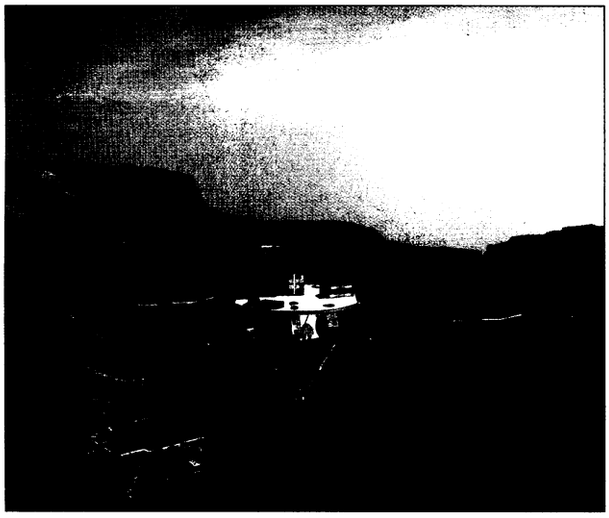
preparation for the planned April 2001 launch, says project manager George Pace of JPL. "We had confidence that the design was going to work [before the polar lander was lost]," he says. "What does it take to return it to flight status? That is a little hard to say. We don't know what the failure was."

To save weight and money, mission designers did not include a transmitter to send back flight data during the lander's entry into the atmosphere, its descent via parachute, and its rocket-assisted landing. Investigators will study all possible failure points, repeating the steps taken by its designers and by outside experts after the September loss of the Mars Climate Orbiter.



Red alert. NASA's 2001 Mars mission and other flights could be revised in the wake of this month's failure.

Goldin appears reluctant to abandon NASA's plans for 2001, saying, "If there's any possibility that we could go back and land, maybe a little different way, we're going to do it." The existing hardware also could be salvaged for a different mission. One option, says Weiler, is to turn the lander spacecraft into an orbiting telecommunications satellite with high-resolution cameras that could scout out safe landing sites for later missions and provide a stronger link between landers and Earth. Although some science would have to be postponed, he says, such an arrangement would boost the chances of success for later spacecraft.

The additional navigational tools reflect NASA's view that martian geography may have contributed to the lander's failure. The craft was headed toward a poorly understood terrain in the south polar region. Although images returned from orbit by the Mars Global Surveyor showed the targeted landing site to be relatively smooth, "we don't have a lot of experience yet in interpreting [those] images," says 2001 project scientist Stephen Saunders of JPL. "Mars looks like a completely different planet at a resolution of a few meters versus the tens of meters" available before Mars Global Surveyor, he says, and it could still harbor lethal hazards too small for Surveyor to see.

Project scientists are currently eyeing two large zones as potential landing sites for the 2001 mission. "It could be we should put more emphasis now on the smoother area" just north of the equator near Sinus Meridiani, says Saunders. The region may be a dried, mineral-laden lake bed.

So far, criticism of NASA and the Mars effort in Washington has been muted. Recent media polls show that a majority of the American public supports continued planetary research, and President Bill Clinton assured reporters on 8 December that he firmly backs Goldin's approach of "faster, cheaper, better" missions. For the moment, members of Congress seem willing to withhold judgment until the panel has had its say.

–ANDREW LAWLER AND RICHARD KERR

SCIENTIFIC MISCONDUCT

Researcher Rebuked for 20-Year-Old Misdeed

The Max Planck Society, Germany's premier research organization, announced on Monday that its president will issue a formal censure to neuroscientist Peter Seeburg, director of the Max Planck Institute for Medical Research in Heidelberg, for publishing data in a 1979 paper that Seeburg has said were false.

Seeburg's censure is the latest chapter in a drawn-out scientific melodrama involving a court battle between the University of California (UC) and biotech pioneer Genentech of South San Francisco over patent rights to engineered human growth hormone (*Science*, 11 June, p. 1752). Seeburg, a co-inventor on a UC patent at the center of the dispute, testified last April that shortly after he moved to Genentech in 1978, he took DNA samples that he had helped prepare while working at UC San Francisco. He also said he and Genentech colleagues falsified technical data in a *Nature* paper to cover up the origin of the samples. Prompted by this testimony, Max Planck president Hubert Markl earlier this year ordered a scientific misconduct investigation.

