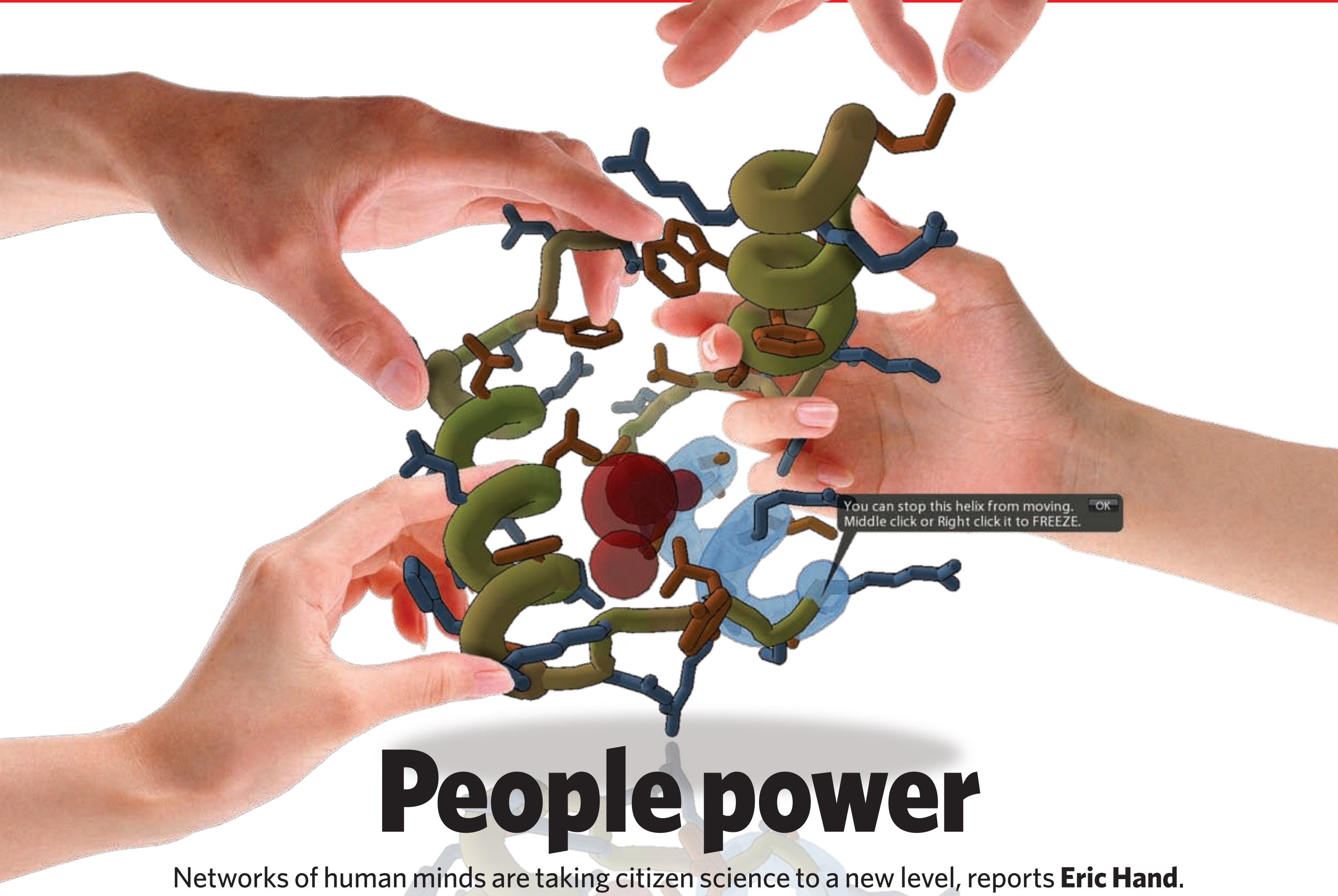


# People power

Networks of human minds are taking citizen science to a new level, reports **Eric Hand**.

The whole thing began by accident, says David Baker, a biochemist at the University of Washington in Seattle. It was 2005, and he and his colleagues had just unveiled Rosetta@home — one of those distributed-computing projects in which volunteers download a small piece of software and let their home computers do some extracurricular work when the machines would otherwise be idle. The downloaded program was devoted to the notoriously difficult problem of protein folding: determining how a linear chain of amino acids curls up into a three-dimensional shape that minimizes the internal stresses and strains — presumably the protein's natural shape. If the users wanted, they could watch on a screen saver as their computer methodically tugged and twisted the protein in search of a more favourable configuration.

