GLOBAL CHANGE

Research Council Says U.S. Climate Models Can't Keep Up

When the U.S. Global Change Research Program (USGCRP) recently began to look at what greenhouse warming might mean for different regions of the United States, it quickly ran up against a problem: No U.S. modelers had simulated changing regional climate in enough detail. So USGCRP policy analysts had to rely on climate models from Canada and Britain until one U.S. model finally made the grade. Even then, that model had to be partly run on computers in Japan and Australia because the United States doesn't have enough computer power at its climate centers. The obvious, but surprising, conclusion is that even as the United States tries to shape the world's greenhouse warming policy, it lags in the race to simulate climate. A new report by a committee of the National Research Council (NRC) makes that judgment official.

According to the report, published last month, the problem is twofold: The United States lacks a coordinated strategy for building models, and it has limited supercomputer power available to run them. "There was a problem, and there is a problem still," says modeler David Randall of Colorado State University in Fort Collins, whose letter with three colleagues jump-started the NRC review 3 years ago. Modelers clearly need more computing power, Randall says, but also "we need newer, better models, newer and better ideas. The U.S. models are competent, but … the U.S. was the best in the business." There are already signs of progress, says NRC Climate Research Committee chair Thomas Karl of the National Climatic Data Center in Asheville, North Carolina, "but we can't lose momentum now; other nations are making significantly faster progress. We have to be sure we do things more wisely."

The shortage of computing power is the most easily quantified problem. As of a year ago, the most powerful climate modeling computer in the United States was a Cray T90, according to information provided to the NRC's Climate Research Committee by Bill Buzbee, recently retired computing director at the National Center for Atmospheric Research (NCAR) in Boulder, Colorado. The Cray runs at a speed of 15 gigaflops, or 15 billion floating point operations per second, but a year ago atmospheric modelers in Australia, France, the United Kingdom, and Canada were running models at 20 to 45 gigaflops, largely on Japanese-brand supercomputers. Today, NCAR has a new and more powerful climate computer, the ORIGIN 2000 system—but at 10 gigaflops, it still ranks only 102nd among world supercomputers as rated by a standard speed test, and it falls well behind the meteorological and climate modeling computers of the United Kingdom, Canada, Australia, and France (see table).

CLIMATE MODELING POWER

Rank[*]	Computer	Rmax[†]	Location
5	SGI T3E900	552,920	Meteorological Office, U.K.
18	NEC SX-4/ 128M4	244,000	Atmospheric Environment Service, Canada
75	NEC SX-4/32	61,770	Bureau of Meteorology, Australia
88	Fujitsu VPP700	58,000	Direction de la Meteorologie Nationale, France
102	SGI ORIGIN 2000	51,440	NCAR, USA

[*] www.netlib.org/benchmark/top500.html [†] Rmax is one standard measure of maximum computing speed.

SOURCE: MANNHEIM UNIVERSITY/NETLIB

Solving the computer power problem will be far harder than measuring it. The computers most sought after by modelers are sold by Japanese companies, but the U.S. Department of Commerce has set huge financial penalties for buying them, because their below-cost price is seen as unfair competition for U.S. computer makers. Commerce's "antidumping" order prevented NCAR from buying its Japanese computer of choice (*Science*, 30 August 1996, p. 1177). That is "a quite serious problem that increasingly affects the international competitiveness of the U.S. climate modeling community," says the NRC report. Even if the trade problem is somehow resolved, warns Buzbee, "federally funded organizations won't be able to go near Japanese computers" because of the political sensitivity of using foreign supercomputers.

Help is on the way, though. Two weeks ago, Vice President Al Gore announced the Clinton Administration's $366 million plan to beef up information technology in the fiscal year 2000 budget (*Science*, 29 January, p. 613). If approved, most of the money would help develop computers that could run at 40 trillion floating point operations per second by 2003. Among the tasks of such "teraflops" machines is boosting regional climate forecasts. Forty teraflops would outpace even the 32 teraflops that Japan's Science and Technology Agency is aiming for by 2002.

Solutions for climate modeling's other problem—the lack of a national strategy—are not so clear. About a decade ago, the climate modeling community rejected a focused, Manhattan Project–style approach to building a single national climate model (*Science*, 22 November 1990, p. 1082). Instead, modelers favored a multiagency strategy that was nevertheless supposed to involve close coordination among the Department of Energy, NASA, the National Oceanic and Atmospheric Administration (NOAA), and the National Science Foundation. But the NRC committee found that each agency independently establishes priorities and that research important to policy-makers, such as regional modeling, falls through the cracks. "We could get better organized in the U.S.," says Karl.

"We abandoned a top-down" approach, agrees Jerry D. Mahlman, a modeler and director of NOAA's Geophysical Fluid Dynamics Laboratory, "but we've also been in anarchy, where everybody does their own thing." Such chaos is common, and often productive, in other research settings. But in this case it has helped to delay the integration of model components such as atmosphere, oceans, and chemistry. Also, there was little cross-fertilization among models, so that researchers effectively worked on "their own pet models," says modeler Tim P. Barnett of the Scripps Institution of Oceanography in La Jolla, California. What American researchers lack, he says, is "a mechanism for easily integrating new research results" from outside groups into their models.

