

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 me-lanogaster* 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 PerkinElmer 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 aca-

demics, 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. 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 -ELIZABETH PENNISI human genomic data.

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 reg-

ulations that require researchers to consider alternatives.

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

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

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