Thousands of people were signing up for Rosetta@home, says Baker, which was gratifying, but not entirely surprising; this kind of digital citizen science had become almost routine by then. It was first popularized in 1999 by the SETI@home project at the University of California, Berkeley (UCB), which harnessed volunteers' computers to sift through radio telescope data in search of alien signals. And in 2002, UCB engineers had released a generalized version of the software known as the Berkeley Open Infrastructure for Network Computing (BOINC). By 2005, there were dozens of active BOINC projects — Rosetta@home among them — and hundreds of thousands of users worldwide.

But what was surprising, says Baker, was that the Rosetta@home volunteers quickly began to chafe at the painfully slow progress of their screen saver. "People started writing in saying, 'I can see where it would fit better this way'," he says.

In retrospect, this should have been obvious: even a small protein can have several hundred amino acids, so computers have to plod through thousands of degrees of freedom to arrive at an optimum energy state. But humans, blessed with a highly evolved talent for spatial manipulation, can often see the solution intuitively.

Recognizing an unexpected opportunity, Baker enlisted the help of computer-scientist colleagues. By mid-2008, they had created an interface for Rosetta@home that not only allows users to assist in the computation, but gives them an incentive to do so by turning it into an online game. In the game Foldit, players compete, collaborate, develop strategies, accumulate game points and move to different playing levels — all while folding proteins.

And it works. This week, Baker and his colleagues publish evidence that top-ranked Foldit players can fold proteins better than a computer (see page 756). By collaborating, these top players often come up with entirely new folding strategies. "There's this incredible amount of human computing power out there that we're starting to capitalize on," says Baker, who is feeding some of the best human tactics back into his Rosetta algorithms.

By harnessing human brains for problem solving, Foldit takes BOINC's distributed-computing concept to a whole new level. And it is not alone: several projects are emerging in this field, sometimes called distributed thinking, and the number of publications based on the approach is increasing.

"We're at the dawn of a new era, in which computation between humans and machines is being mixed," says Michael Kearns, a computer scientist at the University of Pennsylvania in Philadelphia, who evaluated the concept of distributed thinking as part of an unpublished 2008 study funded by the US Defense Advanced Research Projects Agency. Kearns says that the approach has the most promise

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FOLDIT IMAGE: UNIV. WASHINGTON CENTER FOR GAME SCIENCE; ARTWORK BY W. FERNANDES

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in areas such as vision, language and complex logic puzzles — territories in which humans are expected to retain an edge on computers for some time to come.

David Anderson, a UCB computer scientist and the founder of BOINC, admits that the approach is still a long way from becoming mainstream. For many sceptical scientists, he says, "there's this idea that they're giving up control somehow, and that their importance would be diminished".

But advocates of distributed thinking, such as François Grey, a physicist at CERN, Europe's particle-physics centre near Geneva, have few doubts. Last July, Grey helped to establish the Citizen Cyberscience Centre in Geneva, which aims to promote distributed-thinking projects, especially in the developing world. Grey is currently setting up distributed-computing projects in China. And he has helped to organize a workshop to be held in London this September to encourage scientists to adopt the new approaches.

"The whole field has a funny image, that it is just for fun or for PR," says Grey. "That's what we have to break through."

## The eye of the beholder

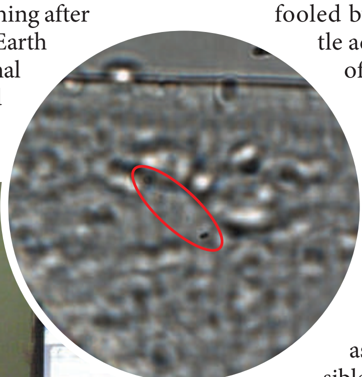
Andrew Westphal, a UCB physicist, started on the road to distributed thinking almost two decades ago, when he was a lead investigator on a cosmic-ray experiment called TREK.

TREK consisted of specially designed glass plates mounted on the outside of the Russian space station Mir in 1991. Cosmic-ray particles pelting the glass left microscopic traces that were revealed by chemical etching after the TREK detector had returned to Earth in 1995. To find those traces, Westphal automatically scanned and recorded images of the plates using a microscope. But image-recognition software wasn't good enough to identify the tracks, so Westphal found himself staring at image after image, counting the tracks by eye. It was excruciating, he recalls. "Despite your best efforts, your mind wanders. You start to think about lunch or whatever."

That reality was on Westphal's mind when he joined NASA's Stardust mission, which was launched in 1999 to collect samples of a comet and return them to Earth. Westphal's focus was not on the comet itself, but on a collecting tray that was exposed to space during the years of cruising required to get there. He and his team were confident that 100 or so microscopic pieces of interstellar dust would burrow into the tray's aerogel, a wispy material designed to decelerate and capture the dust without damaging it. But again, the challenge was to find those particles.

