

structure in the end. "The ultimate goal is crystals in, structures out," he says. He expects that it will be another 2 years before the full process is complete.

—ROBERT F. SERVICE

## STRUCTURAL BIOLOGY

### A Plan to Release Data Within Six Months

**AIRLIE HOUSE, VIRGINIA**—In the 1990s, gene sequencers were under the gun to make their raw data public as rapidly as possible. Now, it's the turn of the gem-cutters of biology—the people who decipher the shape of protein

molecules—and some are not too comfortable with the notion. Last week, international leaders of the field rejected a proposal that labs now gearing up to roboticize the study of proteins give away structural coordinates immediately, or within 3 weeks of completion. Instead, at a meeting at an estate here in Virginia's horse country, they agreed to speed up data release, but on a timetable that will allow for the filing of

**Raising the pace.** NIH's Marvin Cassman plans for accelerated data release from U.S. labs.

patent applications.

The plan for immediate data release was drafted at a meeting a year ago in Hinxton, U.K., home of the Wellcome Trust's genome center.\* Many said it reflected the ideals of British scientists, who were among the leaders in pushing for rapid release of genome data. But several members of the Airlie group said the proposed short deadlines wouldn't allow enough time to refine and validate structural information. Others, noting that structural data may be valuable for drug design, argued frankly that too-rapid data release would impede patenting. In the end, the group endorsed the release of "most" protein structures from high-throughput labs "as rapidly as possible," with a maximum delay of 6 months for proteins of "special interest." Today, the rule is that investigators release coordinates when they publish a structure.

The strongest opposition to the Hinxton plan came from Japanese delegates, who said

it can take many months to process proteins and prepare U.S. patent filings. Toichi Sakata, representing the agency that funds Japanese structural biology—the Ministry of Education, Culture, Sports, Science, and Technology—indicated that Japanese taxpayers want a return on investments in protein analysis in the form of intellectual property. The Japanese group proposed the 6-month limit.

Once the Japanese had spoken, senior European and U.S. scientists said they liked the 6-month delay, too. Udo Heinemann of the Max Delbrück Center for Molecular Medicine in Berlin saw a "fundamental difference" in the way structural genomics is carried out in Europe and the United States. He said his funding agency views his work as being closer to drug development than basic biology. Joel Janin of the Laboratory of Structural Enzymology and Biochemistry in Gif-sur-Yvette, France, felt that "the average European group's view is probably closer to the Japanese position" than the Hinxton model. And biophysicist Stephen Burley of the Rockefeller University in New York City said, "I'm not sure that there's agreement within U.S. groups" that protein structure data are commercially "precompetitive."

A minority objected to the 6-month rule but didn't dissent. "This is a complete reversal" of earlier goals, said Cyrus Chothia, a theoretician of structural biology at the Medical Research Council Laboratory of Molecular Biology in Cambridge, U.K. He chided his colleagues for what he saw as a retreat from data sharing. One meeting organizer detected signs of gambler's fever in the patent discussion: "It reminds me of the lottery," he said. "Very few people will win, but everyone dreams they will."

Participants did agree, however, to increase data sharing and avoid duplication by exchanging lists of "target" proteins in advance. And they outlined a new system of fast peer review and electronic publication, bypassing paper journals to get results out quickly. But they declined to adopt a plan advanced by the U.S. National Institute of General Medical Sciences (NIGMS), part of the National Institutes of Health (NIH), to create a central, public Web site at NIH listing targets claimed by each lab. NIH will do this for its own grantees. One group that specifically opposed listing its own targets is a private consortium led by the Wellcome Trust, which is recruiting about 10 company sponsors for a program to solve and publish 200 protein structures per year (*Science*, 30 March, p. 2531). A trust attorney explained that the companies do not want to tip competitors to potential research plans, but are willing to give away structures once they've been completed.

NIGMS director Marvin Cassman ascribes the difference between the Hinxton and Airlie meetings to the fact that "last

year, structural genomics was pie in the sky; this year, the pie is on the plate," and everyone is looking for a slice. NIGMS is leading the effort to speed up protein analysis, having awarded \$150 million in structural genomics grants to seven centers last year (*Science*, 29 September 2000, p. 2254). The centers funded under this program are likely to be held to more rigorous data-release standards than the rules adopted at Airlie, Cassman said. NIGMS official John Norvell explained that relatively few families of proteins are represented in the public databases at present, and NIGMS is pushing its centers to identify new proteins at the rate of about 200 per year by 2006.

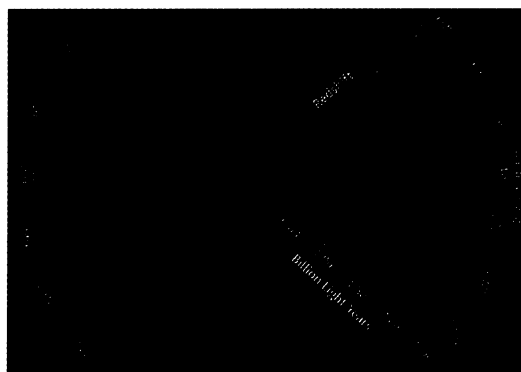
—ELIOT MARSHALL

## ASTROPHYSICS

### Galaxy Mappers Detect Wiggly Cosmic Order

**BALTIMORE, MARYLAND**—A wiggly pattern in the way galaxies are arrayed has yielded a new recipe for the early universe. Last week, at meetings on both sides of the Atlantic Ocean,\* astronomers working on the ambitious Two Degree Field (2dF) galaxy survey announced that they had seen subtle variations in the distribution of matter at different scales. The discovery provides a new method of calculating the amounts of different types of matter in the cosmos shortly after the big bang.

"That would be extremely exciting if they've seen it," says Max Tegmark, a physicist at the University of Pennsylvania in



**Deep space.** Galactic voids and clusters mapped by the Two Degree Field survey trace ripples from the big bang.

Philadelphia. Knowing the ratio of ordinary "baryonic" matter to unseen dark matter in the universe is key to deciding among competing cosmological models, Tegmark says.

The 2dF survey, which uses the 4-meter

\* "The Dark Universe," Baltimore, Maryland, 2–5 April; Royal Astronomical Society National Astronomy Meeting, Cambridge, United Kingdom, 2–6 April.



\* The First International Structural Genomics Meeting took place in Hinxton, U.K., in April 2000; the second, at Airlie House near Warrenton, Virginia, 4 to 6 April, 2001. The third will be in Berlin.