Only after Genentech agreed to pay UC

ScienceScope

Data Grab Hoping to pry open the Clinton Administration's narrow interpretation of a new law that gives the public access to raw research data, the U.S. Chamber of Commerce last week set the stage for a legal challenge by requesting data used to support several Environmental Protection Agency (EPA) regulations and policies.

Universities breathed a sigh of relief earlier this fall when the White House Office of Management and Budget limited the public's reach to published results used in crafting a rule or unpublished data cited in a regulation, and said only data collected under grants made after 6 November were open to scrutiny (*Science*, 8 October, p. 209). But such restrictions are "improper," according to chamber vice president William Kovacs. His group has asked for raw data from several older studies used by EPA, including a 1993 Harvard University air pollution analysis that prompted the campaign to force researchers to share their data. Kovacs expects EPA to deny the requests within a couple of months. If so, the chamber will sue the government.

Try, Try Again French research minister Claude Allègre (below) hasn't given up his idea to reform the CNRS, France's mammoth basic science agency. Allègre laid low much of this year after his first reform plan raised a ruckus (*Science*, 18 December 1998, p. 2162). But Allègre rebounded earlier this month, asking CNRS officials to come up with a more palatable scheme for overhauling the 12,000-researcher agency.

The new plan—dubbed "reform light" by the French daily *Le Monde*—will "blend" previously suggested reforms, such as forging closer ties between the CNRS and universities, with recommendations from the Cohen–Le Déaut report, prepared by two parliamentary deputies for Prime Minister Lionel Jospin (*Science*, 30 July, p. 647), says Vincent Courtillot, the science ministry's research director. But the retooled proposals—which should be ready by February—are already drawing preemptory fire from researchers' unions. Unhappy about a stagnant research budget for 2000, they are planning demonstrations for January.

Contributors: Eliot Marshall, Andrew Lawler, Jocelyn Kaiser, Michael Balter

CREDITS: (LEFT TO RIGHT) C. WASTE/NASA; ANNA CLOPET/BLACK STAR

$200 million in mid-November to settle the suit could the Max Planck investigation finally conclude. While litigation was pending, UC did not answer Max Planck inquiries about whether Seeburg was allowed to take the samples, says Klaus Hahlbrock, Max Planck vice president and a member of the investigating committee. UC ultimately acknowledged that, at the time, there were no unequivocal regulations barring Seeburg from taking the samples, he says. Seeburg himself declared repeatedly that he felt he was entitled to do so according to "most scientists' ethical standards."

Although the committee didn't accept that argument entirely, the investigation focused on the alleged falsified information in the 1979 *Nature* paper. Seeburg's admission was hotly contested by co-author David Goeddel, then at Genentech and now chair of the South San Francisco biotech company Tularik, and several other former colleagues. The Max Planck committee took Seeburg's admission at face value, however. The committee concluded, says Hahlbrock, that "a falsified description in a publication cannot be tolerated, no matter if it dates back 20 years," and recommended that Seeburg be censured —a rare and rather exceptional measure. The censure does not directly affect Seeburg's position at Max Planck, says Markl, but it "will be put into his personnel record."

For his part, Seeburg told *Science* that he may donate part of the $17 million he and four other former UCSF researchers will each receive as part of the settlement to a charity or research foundation. But most of all, he hopes that his censure will be the final episode in this painful saga and that he will once again be able to "concentrate on doing science." **–MICHAEL HAGMANN**

With reporting by Robert Koenig in Berlin.

