Abstractions

LAST AUTHOR

In the quest to understand how the brain processes images, neuroscientists are developing something that sounds like science fiction — a tool for decoding brain activity. Until now, scientists could crudely decode the brain activity that resulted from viewing simple predetermined images, such as faces or places. But on page 352, Jack Gallant, a neuroscientist at the University of California, Berkeley, and his colleagues describe a computational model of the early visual system that can be used to identify natural images being viewed by a person for the first time. Gallant tells *Nature* that it may soon be possible to decode a person's visual experience from brain activity alone.

Is your ultimate goal to build a "brain decoder"?

No, the tool was not the ultimate goal. We want to build a quantitative and predictive model of the brain's visual system, and a brain decoder provides a useful way to test the model.

How were you able to decode novel images?

Our work builds on knowledge gained from more than 50 years of research in many labs. We used a large sample of natural images as stimuli and then constructed a model that links these stimuli to brain responses obtained by functional magnetic resonance imaging — an indicator of brain activity based on blood flow — in the early visual areas of the brain. The model allows us to predict the brain activity in these areas that would be elicited by any arbitrary image. We tested the quality of the model by evaluating the predictions using a separate set of images.

Do you think a model of the entire visual processing circuit will be in place by the time you retire?

I hope so. We know of 30–40 visual areas in the brain, but we currently have good models of how they work for only two of these. It's too early to do meaningful deductive research on visual areas that are essentially unknowns. That's why we use a 'black box' approach — linking random stimuli to brain activity — rather than testing individual hypotheses one at a time.

Do the privacy and ethical issues of 'brain decoding' concern you?

Yes. In science, whenever you learn more about a biological system, you often have to ask if the knowledge gained is worth its potential misuse. A functional model of the brain, our goal, would be a valuable contribution to neuroscience. However, once we have a model, anyone can use it to build a decoder. We're still very far from any potential application, but down the road, ethical and privacy issues must be dealt with. ■

MAKING THE PAPER

Raimund Dutzler

Solving the structure of a ligand-gated ion channel.

The three-dimensional structures of membrane proteins are notoriously difficult to determine. Raimund Dutzler, a biochemist at the University of Zurich, Switzerland, and his graduate student Ricarda Hilf know this only too well: it has taken them two-and-a half years to resolve the structure of a cation-carrying ion channel from the membrane of the bacterium *Erwinia chrysanthemi*. This channel, called ELIC, belongs to a large family of ion channels that also includes neuronal ion channels in animals, and is the first of this type for which such a high-resolution crystal structure has been determined.

The first crystal structure of any ion channel — a potassium ion channel — was produced in 1998 by Roderick MacKinnon, a feat for which he received the 2003 Nobel Prize in Chemistry. Dutzler, who was a postdoc in MacKinnon's lab at the Rockefeller Institute, New York, set his sights on a different type of ion channel that opens only when bound by a particular ligand. These 'ligand-gated ion channels' are made up of five protein subunits and include key players in chemical signalling at neural synapses. The best-known members of the family are the nicotinic acetylcholine receptor, which controls muscle movement, and the γ-aminobutyric acid (GABA) receptor, which is involved in learning and memory.

Dutzler chose the bacterial channel as the simplest and smallest example of this type of channel. It is composed of five identical protein subunits, and a bacterial channel protein should also be easier to produce in large amounts. Even so, the duo encountered many setbacks, but Dutzler credits Hilf with being "incredibly persistent and efficient".

At first they could not produce enough protein to make crystals. "This is usually the end of any crystallography project," says Dutzler. Undaunted, they fused the channel protein to another protein, called maltose-binding protein, to improve production, and obtained crystals. But these first crystals were not of good enough quality to diffract X-rays at the resolution needed. Dutzler and Hilf had to screen many different crystallization conditions before they were able to make crystals that diffracted X-rays at a resolution of 3.3 ångstroms, the resolution required to identify the positions of individual atoms.

And they weren't done yet. To resolve the atomic structure of a protein, one needs several sets of extremely precise X-ray-diffraction measurements in order to construct the electron-density map that is ultimately used to identify atomic positions.

Fortunately, the team had access to a new and highly sensitive X-ray detector called Pilatus at the Swiss Light Source, the synchrotron facility at the Paul Scherrer Institute in Villigen, where the X-ray data were collected. "We had the most optimal infrastructure. Without it, this project could have taken twice as long," says Dutzler.

Dutzler and Hilf believe that the structure that finally emerged (see page 375) is conserved among all pentameric ligand-gated ion channels. "It's the first piece of the puzzle," says Dutzler, adding that they would like to discover what the ligand for this channel is so that they can figure out the mechanics of how it opens to conduct ions. ■

FROM THE BLOGOSPHERE

The recent retraction by Nobel laureate Linda Buck and colleagues of a 2001 *Nature* paper sparked discussions on NPG blogs. On Action Potential, the *Nature Neuroscience* blog (http://tinyurl.com/23bnwg), Debra Speert calls it "the highest profile retraction that I can recall in neuroscience", and on the Nature Network neuroscience forum (http://tinyurl.com/34gxn9) readers are asked for their views on the role of journals and scientists in retracting published work.

The Nature journals correction policy is at http://tinyurl.com/3cluba. For a retraction or other type of correction to be published, all authors typically need to sign it. If some of the authors do not agree, the editors seek advice from peer reviewers and, if necessary, the institution and/or funder. In the event that the retraction or correction is published, the name(s) of the dissenting author(s) are noted in the text of the correction. More information about Buck's retraction is in a News story (*Nature* **452,** 13; 2008), and includes a clarification from one of the paper's authors in the online comment thread. ■

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