predict More Genes Than Do Other Studies

The worm sequencing project is jointly supported by the National Center for Human Genome Research (NCHGR) and MRC. "This accomplishment is an important initial step toward the Human Genome Project's DNA sequencing goals," said Robert Strausberg, who oversees the NCHGR sequencing programs. "Before we commit resources to large-scale sequencing of the human genome, we must first show that such sequencing is technically possible and that it can be done more cost-effectively than previous strategies have allowed." In addition, says Strausberg, the work has shown that sequencing and computer analysis of large genomic regions can turn up valuable information about genes and their organization on chromosomes.

The *C. elegans* genome database (ACEDB) is available at no charge. Contact:

- **Richard Durbin**
  MRC Laboratory of Molecular Biology
  Hills Road
  Cambridge CB2 2QH, U.K.
  (Int.) 44/223-248011
  E-mail: "rd@mrc-lmba.cam.ac.uk"

In the article, Waterston, Sulston, and coworkers described the strategy they used to sequence DNA in three cosmid clones covering a region of chromosome 3 known to be a rich source of genes (see figure). XDAP software, specially developed to speed assembly and editing, has been a key part of progress. Using BLAST and GENEFINDER computer programs to analyze the sequence, the investigators estimated that the region contains at least 32 genes, but further studies must be performed to confirm their identity. Comparisons with existing databases showed that 15 genes were similar to known genes but had not previously been identified in *C. elegans* [see box below]. The remainder of the predicted genes appear to be completely new.

The programs predicted a larger number of genes in the sequenced region than indicated by classical genetic analysis or mutation studies. Analysis of genomic DNA has produced similar surprises in the genomes of yeast, *Escherichia coli*, and the fruit fly. In addition, several duplications and repeated sequences were discovered, including a large stretch of repeats similar to that discovered recently at the site of the human fragile X gene. The authors concluded that "genomic sequence is an efficient means for finding not only genes but also the other information stored in the genome."

The sequences have been submitted to the GenBank® and European Molecular Biology Laboratory databases, and the team has created ACEDB. This *C. elegans* database provides a bibliography and information on genetic maps, mapped clones, and sequence. "The ability to view the sequence in the context of much of the available knowledge about the worm should speed the assignment of function to each sequence," the *Nature* report says. ◊

Reported by Leslie Fink
Office of Communications
NIH NCHGR

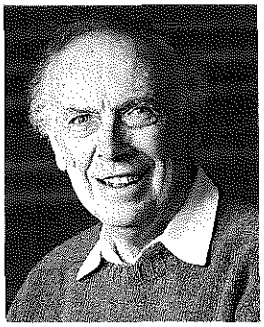
Predicted Genes in *C. elegans*
Similarities to Other Known Genes

- adenylyl cyclase
- phenylethanolamine-N-methyltransferase
- acetyl-CoA acetyltransferase
- Tc3 hypothetical protein
- neutrophil oxidase factor
- SLP1
- giant secretory protein
- 50S ribosomal protein L11
- glucose transporter
- IE110
- arsATPase
- rat proton pump
- glutathione reductase
- CDC25/string
- globin-like host protective antigen

Watson Steps Down As NCHGR Director

Cancer Researcher Michael Gottesman Appointed Acting Director

James D. Watson resigned on April 10 from his position as Director of the NIH National Center for Human Genome Research (NCHGR) and will return full time to his duties as Director of Cold Spring Harbor Laboratory (CSHL). Watson had been NCHGR Director since October 1, 1989.



James D. Watson, Director
Cold Spring Harbor
Laboratory

In a letter of resignation presented to NIH Director Bernadine Healy, Watson wrote, "I have considered it a great pleasure and opportunity to have served at the National Institutes of Health in this capacity. I remain firmly committed to the success of the Human Genome Project."

Accepting the resignation, Healy said, "We have been fortunate to have had [Watson's] expertise and scientific judgment, which have been invaluable to the establishment of the National Center for Human Genome Research."

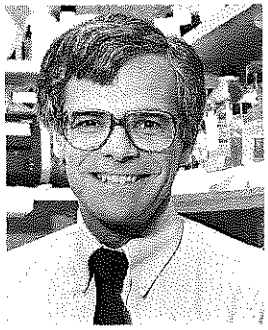
In October 1988 Watson was appointed by James Wyngaarden, then NIH Director, to help guide NIH human genome research in the part-time position of Associate Director for Human Genome Research. When NCHGR was established, Watson became its Director, a part-time position he held along with his CSHL post. He planned to remain in the NCHGR position until its scientific programs were well established and running smoothly.

At the January meeting of the Program Advisory Committee on the Human Genome, Watson commented that he was pleased with the progress of NCHGR and would begin thinking about an appropriate time to step down, probably within the year. In his resignation statement Watson said, "Performing the substantial duties as Director of the National Center for Human Genome Research while simultaneously serving as Director of Cold Spring Harbor Laboratory on Long Island has proved to be increasingly difficult and burdensome to myself and my family. In light of this burden, I have discussed with a number of friends and colleagues over the last several months my intention to leave the project and return full time to Cold Spring Harbor Laboratory."

Healy appointed molecular geneticist and cancer researcher Michael Gottesman to serve as NCHGR Acting Director while the search for a replacement is under way. Gottesman is Chief of the National Cancer Institute Laboratory of Cell Biology, where he studies the resistance of cancer cells to anticancer drugs. Gottesman codiscovered the MDR1 gene, which encodes a membrane protein responsible for transporting substances, including cancer drugs, out of cells.

Gottesman received his M.D. degree magna cum laude from Harvard Medical School and is board certified in internal medicine. He has held research positions since 1971. He is a member of several professional societies, including the Genetics Society of America, the American Society for Cell Biology, the American Society for Microbiology, the American Society for Biochemistry and Molecular Biology, and the American Association for Cancer Research. Gottesman received the 1990 Milken Family Medical Foundation Cancer Research Award and the 1992 Rosenthal Award for Cancer Research. ◇

Reported by Leslie Fink
Office of Communications
NIH NCHGR



Michael Gottesman
NCHGR Acting Director
and
Chief, Laboratory of Cell
Biology, National Cancer
Institute

Watson Returning to Cold Spring Harbor Full Time

Markers Available to Mouse Community

More than 750 polymorphic markers for the mouse genome are offered by Research Genetics at economical rates designed to make the markers widely available to the mouse community. Many of these markers were developed at the Massachusetts Institute of Technology Genome Center.

Each marker consists of two polymerase chain reaction (PCR) primers that have been mapped to a specific mouse chromosome. The allele size of the PCR product for each marker has been determined for 12 mouse strains; further characterization of additional strains is planned. Markers, consisting of one forward and one reverse primer, cost $20 a pair when sold individually; quantity discounts are available. Each primer, sold under the trade name of MapPairs, is sufficient for 1000 PCR reactions. Over 200 human SSLP (microsatellite) markers are also offered. (Contact: Research Genetics; 2130 Memorial Parkway SW; Huntsville, AL 35801; 800/533-4363; Fax: 205/536-9016.) ◇

Reported by Anne Adamson
HGMIS, ORNL

Genome News

NIH-DOE Joint Subcommittee and NIH PACHG

Meetings Held January 3–4 in Irvine, California

Working Groups Report Progress

Joint Subcommittee Meeting

At the January meeting of the NIH-DOE Joint Subcommittee on the Human Genome in Irvine, California, Paul Berg (Stanford University School of Medicine), Chair of the NIH Program Advisory Committee on the Human Genome (PACHG), and Leonard Lerman [Massachusetts Institute of Technology (MIT)] of the DOE Health and Environmental Research Advisory Committee presided as the subcommittee heard reports from several NIH-DOE working groups.

ELSI Working Group. Nancy Wexler (Hereditary Disease Foundation and Columbia University) spoke for the DOE-NIH Joint Working Group on Ethical, Legal, and Social Issues (ELSI) related to data generated by the Human Genome Project. She reviewed progress in five activities: (1) an NIH-funded consortium of eight clinical studies related to cystic fibrosis; (2) ELSI Insurance Task Force meetings to develop guidelines for using genetic information in underwriting (see article, p. 6); (3) a special ELSI initiative on guidelines for protecting the privacy of genetic information; (4) communication of concerns about exclusionary genetic testing by employers; and (5) NIH-DOE funding initiatives for public education on the impact of genetic data.