Unfortunately, that task made TREK look easy. After the spacecraft's sample-return capsule fell to Earth in January 2006, Westphal reused the automatic imaging microscope from TREK to create 1.6 million images of the aerogel. He estimated that it would take a century for one person to peruse them all. So the following August, Westphal and his team launched Stardust@home, a continuing project that enlists the pattern-recognition abilities of thousands of volunteer 'dusters'.

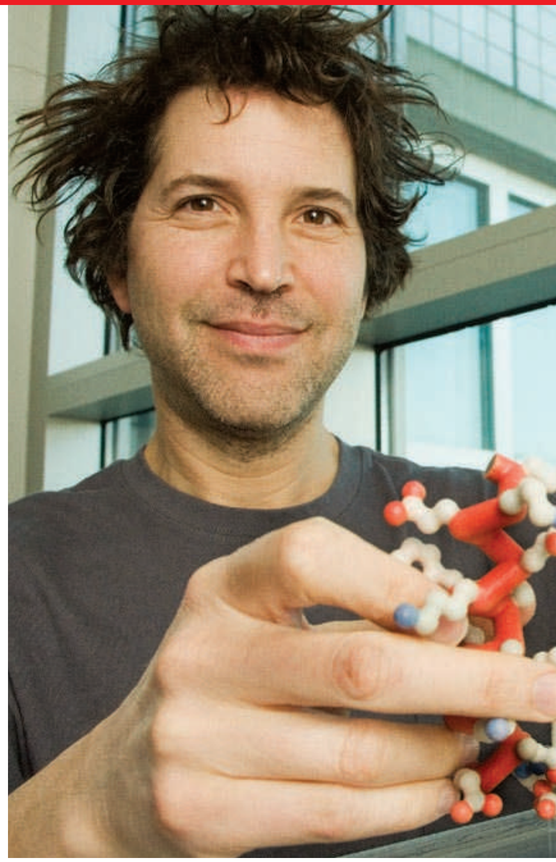
Although the '@home' name pays homage to BOINC volunteer computing programs, Stardust@home is one of the pioneering distributed-thinking projects. As such, it faced plenty of early hurdles. For example, the dusters had to be given lessons on how to avoid being fooled by cracks in the brittle aerogel or by particles of Earth dust that had embedded in the aerogel from the start. Only some of the volunteers worked diligently. Others quickly slacked off. And still others tried to cheat, just flipping through as many images as possible to rise to the top of a scorecard put in place as an incentive.



B. HUDSON; INSET: D. FRANK

Non-scientist Bruce Hudson found the first dust particles from NASA's Stardust mission, naming them Orion (inset) and Sirius.

Westphal, working together with Anderson, realized that they would have to calibrate their volunteers just as they would any instrument. They had to find ways to assign a skill level to each volunteer; to assess how that skill level changes with time; and to determine how many volunteers had to reach the same conclusions about an image before a result could be believed.



C. MCLEAN/UW MEDICINE

David Baker's online game Foldit uses the basic problem-solving skills of volunteers to help solve three-dimensional protein structures.

## Cosmic stardust agents

For Bruce Hudson, a resident of Midland, Ontario, Stardust@home was a perfect way to fill the long days. In 2003, he had a stroke that rendered the right side of his body mostly useless. Even computer games weren't much fun. But somehow, the endless microscope photos of aerogel were enthralling. "I've always liked the stars and the planets and all that kind of stuff," says Hudson, who previously worked as a groundskeeper for a Catholic shrine. He estimates that he spent as much as 15 hours a day on the project.

His hard work paid off. In March 2010, at the Lunar and Planetary Science Conference in Houston, Texas, Westphal announced that Hudson had found the first probable piece of stardust — actually a pair of particles in the same track (see *Nature* doi:10.1038/news.2010.106; 2010). "I still can't believe it," says Hudson, who named the particles Orion and Sirius. Westphal is already using the unique characteristics of Orion and Sirius to calibrate the expectations of a new generation of Stardust volunteers.

Meanwhile, Anderson is reprising what he did with BOINC by generalizing the Stardust@home software, so that it can be used by scientists for other distributed-thinking projects. He calls the result Bossa, which doesn't stand for anything. "At some point, I

got tired of the idea that everything has to have an acronym," he says laconically.

Anderson's intention is that Bossa will always be open source and free, so that any scientist can use the software and adapt it to the task at hand. He foresees applications as diverse as in the BOINC ecosystem, where 68 active projects are engaging nearly two million users worldwide.