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The NRC report urges that USGCRP agencies agree on a national set of goals, coordinate funding, and reorder the priorities of individual modeling groups to achieve them. It notes some encouraging developments along those lines. One is NCAR's "new-generation" model, which was developed and is being improved with outside assistance. After some rocky times, "we are working interactively" to improve model components, says Mahlman. "We're not there yet," adds Barnett, "but I'm very optimistic about the future." **–RICHARD A. KERR**

GENOME SEQUENCING

Fruit Fly Researchers Sign Pact With Celera

It may not be as dramatic as a Capulet-Montague marriage, but the announcement last week that experts from the private and public sectors are joining together to decode the fruit fly's genome could signal a new period of cooperation in genome research.

For years, private entrepreneurs and academics have clashed over how quickly genome data should be released. Now, aided by a huge investment from equipment manufacturer Perkin-Elmer of Norwalk, Connecticut, the two camps have agreed on a joint plan to sequence the DNA of the fruit fly *Drosophila melanogaster* and a timetable for making the sequence public. It could soon become the most complex organism completed; its genome, about 160 million bases, is two-thirds larger than that of the worm *Caenorhabditis elegans*, completed in 1998 (*Science*, 11 December 1998, p. 1972). Yet the partnership aims to finish in record time—by December 1999. The project could also pave the way for a similar collaboration to sequence the human genome.

The details of the fly project were released on 27 January by the National Human Genome Research Institute (NHGRI). It is bringing together a group of NHGRI-funded sequencers led by Gerald Rubin of the University of California (UC), Berkeley, with the staff of Celera Genomics of Rockville, Maryland, a company started last year by Perkin-Elmer and DNA sequencer J. Craig Venter. A memorandum of understanding signed by Venter, Rubin, and UC officials says that by April, Rubin's group will supply 12,500 bacterial clones holding fragments of *Drosophila* DNA to Celera, which aims to do the sequencing by July. Finished data—in groups of 2000 or more bases of contiguous DNA (contigs)—will be released to the public by 1 January 2000 "at the latest."

Venter said he is "delighted" to join forces with the academics. And NHGRI director Francis Collins said last week that the agreement "marks the beginning of a productive collaboration … that should give the research community the fruit fly sequence more rapidly than previously predicted." Collins also predicted a $10 million savings.

Most of the difficult preparatory and finishing tasks will continue to be done by academics, Collins said. Rubin and his colleagues at the Lawrence Berkeley National Laboratory in California, the Baylor College of Medicine in Houston, and the Carnegie Institution of Washington have been identifying landmarks along the 160 million bases of the fly genome and tagging them for mapping purposes. They had hoped to sequence all the gene-rich regions—about 125 million bases long—by the end of 2001. Already, they've completed 20% of this work.

Dealmaker. Venter teams up with fly experts to sequence the *Drosophila* genome.

Instead of the conventional approach of serial sequencing and assembly that most academic groups have been using, Celera will use a battery of new Perkin-Elmer automated machines to sequence all the clones in parallel and fit the results together afterward. By July, the company plans to begin releasing contigs simultaneously to the public and to Rubin's consortium. Rubin's group will fit the puzzle together, relying in part on low-precision sequencing of the genome by a team headed by Richard Gibbs at Baylor. All this will require a "nimble" touch, says Rubin: "Our work will be much more like a scientific experiment" than a normal production job.

If successful, this effort could set the stage for collaboration on sequencing the 3 billion bases of the human genome. Venter last year announced that Celera hoped to do this on its own in 3 years. Federal research officials then offered to collaborate.

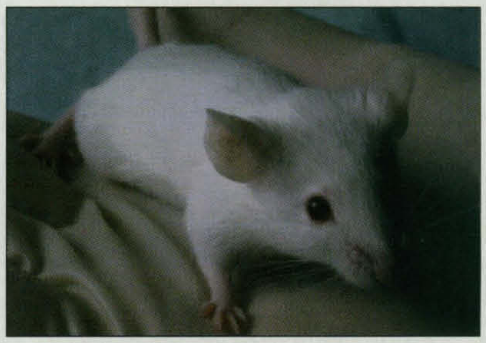
Last week, Collins said he was moderately optimistic about the prospects for a broader agreement that might include Celera. In an interview with *Science*, he said that "active discussions are going on right now on how to put together a memorandum of understanding on the human genome" to include U.S. publicly funded scientists, those supported by the Wellcome Trust in Britain, and "any private entity that's interested." There is still "some tension," he said, over how data will be annotated and released, as nonprofit and private sponsors have different aims. Working out the details will be "complicated," because Celera clearly wants to stake a claim to human genomic data. **–ELIZABETH PENNISI**

ANIMAL RESEARCH

Groups Sue to Tighten Oversight of Rodents

A coalition of animal rights advocates—including three academic scientists and a biomedical supply company—announced this week that it will go to federal court to force the U.S. government to redefine mice, rats, and some birds as animals under a major animal protection law. The change is needed, they argue, to bring the country's most widely used experimental animals under federal regulations that require researchers to consider alternatives.

U.S. Department of Agriculture (USDA) officials say that the redefinition would stretch its cash-strapped enforcement program to the breaking point and could



Painless measures. This assay system measures skin and eye irritation without using lab animals.

CREDITS: (LEFT TO RIGHT) RICK KOZAK; TOM LEVY/PNI; INVITRO INTERNATIONAL