Mapping Working Group. Mark Guyer [National Center for Human Genome Research (NCHGR)] presented a list of quality index markers that have been identified, isolated, and mapped since the index marker project began in April 1991 [see *HGN* **3**(2), 1–2 (July 1991)]; he reported that about half the needed 300 highly polymorphic markers have been assembled. Plans call for a full index marker map of the human genome to be constructed by January 1993, but interim information is being disseminated earlier [see *HGN* **3**(6), 2 (March 1992) for information on an NCHGR catalog of index-quality markers and interim maps].

The subcommittee agreed that, in addition to index marker maps, a "baseline" map for each human chromosome should be constructed and published in a uniform format as soon as feasible. These maps eventually will contain the quality index markers as well as other useful markers. Helen Donis-Keller (Washington University) will coordinate the effort. Discussion followed about format and how best to distribute the baseline maps.

Committee members agreed that increasingly precise mapping goals may warrant supporting research through contracts or center grants with clearly delineated objectives rather than through regular research grants. A working group consisting of Mark Pearson (E. I. du Pont de Nemours & Company), Maynard Olson (Washington University School of Medicine), and Diane Smith (Xerox Corporation) was established to review this issue and make recommendations at the next meeting.

Olson submitted a proposal for measuring physical mapping progress. He commented on the difficulty of comparing "bottom up" and "top down" data and suggested a new "ordered marker" measure that would present information in much the same style as genetic mapping. The committee recommended that six to eight of the research groups involved in physical mapping convene to examine how this approach would affect them.

Mouse Genome Working Group. Verne Chapman (Roswell Park Cancer Institute) summarized the second meeting of the mouse working group and reported on the Mouse Genome Center at MIT [see *HGN* **3**(6), 6–7 (March 1992)]. Information and materials are being distributed through a small business that makes marker kits commercially (see box, p. 3). The recently established Mouse Genome Society plans to sponsor workshops to review data and scrutinize information, chromosome by chromosome.

Sequencing Working Group. Pearson reported that several projects, including some involving bacterial, yeast, nematode, and human genomes, are ready to begin sequencing 1 Mb a year. The current cost of about $1.50 per base pair should be reduced to $0.50 within 5 years. Although technology has improved considerably, the truly novel technologies are still under development.

Intellectual Property Rights. William Smith and Thomas Kiley, California-based patent attorneys, were invited to discuss general issues raised by the recent NIH move to file patent applications for a large series of relatively short cDNA sequences called "expressed sequence tags." Because such patents could carry serious implications for human genome research, the committee

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 and Safety 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.

agreed to develop an opinion letter about these applications and the rationale behind them. The letter will urge federal officials to obtain an authoritative ruling on the patentability of such material.

Smith described several recent patent rulings and expressed the opinion that rights to the composition of matter are the only issue that might cause problems in having a patent granted in the NIH case. In Kiley's view, the NIH case illustrates problems in the biotechnology industry, where the tendency is to try patenting at every stage of discovery. He outlined several potential remedies to weaknesses in the law, including the need for a clear research exemption and a stronger standard of utility. Kiley expressed concern that ambiguities in current law could lead to costly legal battles among biotechnology companies and recommended that basic sequence information should always be placed in the public domain.

Genome Informatics. Several investigators described substantial efforts to develop computer systems to handle the specialized and voluminous information being generated by gene mapping and sequencing research projects. Attention focused on very rapid analysis and dissemination of the newly developed data.

Nathan Goodman (Whitehead Institute for Biomedical Research) reviewed genetic mapping automation and reported an interactive program that helps plan and analyze experiments and automatically completes order forms for appropriate reagents. This program has enabled a small research group to rapidly accumulate and map 500 markers on the mouse genome.

Philip Green (Washington University) outlined an informatics approach that involves two complementary components: one statistical in which the "likelihood" of marker order is calculated by computer, and one combinatorial in which the program helps determine probable errors in the data set.

Elbert Branscomb [Lawrence Livermore National Laboratory (LLNL)] reported on a system that will enable research groups at different sites to exchange and analyze each other's data while maintaining the integrity of their own hardware and software. A prototype system involving Genome Data Base, IntelliGenetics, and LLNL is already functioning [see *HGN* **3**(5), 5–7 (January 1992)].

James Fickett (Los Alamos National Laboratory) described Software for Integrated Genome Map Assembly, a system that eventually will automate mapmaking. Robert Waterston (Washington University) discussed data management for large-scale sequencing, especially of *Caenorhabditus elegans* (see article, p. 1). Dieter Soll (Yale University), Chair of the Joint Informatics Task Force, outlined the recently completed 2-year effort to describe the state of genome informatics and to specify needs in the field. This work has been summarized in a major draft report, which subcommittee members recommended should be edited professionally and distributed as soon as possible. The subcommittee also endorsed the report's main recommendations for increased support of interdisciplinary research and training in informatics.

NIH PACHG

At the NIH PACHG meeting, presided over by Berg, Elke Jordan (Deputy Director, NCHGR) reported that a delay in nominating new committee members may necessitate extending the terms of some members.

Budget. Several participants requested an explanation of the congressional appropriations process. Jordan explained that any significant shift of funds in future budgets from grants to contracts would necessitate considerable planning and a lead time of several years. The committee anticipated a need within a few years to conduct more of the overall program with contract rather than grant support. Participants noted that contracts will provide a more efficient means of support when large-scale sequencing projects begin. As an alternative to a complete switchover to contracts, members suggested that research grants be used more flexibly to achieve program goals.

Concept Clearance for Initiatives. Bettie Graham (NCHGR) summarized several NIH initiatives, including a request for applications for mouse genetics and a new program to support Russian and other East European scientists [see *HGN* **3**(5), 5 (March 1992)]. A July meeting is planned in St. Petersburg to develop contacts between U.S. and Russian scientists.

David Benton (NCHGR) described an announcement of funding for a genome

(see PACHG, p. 6)

Subcommittee Addresses Patent Applications

Informatics Investigators Developing Rapid Data Analysis and Dissemination

Participants Discuss Budget Process

To receive minutes of Subcommittee and PACHG meetings, contact:

- Office of Communications
NIH NCHGR
Bldg. 38A, Rm. 617
Bethesda, MD 20892
301/402-0911
Fax: 301/480-2770

Genome News

Task Force on Genetics and Insurance

Task Force Explores Insurance Industry's Use of Genetic Information

The Task Force on Genetics and Insurance of the NIH-DOE Joint Working Group on Ethical, Legal, and Social Issues held an information-seeking meeting in Washington, D.C., on December 2 and 3, 1991. The task force is charged with studying how the increased ability to predict future illness will affect insurance access and practices. The first year is being spent in gathering information; the second year the task force will look for solutions.

The meeting had two principal goals: (1) to learn more about the insurance industry's use of genetic information and (2) to examine clinical, scientific, and technological advances that might affect the availability of genetic information.

Speaking on behalf of the insurance industry were Warren Schreier (Benefit Trust Life), Harvie Raymond, John Cova, and Jude Payne (Health Insurance Association of America), and Sandy Lowden (Crown Life Insurance Company). Reed Pyeritz (Johns Hopkins University School of Medicine), Katherine Klinger (Integrated Genetics, Inc.), and Philip Reilly (Shriver Center for Mental Retardation) spoke, respectively, on the clinical, technological, and scientific advances that are likely to shape the future role of genetic information in insurance. These speakers and the ensuing discussions brought out the following points.

According to the speakers, insurers are not currently doing genetic testing to determine policy eligibility or rates. They do consider genetic data gathered through other means, such as from an individual's file that includes a family history or other information on the risk of illness or early death. Insurers argue that they do not want to decrease their business by excluding large numbers of people from coverage; some conditions that cause substantial morbidity and mortality have genetic contributions but are not commonly thought of as genetic.

