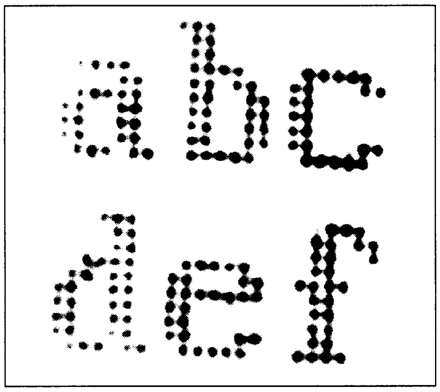
achievement," says Eaton Lattman, an x-ray crystallographer at The Johns Hopkins University in Baltimore. Sayre and his colleagues—Jianwei Miao and Janos Kirz at the State University of New York (SUNY), Stony Brook, and Pambos Charalambous at Kings College in London—used their new technique to produce images of an array of tiny gold dots with a resolution of 75 nanometers. That doesn't match the resolution available from crystalline samples, which can be hundreds of times finer, but it's already better than the best optical microscopes. And Miao told *Science* the team has already improved the resolution to about 65 nanometers and expects to do considerably better.

The technique is an outgrowth of conventional x-ray diffraction, which requires knowing two properties of the diffracted x-rays to make an image. The first is the intensity of the diffraction spots—easily determined with a photon counter. The second property is the relative timing of the waveforms of the x-rays, known as their phase. Figuring out the phase is more troublesome, traditionally requiring researchers to compare the diffraction pattern from a pure crystal with one from a similar crystal in which heavy metal atoms substitute for some components of the crystal. The signals from the metal atoms provide reference points from which the phase of the other x-rays can be worked out.

That's all well and good for working with orderly crystals. But with noncrystalline samples, x-rays don't produce the clear diffraction patterns studded with sharp and isolated spots. Instead, they generate splotchy patterns. The key is that in these splotches, the intensity varies smoothly from one pixel in the diffraction image to the next in a manner related to the phase. In the early 1980s, other researchers suggested that it might be possible to use that information to work out the phase of x-rays diffracted from such samples. So, the SUNY–Kings College team created an algorithm that is designed to extract an image from this fuzzy diffraction data by first making a wild guess, assessing its accuracy, making adjustments, and then repeatedly trying again.

The program starts with the intensity data in the splotchy diffraction pattern and combines this with random phase information generated by the computer to churn out an approximate image of the target responsible for the diffraction. It then adjusts this image by comparing it to a set of known mathematical constraints. Next, it reconverts the revised image back into the corresponding diffraction intensity data and phase information. It combines the new phase information with the original intensity data to generate a new picture. Repeating this cycle about 1000 times, the computer homes in on a final image.

The new algorithm is designed to work with low-energy, "soft" x-rays, which are ideal for imaging biological materials. Such samples vary greatly in the amount of soft x-ray photons they diffract at different wavelengths, says Ian Robinson, a physicist at the University of Illinois, Urbana-Champaign. So, researchers should be able to create high-resolution, high-contrast composite images of cells by combining separate images taken at different soft x-ray wavelengths, he says. Down the road, adds Louise Johnson, a biochemist at Oxford University, the technique could make it possible to image single protein molecules, eliminating the need to crystallize them first, often a major hurdle for protein crystallographers. But generating enough diffraction data from a single molecule will require new x-ray sources billions of times brighter than today's.



Letter perfect. Micrometer-sized letters, formed from gold dots imaged with x-ray diffraction.

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—**ROBERT F. SERVICE**

DATA DISCLOSURE

Congress Votes Down Delay in Access Law

Congress last week rejected a proposal to overturn a controversial new law that would force the release of scientific data from federally funded research. Universities and other scientific groups concerned about the impact of the legislation are now shifting their focus to a statement due out shortly from the White House Office of Management and Budget (OMB) on how it plans to implement the law, which is expected to go into effect this fall.

The law requires "all data" funded by federal grants to be subject to the Freedom of Information Act (FOIA), which gives the public access to government documents. It was tucked into last fall's omnibus appropriations bill by Senator Richard Shelby (R–AL), who argued that the raw data underlying regulations—such as recent new air pollution rules—should be publicly available. Scientific and university organizations have weighed in heavily against it, saying the new law would harass researchers, violate confidentiality agreements, and hinder the conduct of science (*Science*, 12 February, p. 914).

Legislators who had hoped to block the law suffered a major blow on 13 July, when the House Appropriations Committee voted 33 to 25 to reject an amendment to a bill funding OMB that would have delayed implementing the legislation for 1 year pending a study. The amendment was sponsored by James Walsh (R–NY) and David Price (D–NC). Two days later, National Institutes of Health director Harold Varmus and National Academy of Sciences president Bruce Alberts testified before another House panel on another bill to repeal the law. "We should go back to ground zero and ask, 'What is it we're trying to solve?' " Varmus said about the bill, sponsored by Representative George Brown (D–CA), who died last week (see p. 509). But with the defeat of the Walsh-Price amendment, supporters of Brown's bill say its chances of passage appear slim.

The vote shifted attention to OMB, which is expected to issue within a few days a second version of a proposal released in February that drew more than 9000 comments. An unofficial copy circulating in Washington has eased the concerns of some who felt FOIA's exemptions for intellectual property rights and medical privacy weren't sufficient and that experimental results might be released before they had even been published. For example, the draft OMB document defines "data" as "any raw underlying information necessary to validate [research] findings, but not information that would violate the privacy rights of research subjects or the intellectual property rights of researchers." The draft also restricts the law's reach to data "published in a peer-reviewed journal" or when cited "in a proposed rule." Says Nils Hasselmo, president of the Association of American Universities: "It does address some of the critical issues that the scientific community had raised."

It was unclear as *Science* went to press whether OMB will tinker further with this version before publishing it. Shelby's staff declined to comment until it appears in the *Federal Register*. Louis Renjel of the U.S. Chamber of Commerce—a strong supporter of the law—said the chamber believes OMB should apply the law not just to major rules but also to things like risk assessments. Right now, the draft defines "rule" as "an agency statement … intend[ed] to have the force and effect of law … designed to implement, interpret or prescribe law or policy. …"

Whatever it decides, OMB faces a tight schedule. The agency will allow for another 30-day comment period before issuing a final rule by 30 September.

—**JOCELYN KAISER**