COMPUTER SCIENCE

Big Blue Aims to Crack Protein Riddle

IBM last week announced a $100 million research initiative to build a supercomputer 500 times more powerful than the current record holder. Dubbed "Blue Gene," the technology test-bed's initial goal will be to model how proteins fold into the three-dimensional shapes that allow them to orchestrate life within the cell. If successful, the 5-year effort could allow drug researchers to go right from the sequence of a disease-related gene to the predicted structure of its protein, in order to identify targets for therapeutic drugs. Down the road, Blue Gene and its kin could also revolutionize other computationally intensive disciplines, such as modeling climate change and the evolution of galaxies.

Researchers who model protein folding agree that Blue Gene's ability to run 1 quadrillion (10^{15}) mathematical operations per second (also known as 1 petaflops) will be a big step for the field. "Petaflops computers certainly make you salivate," says Stephen Mayo, a protein-folding expert at the California Institute of Technology in Pasadena. It won't be easy to serve up this feast, however. Supercomputers built by IBM and Intel for the national weapons laboratories currently reign as the world's fastest, at 2 trillion operations per second (2 teraflops). "But there's no way to get up to a petaflops using [the same] technology," says Monty Denneau, a mathematician at IBM's T. J. Watson Research Center in Yorktown Heights, New York, and Blue Gene's chief architect.

Nature makes it look easy. The bubbles illustrate stages in the folding of a protein—a process that researchers would like to predict.

The chief obstacle is power consumption and heat: Denneau says a petaflops machine that used the same amount of energy for each operation as current teraflops machines "would take a dedicated [power] reactor"—and would quickly immolate itself. To speed computation while cutting power consumption, IBM plans to come up with an "ultraminimalist approach" for both hardware and software, which will reduce the complexity of the processors but increase their ability to communicate and work in tandem. Both the new chips and the software are still on the drawing boards, but "I think the plan makes a lot of sense," says Arvind, a computer architecture expert at the Massachusetts Institute of Technology, who goes by a single name.

As a test for their new machine, Denneau and his colleagues have chosen one of the toughest challenges in biology. Inside cells, newly synthesized chains of amino acids take a second or less to fold into a functional protein. Every one of tens of thousands of atoms in the chain and surrounding water molecules pulls or pushes on its neighbors to determine the final shape. But even though researchers have measured the forces between atoms in great detail and can easily predict how a handful of amino acids will interact, precisely modeling the folding of proteins has been out of reach.

The most ambitious efforts, called all-atom simulations, calculate the interatomic forces and their effects for every possible pair of atoms in the protein chain. Even for a small protein, an all-atom simulation of just a fraction of the folding process takes months of supercomputing time.

IBM's answer, Blue Gene, will consist of more than 1 million processors, each capable of 1 billion operations per second (1 gigaflops), assembled on 64 racks. To reduce power consumption, IBM researchers are doing away with a type of fast but power-hungry on-chip memory called cache. In its place, they're moving onboard a slower type of memory called DRAM, which is traditionally located off the chip. This should bring big power savings by eliminating the need to send off the chip for additional data.

To compensate for the slower memory speeds, the IBM team is planning to turn to a technique known as multithreading, the computer equivalent of a multitasking commuter who eats breakfast, drives, and talks on the phone all at the same time. In this case, each processor will work simultaneously on eight separate problems. That way if a processor is waiting for a bit of data to come in from memory to complete one computation, it can still be working on others at the same time. Finally, because chip failures are inevitable in an array of a million processors, Blue Gene's software will be designed to reroute data to working devices if a processor or connection fails in midsimulation.

Even with a new petaflops machine, it will take about 1 year to simulate the complete folding of a typical protein. And even then the protein-folding problem may not be solved. Peter Wolynes, a protein-folding expert at the University of Illinois, Urbana-Champaign, explains that the all-atom approach of computing the interactions between pairs of atoms may not be enough. It may turn out that to get the right answer, researchers will have to compute the interactions among many atoms at once as they tug and push on each other, which would vastly increase the problem's complexity and require still more computing muscle. "My suspicion is that you won't need all that additional stuff," says Wolynes. But if it turns out you do, at the end of the day "you would have learned that you can't solve it."

–ROBERT F. SERVICE

CREDIT: KOLLMAN *ET AL.*, UCSF