Factors are presently not favorable to the use of genetic testing by insurance companies, but participants expect these factors to change. Testing costs will decline, possibly sharply; predictive value of the tests may increase; competition may intensify as some companies perceive a competitive advantage in using genetic predictors; and the cost-benefit ratio of genetic testing will become more appealing. Automation of genetic tests will lower personnel costs considerably, and single-cycle panels of tests will decrease the per-unit cost. Basic research on the pathophysiology of genetic diseases may allow the use of cheaper test systems that do not rely on analyzing the DNA itself. Also, the technology for generating genetic information is developing very rapidly. Ten years ago, direct DNA testing was virtually impossible; today, the polymerase chain reaction makes testing a common practice.

Insurers cited underwriters' lack of sophistication about genetics as the reason for insurance being denied for genetic reasons even when little chance existed for morbidity or mortality increase. Improved understanding among underwriters could reduce the number of baseless rejections of people unlikely to fall ill or die prematurely, but individuals who carry detectable genetic risks could still be rejected or charged higher premiums according to the definition of fairness used by the insurance industry.

Experts at the meeting estimated that over 50% of U.S. companies, particularly larger ones, are self-insured—the largest and fastest-growing method of providing health insurance. This trend toward self-insurance complicates public policy regarding genetic information and insurance; the federal government leaves insurance regulation mostly to the states, but the federal

(see Insurance, p. 7)

Task Force Contact:

- **Elinor Langfelder**
  NIH NCHGR
  Ethical, Legal, and Social Implications Program
  Bldg. 38A, Rm. 617
  9000 Rockville Pike
  Bethesda, MD 20892
  301/480-0911
  Fax: 301/480-2770

PACHG *(from p. 5)*

informatics program, and Berg recommended that NIH staff visit leading universities to recruit researchers into this field. Graham pointed out that NCHGR offers a new special-emphasis research career award (SERAC) that can provide computer scientists with support of up to $50,000 a year for 3 to 5 years.

The dates of the next Joint Subcommittee and PACHG meetings have not been set. ◇

Reported by Leslie Fink
Office of Communications
NIH NCHGR

Agencies Hear ELSI Working Group Priorities

The NIH-DOE Joint Working Group on the Ethical, Legal, and Social Issues (ELSI) related to data generated by the Human Genome Project met in Washington, D.C., on February 10 to advise the agencies' ELSI program staff on priorities for program initiatives. Topics considered were (1) testing and counseling for p53 mutations, (2) guidelines for pedigree research, (3) the psychosocial impact of prenatal testing on women, and (4) public and professional education. Experts in each area were invited to participate in the discussion.

Frederick Li (Dana-Farber Cancer Center) provided background on testing for mutations in the p53 gene, which has been associated with several types of cancer. Predictive testing of healthy members of p53 cancer families would help determine their risk of developing cancer, while testing cancer patients for the p53 gene mutation would inform family members of a possible hereditary component of the cancer.

Li reported that a conference jointly sponsored by the National Cancer Institute and the NIH National Center for Human Genome Research (NCHGR) had recommended that testing be limited to relatives of known p53 cancer patients and confined to a research setting until specific, accurate, and sensitive tests are developed. ELSI working group members suggested to NCHGR staff that a request for applications (RFA) be developed to address issues in p53 testing on adults.

The working group discussed the necessity for a coordinated effort to develop guidelines for investigators involved in pedigree research. Dorene Markel, Director of the Family Studies Core at the University of Michigan Human Genome Center, described considerations in attempts to pinpoint the breast cancer mutation: (1) protection of the confidentiality of subjects, (2) appropriateness of releasing preliminary data, and (3) suitable mechanisms for contact and subject recruitment.

NCHGR has also funded an American Association for the Advancement of Science conference to discuss this issue and begin developing guidelines for institutional review boards or NIH study sections to use in

⇒

Working Group Discusses Need for Pedigree Research Guidelines

Insurance *(from p. 6)*

Employment Retirement Income Security Act (ERISA) gives states very little regulatory authority over self-insurance plans. The effect is to create a public policy vacuum in the regulation of health-care benefit plans provided by self-insured companies.

The task force established two subcommittees. One, chaired by Paul Billings (Pacific Presbyterian Medical Center), will examine allegations that insurers engage in genetic discrimination. The second, chaired by David Tannenbaum (Blue Cross/Blue Shield Association), will explore questions about the role that genetic information is likely to play with and without individual underwriting. The task force expects to complete its final report with recommendations in May 1993.

The full report of the task force meeting is available from Elinor Langfelder (see box, p. 6, for contact information). ◇

Reported by Thomas H. Murray
Case Western Reserve University

Announcements

DOE Contractor-Grantee Workshop

DOE plans to hold its 1993 Contractor-Grantee Workshop on February 7–11 in Santa Fe, New Mexico. Abstracts are due November 1, 1992. Contractors and grantees should receive a letter from DOE in early June. Each DOE-funded project is expected to be represented at the meeting. [Contact: Sylvia J. Spengler, Lawrence Berkeley Laboratory Human Genome Center (415/486-4879, Fax: 415/486-5717; Internet: "sylviaj@ux5.lbl.gov").]

NIH, DOE To Hold Meeting for ELSI Grantees

NIH and DOE grantees in Ethical, Legal, and Social Issues (ELSI) related to data produced by the Human Genome Project will hold a 2-day meeting September 14–15. [Contact: Elinor Langfelder, NIH (301/402-0911).] ◇

Chromosome 11 Workshop Scheduled

The Third Annual International Chromosome 11 Workshop will be held September 13–15 in San Diego, California. The meeting will involve all international groups working on chromosome 11 genetic and physical mapping, disease genes, syntenic mouse chromosomes, informatics, and new technology. [Contact: Salk Institute; P.O. Box 85800; San Diego, CA 92138; Attn: Suzanne Clancy, Molecular Genetics Laboratory (Fax: 619/558-9513).] ◇

Genome News

ELSI Groups Set Areas for Further Study

evaluating the protection of human subjects involved in large family studies. NCHGR and the NIH Office of Protection from Research Risks will hold a workshop this year to continue this discussion.

In November 1991, NCHGR sponsored an agenda-setting conference that enumerated issues requiring further research and consideration. Karen Rothenberg (University of Maryland School of Law), cochair of the conference, informed the working group of suggested strategies for addressing research gaps. These strategies include (1) reframing the discussion of prenatal diagnosis in terms of preserving reproductive health rather than reducing the number of children born with chromosomal abnormalities; (2) determining whether prenatal testing will be made available, accessible, or mandatory for women; (3) ensuring that counselors are equipped to address scientific and psychosocial value-sensitive issues; (4) defining whether the goal of prenatal testing is to get consent or to allow women to make a decision; (5) informing women of the ethical, legal, and social issues involved in prenatal testing; and (6) eliminating communication and language barriers between the biomedical and disabled communities. Working group members agreed that prenatal testing and diagnosis is an important area requiring further attention and research and recommended that staff develop an RFA to address these issues.

NIH and DOE ELSI staff presented the scope of education projects being funded by the two programs, including curriculum development, training of science teachers, public broadcasting, and public discussions. The working group advised NIH and DOE ELSI staff to follow up the March 1991 NCHGR workshop with a similar meeting to set an agenda for the solicitation of quality education projects. The group also concurred that education issues continue to receive prominent billing in the NIH and DOE regular program funding announcements.

Progress of the Insurance Task Force and Privacy initiatives was also discussed. The Privacy Initiative is led by DOE Human Genome Program staff, who recently issued the FY 1993 DOE ELSI program announcement, which has a focus on privacy of genetic information [see *Fed. Reg.* **57**(78), 14710 (April 22, 1992)]. DOE is contracting for a series of commissioned papers on privacy issues to complement the grant projects. The papers are expected to be completed and distributed within 1 year.

The ELSI working group will meet with NIH and DOE ELSI grantees on September 14–16 in Washington, D.C. ◇

Reported by Elinor Langfelder
ELSI Program, NIH NCHGR

HUGO Invites Applications for Membership

The Human Genome Organization (HUGO) will hold its annual election of new members this summer. Now composed of 427 members from 32 countries, HUGO invites membership applications from anyone actively interested in human genome research. Application forms are available from the offices of HUGO Europe and HUGO Americas and from HUGO members.