An early recruit is Tim White, a UCB palaeontologist, whose research involves searching for early hominid fossils in the Great Rift Valley of east Africa. For decades, his teams have searched in the same way: slowly. Bent over. Crawling across the dry desert soil in temperatures of up to 50 °C. But with their planned Bossa-based project, which they intend to call Hominids@home, much of that work could be taken over by volunteers who would look for the white gleam of bone in pictures. "A kid in front of a monitor isn't going to know the difference between the tooth of a colobus monkey and a baboon," says White, "but they're going to know it's a tooth."

> "It needs to be an exciting, compelling experience that's not always the same."

## Galaxy Zoo

The online astronomy project Galaxy Zoo, which launched in 2007 at the University of Oxford, UK, is taking a rather different tack. Co-founder Chris Lintott says that the project was directly inspired by Stardust@home. "If people would look at dust grains," he says, "then surely they'd look at our beautiful images of galaxies" — images that have been collected in the millions by the international Sloan Digital Sky Survey consortium.

The idea is for volunteers to determine by eye whether the galaxies are spiral or elliptical — a task for which computers are almost worthless. Galaxy Zoo has already published 17 papers after classifying 1.25 million different galaxies, and has just begun another stage of galaxy classification with data from the Hubble Space Telescope.

But as Lintott expands his domain to a 'Zooniverse' of projects — not just for galaxy classification, but for galactic mergers, supernovae, solar storms and lunar craters — he has been much pickier than Anderson is being with Bossa, where anyone can try anything. Lintott worries that Bossa projects might be hasty affairs that end up wasting the goodwill of citizen scientists. "Rather than letting anyone pitch for volunteers, we'd like to be a place where people can come and expect a certain level of commitment," he says.

Anderson, not surprisingly, disagrees. He says he likes the commitment of Galaxy Zoo to distributed thinking, but not its 'walled garden' approach. Galaxy Zoo "doesn't provide flexibility to the individual scientist", he says.

Baker says that he also drew his inspiration for Foldit from Stardust@home. But any similarities to that program or to Galaxy Zoo end there. For one thing, Foldit players aren't just engaged in basic image recognition and classification tasks — they are intuitively solving much harder optimization problems. Baker argues that the program is exploiting three uniquely human talents: a superior spatial awareness; an ability to take short-term risks for long-term gain; and the converse, recognizing a dead-end early and knowing when to quit.

The other important difference is that the Foldit designers take the gaming element more seriously. Neither Galaxy Zoo nor Stardust has the immersive qualities of Foldit, with its chat rooms, wikis and increasingly difficult levels of play. Zoran Popović, Baker's computer-science collaborator at the University of Washington, points out that holding the volunteers' interest is necessary if they are to learn quickly the skills required to make a real contribution. "It needs to be an exciting, compelling experience that's not always the same," says Popović.

There are also limits to games. If nothing else, says Kearns, as human computing becomes ubiquitous, "people will no longer marvel at being a part of these networks and may start to feel exploited by them". The day may come when scientists have to seduce volunteers by doing what many consider anathema at present: paying them. "There will be a whole economics of this field," says Kearns.

S. ZACCANELLI


Scott Zaccanelli designed a fibronectin variant that was synthesized in the lab.

For now, there are still plenty of volunteers who are not jaded. Scott 'Boots' Zaccanelli is one of them. A resident of McKinney, Texas, he splits his time between a day job as a buyer for a valve factory and a personal business — Good For You Massage Therapy — that takes him and his massage chair to rodeos, county fairs and flea markets. But he has also been hooked on Foldit since 2008. "I'm pretty much there every night," says Zaccanelli, who has used his undergraduate biology degree to help him rise to a number-6 global Foldit ranking. "I can look at something and see that it's not right."

The skills of players such as Zaccanelli are so impressive that Baker has moved past protein folding and is now offering them chances to design completely new proteins. Tasks include searches for new catalysts for photosynthesis, and for proteins that can bind to pathogens such as HIV or the H1N1 influenza virus.

One puzzle asked players to create a more stable variant of fibronectin, a protein scaffold that is useful for creating antibody-like compounds. Last October, Baker thought Zaccanelli's design was promising enough to be synthesized in the lab — the first time a player's recipe had been tested. It turned out that Zaccanelli's fibronectin wasn't any more stable, but Baker says it is just a matter of time before a player designs something that is.

And that is a good enough motivation for Zaccanelli. "Maybe something I do will help contribute an answer to curing cancer or AIDS or the common cold," he says. ■

**Eric Hand is a reporter for *Nature* in Washington DC.**