For consideration this year, completed forms should be mailed, not faxed, to arrive at HUGO Europe by June 15. Applications must be supported by two HUGO members (not five, as was previously the case) and must be accompanied by a one-page curriculum vitae and a list of up to five key publications. Contact one of the HUGO addresses below (note new address for HUGO Americas):

HUGO Europe
179 Great Portland Street,
Fifth Floor,
London W1N 5TB
United Kingdom
(Int.) 44-71/436-7178
Fax: (Int.) 44-71/436-1988

HUGO Americas
Diane Hinton
7986-D Old Georgetown Road
Bethesda, MD 20814
301/654-1477
Fax: 301/652-3368

Genome-Related Publications

FCCSET Report

¶*Biotechnology for the 21st Century* is a report on the U.S. Biotechnology Research Initiative, which recognizes the critical role of biotechnology in the nation's future. This document from the Federal Coordinating Council for Science, Engineering, and Technology (FCCSET) consists of major sections on 11 biotechnology research areas, the contributions of 12 federal agencies, and budget tables. Coordination and integration of interagency research and development strategy for the initiative and the report were led by James Mason, Chairman of the Committee on Life Sciences and Health, and by David Galas, Chairman of the Biotechnology Research Subcommittee. 1992. [Committee on Life Sciences and Health; c/o Office of Energy Research ER-70; U.S. Department of Energy; Washington, DC 20585.] ◇

GDB™ Database Access Toolkit Available

The Genome Data Base (GDB) product development staff have developed the GDB Database Access Toolkit (DAT) to aid in making genetic and physical mapping data readily available in various formats through a variety of mechanisms. The GDB DAT—an application programming interface (API) to GDB—is a collection (stored in SYBASE™*) of procedures, views, triggers, rules, defaults, and C routines that reside within the database. This collection of software provides the means to access and update the database.

The NIH-DOE Ad Hoc Committee on Future Human Genome Map Databases recommended development of a stable, documented API to the database at its meeting on December 17, 1990. The GDB DAT was developed using established software-engineering practices and coding standards to create software that is well-documented, tested, and maintainable. Because DAT allows access to data independent of the physical database design, changes in the physical database schema should necessitate minimal change to front-end applications.

DAT is an important software tool for accessing data, embedding GDB functionality within other applications, and developing new tools to browse the GDB database. The toolkit will become a significant architectural component of all future GDB software products beginning with the next major release of the GDB application (version 5.0) expected this fall. Through the use of high-level stored procedures the end user will be able to retrieve data without needing to understand the physical design of the database. For example, the user might call a DAT routine by entering the GDB source identification number and receive the complete information about that reference.

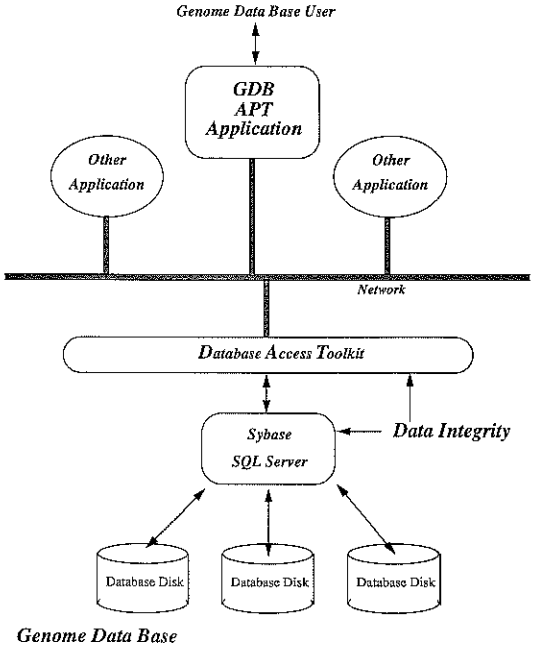
As a part of GDB software architecture (see figure), DAT provides important routines that maintain both the semantic and syntactic integrity of the database by validating the data that are passed to the routines and allowing updates only upon successful validation. To ensure data integrity, DAT handles its own transaction processing, error detection, reporting, and recovery. Separation of the front-end application from database processing will facilitate migration of the

*SYBASE™ is a trademark of Sybase, Inc.)

(GDB Forum continued on p. 10)

■ Notify GDB When Data Are Published

In addition to data from published journal articles, personal communications from researchers are an important source of information for GDB. Researchers who have made submissions through personal communications are asked to notify the appropriate chromosome committee editor and GDB staff when data are published, so the journal citation can be added to GDB.



The GDB Database Access Toolkit maintains database integrity.

APT = Application Productivity Tool.

GDB and OMIM Training Course Schedule

Two comprehensive hands-on training courses on the use of GDB and OMIM are being scheduled in Baltimore and other locations:

- The general course for scientific users provides a basic understanding of the databases and the relationships among the different types of data.
- The course for users with editing privileges includes instructions on adding, modifying, and deleting GDB data.

Class frequency and location will be determined by demand (schedule at right). Courses are free, but attendees must pay their own travel and lodging expenses. Hotel information and directions will be mailed with registration materials.

As interest in GDB continues to grow, organizations around the world will offer training that requires access to GDB in Baltimore. Notifying GDB User Support about planned training activities will enable the staff to ensure database availability by scheduling maintenance and repairs at other times.

Contact: GDB User Support; 410/955-7058, press 4 after greeting; Fax: 410/614-0434; Internet: "help@welch.jhu.edu".

Planned Exhibitions

- ASHG, San Francisco, Calif., Nov. 10–12.

Course	Dates
BALTIMORE	
General User	June 15–16
General User	July 12–13
Editing	Sept. 13–15
General User	Sept. 21–22
General User	Nov. 23–24
LONDON (HARROW)	
Editing	Aug. 17–18
Editing	Aug. 19–20
General User	Aug. 21
SAN FRANCISCO	
Editing	Nov. 6–7
General User 1-day course for ASHG meeting attendees	Nov. 8

GDB Forum

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.

USER SUPPORT OFFICES

United States
GDB User Support
Welch Medical Library
1830 E. Monument Street,
Third Floor
Baltimore, MD 21205
410/955-7058
Fax: 410/614-0434
Internet:
"help@welch.jhu.edu"

The Help Line is staffed from 9 a.m. to 5 p.m. EST for information on accounts, technical support, data questions, and training courses. 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.

United Kingdom
Christine Bates
Human Gene Mapping
Program Resource Center
CRC, Watford Road
Harrow, Middx HA1 3UJ, U.K.
(Int.) 44/81-869-3446
Fax: (Int.) 44/81-869-3807
Internet: "cbates@uk.ac.crc"

Germany
Otto Ritter
Molecular Biophysics Group
German Cancer
Research Center
Im Neuenheimer Feld 280
D-6900 Heidelberg 1, FRG
(Int.) 49/6221-42-2372
Fax: (Int.) 49/6221-40-1271
Internet:
"dok261@cvx12.dkfz-heidelberg.de"

Australia
Alex Reisner
ANGIS
Electrical Engineering
Building, J03
University of Sydney
Sydney, N.S.W. 2006
Australia
(Int.) 61/2-692-2948
Fax: (Int.) 61/2-692-3847
Internet:
"reisner@ee.su.oz.au"

GDB application to new releases of SYBASE or other vendor software and development of new applications such as graphical user interfaces. The DAT library makes existing GDB functions extensible to other applications. ◊

Reported by Christopher Brunn
and
François Schiettecatte
GDB, Johns Hopkins University

SQL Access to GDB SYBASE Tables

A SYBASE server containing the GDB SYBASE tables now enables utilization of the structured query language (SQL) to query GDB directly at the general-access computer in Baltimore. Requirements for using this service include Internet access and a license from Sybase, Inc., to run front-end software such as interactive SQL (ISQL) or Data Workbench (DWB). To obtain an SQL account, users should contact GDB User Support for a registration form. An SQL user may also have a GDB account for accessing GDB though front-end software, but this is not required.

GDB Statistics and OMIM Documents Available via Anonymous FTP*

Two new types of files in ASCII format, GDB statistics and OMIM documents, are now available via Anonymous FTP (file transfer protocol) from the host:

- "mendel.welch.jhu.edu" (128.220.59.42).

GDB Statistics

Two types of statistics are updated weekly and added to the gdb/stats directory. One set of files shows the number of genes and markers mapped to each chromosome, and the other shows the number of identified loci, probes, polymorphisms, sources, and contacts. A README file in the gdb/stats directory describes the file name format.

OMIM Documents

All MIM documents that can be retrieved and displayed through the OMIM database are available as individual files with the MIM number as the filename. Users who have searched OMIM for relevant MIM numbers can use FTP to download the full text of the documents. A README file in the OMIM directory describes how to locate specific MIM documents. ◊

*A beginner's guide to FTP access and downloading procedures is available from GDB User Support. This guide is in ASCII format and can be sent via e-mail or U.S. mail.

Genome-Related Publications

Bibliography on Computational Molecular Biology

¶The GenTools™ *CMB-Bibliography*, a database of bibliographic references on computer and mathematical aspects of molecular biology and genetics, contains about 2500 citations and is expanding rapidly. Available to the general public, the database is maintained as part of the GenTools Project at the University of Texas System Center for High Performance Computing. Contributions of citations, preprints, and suggestions are welcome. [Contact: Sarah Barron; U.T. System Center for High Performance Computing; Balcones Research Center; 1.154CMS; 101000 Burnet Road; Austin, TX 87812; Internet: "gentools@chpc.utexas.edu".]

New Journal

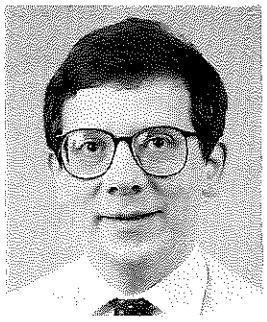
Nature Genetics, a new monthly journal designed to supplement *Nature*, focuses on the link between human genome structure and disease. The journal will publish a broad spectrum of papers on the latest findings in gene mapping, linkage analysis, candidate genes, positional cloning of important chromosomal regions, clinical genetics, aspects of developmental biology, imprinting, and fundamental advances in the Human Genome Project's research for humans and other organisms. Individual subscription, $195 or £175. [North America: Nature Genetics; 65 Bleecker Street; New York, NY 10012; 212/477-9600, Fax:202/628-1609. Outside North America: Macmillan Magazines Ltd.; 4 Little Essex Street; London WC2R 3LF, U.K.] ◊

Jay Snoddy Joins DOE Human Genome Staff

Jay Russell Snoddy, a detailee from Argonne National Laboratory (ANL), was recently named the fifth member of the Human Genome Program staff of the DOE Office of Health and Environmental Research (OHER) in Germantown, Maryland. His responsibilities involve molecular and cellular biology within the DOE Human Genome Program and the Health Effects and Life Sciences Research Division; he also serves as a member of the OHER Human Genome Task Group and Health Effects Task Group.

Snoddy received his B.S. degree in 1980 from Bucknell University with honors in Biology. His Ph.D. thesis research in the laboratory of Peter Lengyel at Yale University involved genetic mapping and DNA sequencing of a family of mouse genes whose expression is strongly unregulated by interferons.

Snoddy worked for 2 years with Harinder Singh at the University of Chicago on the DNA transcription factors in B-cell lines. The primary focus of this research was somatic cell selection strategies using selectable markers under the tight transcriptional control of transcription-factor binding sites. Snoddy then joined Radomir Crkvenjakov and Radoje Drmanac in their work on sequencing by hybridization at ANL, where he designed an interface for data input and assisted in the computer-aided storage and interpretation of hybridization data. ◇



Jay Russell Snoddy
DOE Human Genome Program
and
Argonne National Laboratory

LBL Names Rine Genome Center Director

Jasper Rine was recently named Director of the Human Genome Center at the Lawrence Berkeley Laboratory (LBL), a position he has held in an acting capacity since last July. He is also a Professor of Genetics in the Department of Molecular and Cellular Biology at the University of California, Berkeley, and in his capacity as center director serves as a member of the DOE Human Genome Coordinating Committee.

The LBL Human Genome Center has specific responsibilities for mapping and sequencing chromosome 21. Under Rine's leadership, the center has undergone organizational and scientific changes culminating in a well-received DOE site review at the beginning of this year.

Mina Bissel, Director of the LBL Cell and Molecular Biology Division, which oversees the center, said, "Jasper Rine is the ideal Director for our Human Genome Center." According to Bissel, Rine is known as both a superb bench scientist and as an administrator genuinely fascinated by and interested in bringing focus and excitement to this project. "We are fortunate to have him," she said.

Rine holds a Ph.D in molecular genetics from the University of Oregon and was a postdoctoral fellow at the Stanford University School of Medicine. For a number of years his laboratory research has focused on the use of genetically tractable organisms to study human disease. His more recent research has turned toward developing the methodology for exploiting natural genetic polymorphisms to study the inheritance of natural variation. ◇

Reported by Anne Adamson
HGMIS, ORNL

Jasper Rine, Director
LBL Human Genome Center

GenBank® Update

Sequence-Submission Software

AUTHORIN™ is free software that facilitates submission of nucleic acid and protein sequences to GenBank, European Molecular Biology Laboratory (EMBL) Data Library, DNA Data Library of Japan (DDBJ), and Protein Information Resource (PIR). The latest release for IBM PC clones can perform many of the advanced features found in the Authorin Macintosh® version, including those that allow the user to (1) include an amino acid translation of the sequence within a nucleic acid submission file; (2) produce improved submission files that the databanks can process more quickly; (3) identify at a glance the fields that are mandatory on each form; and (4) use the Authorin Quick Guide for frequently asked questions. Because Authorin submissions take less time for the databanks to process, investigators often receive an accession number the same day the sequence is submitted. When ordering AUTHORIN, specify IBM PC or Apple Macintosh format and give mailing address to which software should be sent. (Contact: GenBank; IntelliGenetics, Inc.; 700 East El Camino Real; Mountain View, CA 94040; 800/477-2459, Fax: 415/962-7302; Internet: "authorin@genbank.bio.net".)

Software Database

GenBank invites software developers to add their products to the GenBank Software Clearinghouse database of molecular biology software available from vendors. To add sequence analysis programs or to obtain a copy of the clearinghouse, which is stored in relational database format, contact: Yuki Abe; GenBank c/o IntelliGenetics, Inc.; 700 E. El Camino Real; Mountain View, CA 94040; 415/962-7364; "abe@genbank.bio.net". ◇

Meeting Reports

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.

Managing Editor
Betty K. Mansfield

Editors/Writers
Anne E. Adamson
Denise K. Casey
Kathleen H. Mavournin

Production Manager/Editor
Judy M. Wyrick

Production Assistants
K. Alicia Davidson
Larry W. Davis
Sheryl A. Martin
Laura N. Yust

Special thanks to

Correspondence Address:
Betty K. Mansfield
ORNL
P.O. Box 2008
Oak Ridge,TN 37831-6050

Phone: 615/576-6669
Fax: 615/574-9888

BITNET: "bkq@ornlstc"
Internet: "bkq@ornl.gov"

Sponsor Contacts:

Daniel W. Drell
DOE Program Office
Germantown, MD 20545
301/903-4742
Fax: 301/903-5051
Internet:
"drell@mailgw.er.doe.gov"

Leslie Fink
NIH National Center for
Human Genome Research
Bethesda, MD 20892
301/402-0911
Fax: 301/480-2770

Genome-Related Publications

¶ Newsletters

Genome (University of Michigan Human Genome Center): A newsletter for educators that is designed to describe the status of the Human Genome Project throughout the United States and particularly at the University of Michigan. A current topic in genetics is featured in each issue. National education news, new resources for the classroom teacher, educational activities, and materials available through the center's education program are included. Quarterly. [Contact: Paula Gregory, Education Director; Human Genome Center; University of Michigan; Ann Arbor, MI 48109; 313/764-8050.]

Baylor Genome Center News (Baylor College of Medicine): Covers recent advances related to the center's areas of genome research, details of data and materials that are available to other researchers, lists of recent publications, and reports on other center activities. Quarterly. [Contact: Belinda J. F. Rossiter; Human Genome Center; Baylor College of Medicine; One Baylor Plaza; Houston, TX 77030; 713/796-6522, Fax: 713/798-6521.]

Probe (U.S. Department of Agriculture): Designed to facilitate interaction throughout the plant genome mapping community and beyond, **Probe** presents articles on pertinent topics, technologies, and people in plant genome research; informatics; and funding opportunities. A calendar of genome events is included. Quarterly. [Contact: Susan McCarthy; National Agricultural Library, Room 1402; 10301 Baltimore Boulevard; Beltsville, MD 20705-2351; 301/504-6875, Fax: 301/504-7098.]

Linkage Newsletter (Columbia University): Produced by Jurg Ott and focused on human linkage analysis with particular emphasis on statistical problems and computer programs. Now in its sixth year, the newsletter also includes information on available courses, software bugs and possible remedies, and electronic bulletin boards, as well as a question-and-answer column. Two to three issues yearly. [Contact: Katherine Montague, Editorial Assistant; Columbia University, Box 58; 722 West 168th Street; New York, NY 10032; 212/960-2507, Fax 212/568-2750, BITNET: "ott@nyspi.bitnet".]

Bioinformatics (ASFRA): Devoted to databases, databanks, and related technologies being developed in the biomedical arena and the use of such tools to record and analyze results, identify organisms, and locate properties. The magazine publishes critiques of products and processes and descriptions of systems, services, and projects. The aim is to inform investigators in different areas so developments can be seen against other backgrounds. Eight issues yearly. Institutional subscription, $162; personal, $90. [ASFRA BV; Publishing Division; Voorhaven 33; 1135 BL EDAM; Netherlands; (Int.) 31/29-93-72751, Fax: (Int.) 31/29-93-72877.] ◊

California Educational Linkages in the Life Sciences (CELLS) (Lawrence Hall of Science): Aims to promote development of collaborative programs for bringing recent biological science advances into the classroom through interaction and cooperation among schools, universities, industry, government, environmental and consumer groups, the media, and the public. Issues highlight educational programs and feature topics of interest to teachers and students. Two issues yearly. [Contact: Susan Brady or Mary Connolly; **CELLS** Project; Lawrence Hall of Science; University of California; Berkeley, CA 94720; 510/643-5547.]

NCBI News [National Center for Biotechnology Information (NCBI)]: Informs the biology community about NCBI research activities and the availability of database and software services. The NCBI mission is to develop new information technologies to aid in the understanding of fundamental molecular and genetic processes that control health and disease. This goal involves (1) creating automated systems for storing and analyzing knowledge about molecular biology, biochemistry, and genetics; (2) performing research into advanced methods of computer-based information processing; (3) facilitating the use of databases and software; and (4) coordinating efforts to gather biotechnology information worldwide. Three issues yearly. [Contact: NCBI; NLM; NIH; Building 38A, Room 8N-803; 8600 Rockville Pike; Bethesda, MD 20894; Fax: 301/480-9241; Internet: "info@ncbi.nlm.nih.gov".]

New Mapping Kit for Human Chromosome 1

The American *Type Culture* Collection (ATCC), in conjunction with the Centre d'Etude du Polymorphisme Human (CEPH) and supported by the NIH National Center for Research Resources, is distributing a mapping kit (ATCC #77175) for human chromosome 1. The kit contains 16 DNA probes (15 recombinant plasmids and 1 cosmid, 5 μg DNA each) to detect a subset of ordered genetic markers from the CEPH consortium linkage map of human chromosome 1 [*Genomics* 9, 686–700 (1991)]. $225. [Contact for ordering kit: 12301 Parklawn Drive; Rockville, MD 20852-1776 (301/881-2600; Fax: 301/231-5826). Contact for technical information on using the probes in the kit: William Nierman at ATCC address above (Fax: 301/770-1848) or Howard Cann at CEPH in Paris (Fax: {Int.} 33/1-40-18-02-55)].

For Your Information

NCHGR Initiates Eastern European Programs

PA 92-67 and PA 92-68

To facilitate collaboration between U.S. and Central and Eastern European scientists, NIH NCHGR and the Fogarty International Center are sponsoring research opportunities and extended visits for foreign investigators in U.S. laboratories [see **HGN 3**(6), 5 (March 1992)]. Support will be through the small-grants mechanism (R03) for the International Genome Research Collaborative Program and through the international fellowships mechanism (F05) for the International Genome Research Fellowship Program. Central and Eastern Europe are defined as Bulgaria, the Czech and Slovak Federal Republic, Hungary, Estonia, Latvia, Lithuania, Poland, Romania, all other republics of the former U.S.S.R., and Yugoslavia.

Applications are encouraged in both categories for the construction of high-resolution genetic and physical maps and the development of (1) new or improved DNA sequencing methods; (2) computer tools, information systems, and strategies for collecting, storing, retrieving, analyzing, interpreting, and distributing large amounts of mapping and sequencing data; or (3) technology to support Human Genome Project objectives. Foreign applicants must have U.S. collaborators (in the case of small grants) or U.S. sponsors (in the case of fellowships) who hold NCHGR grants.

Application receipt dates each year:

- PA 92-67 (collaborative program) – June 1, October 1, and February 1.
- PA 92-68 (fellowship program) – September 10, January 10, and May 10.

For further information and to request the special application instructions, contact:

- David A. Wolff; International Research and Awards Branch; Fogarty International Center; Bldg. 31, Room B2C21; 9000 Rockville Pike; Bethesda, MD 20892; 301/496-1653; Fax: 301/402-0779. ◊

NCHGR Genome Informatics Research

PA-92-59

NIH NCHGR supports informatics research in several targeted areas as well as in the establishment and operation of repositories for collecting and disseminating data derived from the Human Genome Project.

Support for informatics research, development, and infrastructure is furnished through a number of funding mechanisms. Applicants are encouraged to contact NCHGR staff (listed below) to discuss the appropriateness of a particular support mechanism and any special application requirements.

- David Benton, Director; Genome Informatics Program; Bldg. 38A, Room 610; Bethesda, MD 20894; 301/496-7531.

U.S. Genome Research Funding Guidelines

Note: Investigators wishing to apply for NIH and DOE funding are urged to discuss their projects with 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 and 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 staff during application development phases.

Program announcements are listed in the weekly **NIH Guide for Grants and Contracts**,* which is available by

- Hard-copy subscription – call 301/496-7441.
- Remote login via modem to NIH Grant Line – call John James, 301/496-7554.
- Listserver computer network subscription – call Dottie Baker, 919/966-5625; BITNET: "pjones@uncvx1.bitnet" or Internet: "jones@samba.acs.unc.edu".

*Expanded statements of RFAs listed in the NIH grants guide may be obtained from either of the two electronic sources or from NIH NCHGR in Bethesda, Maryland (301/496-0844).

DOE Human Genome Program

Special Research Grants: Program Notice 92-13

Solicitations for technology research proposals were announced in the April 23 issue of the **Federal Register** [57(79), 14833–34 (1992)]and in recent issues of **Science** and other publications. The DOE Office of Health and Environmental Research (OHER) of the Office of Energy Research invites applications for the development and implementation of automated mapping and advanced sequencing technologies and informatics/computational/interpretive capacities that are broadly supportive of the Human Genome Program. Preproposals encouraged by June 15. Formal proposals due August 7. For more information, contact

- David Smith, OHER, ER-72 (GTN), DOE Office of Energy Research, Washington, D.C. (301/903-6488).

Special Research Grants: Program Notice 92-14

OHER invites applications for special research grants to support activities on Ethical, Legal, and Social Issues (ELSI) that may arise from the use of data resulting from the Human Genome Project [**Fed. Reg.**, **57**(78), 14710–11 (April 22, 1992)]. These activities include (1) conducting multidisciplinary empirical research on privacy as it pertains to genetic information, (2) preparation and dissemination of educational materials to enhance public understanding of both the scientific and ELSI aspects of the Human Genome Project, and (3) planning and implementing conferences focused on relevant issues. Applicants are urged to discuss proposals with

- Daniel Drell, OHER (301/903-4742, Fax: 301/903-5051, Internet: "drell@mailgw.er.doe.gov"). Preposals due June 15; proposals due August 7.

SBIR Grants

DOE also invites small business firms to submit grant applications addressing the human genome topic of SBIR programs, which are designed to strengthen innovative firms in areas of research and development and to contribute to the growth and strength of the nation's economy. The human genome topic emphasizes instrumentation development for automated clone processing, improvements in DNA sequencing technologies, and enhanced sequence data storage and processing capabilities. Next submission date: fall 1992. For more information, contact

- Samuel Barish; SBIR Program Manager, ER-16; DOE; Washington, DC 20585; 301/903-5707.

Human Genome Distinguished Postdoctoral Fellowships

Next deadline: February 1, 1993. For further information, see **HGN 3**(3), 5 (September 1991) or contact

- Linda Holmes, Oak Ridge Associated Universities: 615/576-4805. ◊

Calendar of Genome Events*

May

31–June 1. ELSI Insurance Task Force; Washington, DC [E. Langfelder, 301/402-0911, Fax: /480-2770]

June

2–3. NIH Cystic Fibrosis Studies Consortium Meeting; Washington, DC [see contact: May 31–June 1]

4–7. Second International Conference on Bioinformatics, Supercomputing, and Complex Genome Analysis; St. Petersburg Beach, FL [H. Lim, 904/644-7046, Internet: "genome@scri.fsu.edu"]

7–9. First International Workshop on Chromosome 6; Ann Arbor, MI [J. Trent, 313/764-4509, Fax: -4534, A. Ziegler, (Int.) 49/30-30-35-2617, Fax: -3778]

12–14. Second Chromosome 4 Workshop; Leiden, Netherlands [G. van Ommen, (Int.) 31/71-276293, Fax: -276075, J. Murray, 319/356-2674, Fax: -3347]

18–19. Chromosome 15 Workshop; Tucson, AZ [T. Donlon, 415/723-4923, Fax: -3147]

20–25. 1992 World Congress on Cell and Tissue Culture; Tissue Culture Assoc., Washington, DC [P. Reinsfelder, 301/992-0948, Fax: -0949]

22–24. Annual Meeting of the Electrophoresis Society; Barr Enterprises, Research Triangle Park, NC [J. Cunningham, 301/898-3772, Fax: -5596]

July

19–Aug. 2. *Second International Workshop: Open Problems in Computational Molecular Biology; Telluride, CO [A. Konopka, 301/846-5396, E-mail: "konopka@fcrfv1.ncifcrf.gov"]

20–21. First International Workshop on Chromosome 18; Chicago, IL [M. LeBeau, 312/702-0795, Fax: -3163]

21–25. Science Innovation '92: New Techniques and Instruments in Biomedical Research; San Francisco, CA [Am. Assoc. for the Advancement of Sci. (AAAS), 202/326-6450, Fax: /289-4021]

23–25. 11th Summer Symposium in Molecular Biology; University Park, PA [P. Phillips, 814/863-3650, Fax: -1357]

August

16–21. Ninth International Biotechnology Symposium & Exhibit; Crystal City, VA (poster deadline: Mar. 31) [Am. Chem. Soc. (ACS), 202/872-6286, Fax: -6128]

18–23. Molecular Genetics of Bacteria & Phages; Cold Spring Harbor, NY [Cold Spring Harbor Laboratory (CSHL), 516/367-8346, Fax: -8845]

26–30. Mouse Molecular Genetics; CSHL, Cold Spring Harbor, NY [see contact: Aug. 18–23]

September

2–6. Cancer Cells: Genetics & Molecular Biology of Breast Cancer; CSHL, Cold Spring Harbor, NY [see contact: Aug. 18–23]

7–11. Eighth Workshop on Molecular Genetics of the Mouse; Dourdan, France [J.-L. Guenet, (Int.) 33/1-4568-8555, Fax: -8639]

10–14. *First International E. coli Genome Meeting; Madison, WI [M. Ellingson, 608/262-2755, Fax: -5487]

13–15. Third International Workshop on Human Chromosome 11; San Diego, CA [G. Evans, 619/453-4100, ext. 279, Fax: /558-9513]

14–16. ELSI Grantee Workshop; Washington, DC [see contact: May 31–June 1]

17–20. Third International Chromosome 22 Workshop; Philadelphia, PA [B. Emanuel, 215/590-3856, Fax: -3764]

18–20. Chromosome 12 Gene Mapping Workshop; Oxford, England [R. Gemmill, 303/333-4515, Fax: -8423 or I. Craig, (Int.) 44/865-275-327, Fax: -318]

20–21. *National Advisory Council for Human Genome Research; Bethesda, MD [J. Ades, 301/402-2205, Fax: 2218]

20–23. Chromosome 13 Workshop; Dallas, TX [A. Bowcock, 214/688-3896, Fax: -8617]

22–26. Gene Therapy; CSHL, Cold Spring Harbor, NY [see contact: Aug. 18–23]

23–24. The Birth of Bioethics; Seattle, WA [Dept. of Medical History and Ethics, 206/543-5447, Fax:/685-7515]

26–30. Genome Sequencing and Analysis IV; Hilton Head, SC [S. Wallace, 301/480-0634, Fax: -8588]

October

7–9. "The Impact of Molecular Medicine on Clinical Practice" at the Anglo-American Conference; London, England [W. O'Reilly, 212/371-1150, Fax: -1151]

9–11. Genetic Factors in Crime: Findings, Uses, and Implications; College Park, MD [D. Wasserman, 301/405-4753, Fax:/314-9346]

11–15. Sixth International Mouse Genome Conference; Buffalo, NY [V. Chapman, 716/845-5840, Fax: -8169]

15–18. Human Genome '92; Nice, France [AAAS, 202/326-6450, Fax: /289-4021]

17–21. First International Conference on Mathematical and Computational Analysis of the Human Genome and Its Mutation Load; Szeged, Hungary [Human Genome Research Ltd., (Int.) 36/62-23855, Fax: -23844]

November

4–6. Third Meeting of Mammalian Genetics and Development Workshop; London [S. Rastan, (Int.) 44/81-869-3266, Fax: -423-1275]

4–8. Genetics of Cancer; Hilton Head, SC [AACR, 215/440-9300, Fax: -9313]

6–8. Chromosome 2 Workshop; Half Moon Bay, CA [S. Naylor, 512/567-3842, Fax: -6781]

6–8. Human Genome Project: Impact, Implications, and Issues; San Francisco, CA (submission of papers deadline: May 29) [B. Leopold, 215/872-7608, Fax: -1192]

9–11. Plant Genome I; San Diego, CA (abstract deadline: Oct. 1) [Scherago International, Inc., 212/643-1750, Fax: -1758]

9–13. 42nd Annual Meeting of the American Society of Human Genetics (ASHG); San Francisco, CA [M. Ryan, 301/571-1825, Fax:/530-7079]

11. Planning meeting for the First International Chromosome 8 Workshop at ASHG; San Francisco, CA [D. Drayna, 415/266-1413, Fax: -2739]

15–17. *Chromosome Coordinating Committee Meeting; Baltimore, MD [P. Pearson, 410/955-9705, Fax: -0054]

December

7–8. DOE/NIH Joint Subcommittee on the Human Genome; NIH Program Advisory Committee on the Human Genome; Bethesda, MD [see contact: Sept. 20–21]

7. *DOE Human Genome Coordinating Committee; Bethesda, MD

January 1993

5–8. Biotechnology Computing Track of the 26th Hawaii Conference on System Sciences; Kauai, HI (submission of paper deadline: June 5) [L. Hunter, 301/496-9300, Fax: -0673, Internet: "hunter@nlm.nih.gov"]

17–22. "Advances in Gene Technology: Protein Engineering and Beyond" at the 1993 Miami Bio/Technology Winter Symposia; Miami Beach, FL [S. Black, 305/547-3597, Fax: /324-5665]

25. *National Advisory Council for Human Genome Research; Bethesda, MD [see contact: Sept. 20–21]

February 1993

1–6. Oncogenes and Tumor Suppressor Genes in Cancer Etiology and Mammalian Development; Big Sky, MT [see contact: Nov. 4–8]

7–11. *Third DOE Contractor-Grantee Workshop; Santa Fe, NM (abstract deadline: Nov. 1) [S. Spengler, 510/486-4879, Fax: -5717]

March 1993

6–8. Chromosome 20 Workshop; Paris [C. Smith, 510/643-6376, Fax: -1188]

April 1993

12–18. 1993 Keystone Symposia Meetings: Gene Therapy; Keystone, CO [Keystone Symposia, 303/262-1230, Fax: -1525]

12–18. 1993 Keystone Symposia Meetings: Genetically Targeted Research & Therapeutics-Antisense & Gene Therapy; Keystone, CO [see contact: April 12–18]

May 1993

17. *National Advisory Council for Human Genome Research; Bethesda, MD [see contact: Sept. 20–21]

19–22. 84th Annual Meeting of the AACR; Orlando, FL [see contact: Nov. 4–8, 1992]

*Attendance at meetings listed with asterisk is either limited or restricted. Dates may change; check with contact person.

Training Calendar: Workshops and Coursework*

June

1–5. YACs and Phage Vectors in Large DNA Analysis; CATCMB/CUA, Washington, DC [Office Manager, 202/319-6161, Fax: -5721]

5–25. Advanced Bacterial Genetics; CSHL, Cold Spring Harbor, NY (application deadline: Mar. 15) [CSHL, 516/367-8343, Fax: -8845]

15–16. GDB/OMIM Training Courses [see schedule, p. 9]

15–19. Current Techniques for Plant Biotechnology; CATCMB/CUA, Washington, DC [see contact: June 1–5]

15–19. †Ethics and the Human Genome Project; Seattle, WA (application deadline: Mar. 15) [B. Brownfield, 206/543-5447]

15–19. Recombinant DNA and Cytogenetic Approaches for the Study of Genetic Disease and Gene Mapping; CATCMB/CUA, Washington, DC [see contact: June 1–5]

15–19. Recombinant DNA Methodology; Exon-Intron, Inc. (also offered at later dates) Columbia, MD [Workshop Coordinator: 410/730-3984, Fax: -3983]

15–19. Recombinant DNA Techniques; Rochester, NY [RIT, 716/475-5000, Fax: -7000]

15–25. Principles of Flow Cytometry; BTP, Colorado Springs, CO [S. Chance, 515/232-8306]

15–29. Advanced Drosophila Genetics; CSHL, Cold Spring Harbor, NY (application deadline: Mar. 15) [see contact: June 5–25]

18–19. Molecular Cytogenetics: Chromosome In Situ Workshop; Gaithersburg, MD (also offered later dates) [Oncor, Inc., 301/963-3500, Fax: /926-6129]

22–26. Advanced Topics in Recombinant DNA; Exon-Intron, Inc., Columbia, MD (also offered July 20–24) [see contact: June 15–19]

22–26. Expression of Recombinant DNA in Mammalian Cells; CATCMB/CUA, Washington, DC [see contact: June 1–5]

29–July 19. Molecular Cloning of Neural Genes; CSHL, Cold Spring Harbor, NY (application deadline: Mar. 15) [see contact: June 5–25]

July

9–18. Gene Targeting & Homologous Recombination; London [P. Faik, (Int). 44/71-403-6998, Fax: -407-5281]

12–18. Technical Skill & Art of DNA Sequencing; Salt Lake City, UT (application deadline: April 15) [Genome Tech. Workshop, 801/581-5190, Fax: /585-3910]

13–Aug. 1. Genome Technology; Salt Lake City, UT [see contact: July 12–18]

19–25. Physical Mapping; Salt Lake City, UT (application deadline: April 15) [see contact: July 12–18]

19–Aug. 1. Carolina Workshops on Mouse Genetics; Chapel Hill, NC (application deadline: May 22) [W. Litaker, 919/966-1730, Fax: -6821]

20–31. Recombinant DNA Methodology and Applications; Baltimore, MD [R. Halle, 410/455-2336, Fax: -1074]

20–31. Short Course in Medical & Experimental Mammalian Genetics; Bar Harbor, ME [Jackson Laboratory, 207/288-3371, ext. 1253]

21–Aug. 10. Advanced Molecular Cloning & Expression of Eukaryotic Genes; CSHL, Cold Spring Harbor, NY (application deadline: Mar. 15) [see contact: June 5–25]

21–Aug. 10. Yeast Genetics; CSHL, Cold Spring Harbor, NY (application deadline: Mar. 15) [see contact: June 5–25]

26–Aug. 1. Human Disease & Medical Applications for Genome Tech.; Salt Lake City, UT (application deadline: April 15) [see contact: July 12–18]

26–Aug. 14. †Societal Institute of the Mathematical Sciences Tutorial: Mathematical Sciences in Genomic Analysis; New Brunswick, NJ [D. Thomsen, 203/966-1008, Fax: /972-6069]

31–Aug. 8. DNA Related Methods in Human Genetics: YAC Cloning in Genome Analysis; London [see contact: July 9–18]

August

2–14. Molecular Evolution; Marine Biological Laboratory, Woods Hole, MA [F. Dwane, 508/548-3705, ext. 216]

3–7. *Nucleic Acid and Protein Sequence Analysis Workshop; Pittsburgh, PA (application deadline: June 12) [N. Blankenstein, 412/268-4960, Internet: "blankens@a.psc.edu"]

10–14. RNA Isolation and Characterization; Exon-Intron, Inc., Columbia, MD [see contact: June 15–19]

17–18. PC/GENE; IG, Mountain View, CA [N. Robinson, 415/962-7300, Fax: -7302]

19–20. GeneWorks; IG, Mountain View, CA [see contact: Aug. 17–18][]

24–27. †Partnerships in Teaching Biotechnology: Human Genome Technology Workshop; Ann Arbor, MI (also offered Aug. 28–29) [P. Gregory, 313/764-8050, Fax: -4133]

24–28. Advanced Recombinant DNA Methodology; Rockville, MD [ATCC, 301/231-5566, Fax: /770-1805]

September

30–Oct. 2. Basic Cytogenetics; Rockville, MD [see contact: Aug. 24–28]

October

8–21. Analysis & Genetic Manipulation of YACs; CSHL, Cold Spring Harbor, NY [see contact: June 5–25]

12–14. PCR Techniques; Lake Tahoe, NV [CATCMB/CUA, 202/319-6161, Fax: -4467]

12–14. Recombinant DNA Methodology; Lake Tahoe, NV [see contact: Oct. 12–14]

18–Nov. 1. Carolina Workshops on cDNA and Gene Expression; Chapel Hill, NC [see contact: July 19–Aug. 1]

26–30. Recombinant DNA Techniques & Applications; Rockville, MD [see contact: Aug. 24–28]

26–Nov. 4. †Essential Computational Genomics for Biologists; CSHL, Cold Spring Harbor, NY [T. Marr, 516/367-8393, Fax: -8389]

November

2–4. PCR/Cycle DNA Sequencing; Rockville, MD (also offered Nov. 5–7) [see contact: Aug. 24–28]

11–12. Advanced Data Banks; IG, Mountain View, CA [see contact: Aug. 17–18]

AAAS Am. Assoc. for the Advancement of Science.
AACR Am. Assoc. for Cancer Research
ACS Am. Chemical Soc.
ASHG Am. Soc. of Human Genetics
ATCC Am. **Type Culture** Collection
BTP Biotechnology Training Programs
CATCMB/CUA Center for Advanced Training in Cell and Molecular Biology/Catholic Univ. of America
CSHL Cold Spring Harbor Laboratory
ELSI Ethical, Legal, and Social Issues
ESHG European Soc. of Human Genetics
IG IntelliGenetics
LTI Life Technologies, Inc.
NCHGR National Center for Human Genome Research
UNESCO United Nations Educational, Scientific, and Cultural Organization

*Dates and course status may change, and courses may be offered at other times and places; check with contact person.
†NCHGR-funded event.

Human Genome Management Information System

Subscription/Document Request (Vol. 4, No. 1)

1. ___ **Human Genome News**

___ New Subscriber ___ Change of Name/Affiliation/Address ___ Drop Name from Mailing List

2. ___ **Understanding Our Genetic Inheritance, The U.S. Human Genome Project: The First Five Years, FY 1991–1995 (Joint DOE-NIH 5-Year Plan)**

3. ___ **DOE Contractor-Grantee Workshop Report (complete report with abstracts)**

Please type or print. Enclose previous newsletter address label or business card, if possible.

Name: _____ **Phone:** _____
(First) (MI) (Last)

Affiliation: _____

Mailing Address (business or home, please circle): _____

_____

E-Mail Address: _____ **Fax:** _____

Reader Comments:

HGMIS MAILING ADDRESS
Betty K. Mansfield
Oak Ridge National Laboratory
P.O. Box 2008
Oak Ridge, TN 37831-6050
U.S.A.