

The situation at ICLR 2026 highlights the mounting pressure on peer reviewers to keep pace with a fast-growing field. “In AI and machine learning right now, we have a crisis in terms of reviewing, because the field has expanded exponentially for the past five years,” says Neubig.

Hariharan says each ICLR reviewer was

assigned five papers that they had to review in two weeks, on average. “That is a very significant load. It is much higher than what has been done in the past.” He says discussions are taking place on how to manage this. “Everyone in the community is aware that we are in a regime where all of us are doing significantly more volunteer work than we used to.”

magnetic information is sensed in animals’ brains and how sensory neurons confer sensitivity to electromagnetic changes.

In 2011, researchers found hints that magnetic fields triggered pigeons’ vestibular system, which enables vertebrates to sense accelerations (including gravity) and helps them to stay balanced². The structure is made of three fluid-filled loops which are mutually perpendicular, so they can communicate the direction of an acceleration to the brain by breaking it down into three *x*, *y* and *z* components.

In the present study, David Keays, a neuroscientist at Ludwig Maximilian University of Munich in Germany, and his colleagues designed an experiment that could reveal how pigeons’ brains respond to magnetic fields.

Keays’ team exposed pigeons to a magnetic field slightly stronger than Earth’s for more than an hour. The birds’ heads were immobilized and the magnetic field was continually rotated to simulate the heads’ motions with respect to Earth’s geomagnetic field.

Next, the team used a method for measuring activation patterns of neurons across the brain – by using a genetic marker of cell activity in pigeon brains, which were made transparent by a technique called clearing. Maps of brain activity in birds that had been exposed to magnetic fields were compared with a control group that had not been exposed to magnetic fields.

The results showed neuronal activity related to magnetic fields in the brain region that receives input from the vestibular system, as well as in regions that help to integrate various sensory stimuli. This result narrowed down the list of potential compasses to one – the vestibular system – although it did not explain how pigeon neurons can physically sense magnetic fields.

A magnetic sense organ

In principle, a conducting material in an organism could produce electric currents in response to magnetic fields, giving an animal a ‘magnetic sense’ – a mechanism that was proposed as early as 1882 by French zoologist Camille Viguier³.

In previous research, Keays had looked for a molecular mechanism of this magnetoreception by following inspiration from the biophysics of sharks and skates, which have organs that sense minute electric fields to help them find prey⁴. These animals express a protein that is sensitive to changes in neurons’ electrical activity. They have a ten-amino-acid-long insertion that allows them to sense electric currents that are generated from magnetic fields.

“We asked, does it exist in pigeons? And it does,” Keays says. In 2019, he and his collaborators found that a similar modification exists in the pigeon genome⁵.



Studies show that several animals can sense the direction and strength of magnetic fields.

HAS THE ‘COMPASS’ ORGAN OF BIRDS BEEN FOUND AT LAST?

Evidence suggests that pigeons sense magnetic fields by detecting electric currents in their inner ears.

By Davide Castelvecchi

Pigeons can sense Earth’s magnetic field by detecting tiny electric currents in their inner ears, a team of researchers suggest. Such an inner compass could help to explain how certain animals can achieve astonishing feats of long-distance navigation.

The team performed advanced brain mapping as well single-cell RNA sequencing of pigeon inner-ear cells. Both lines of evidence point to the inner ear as the birds’ ‘magnetoreception’ organ. The results were published in *Science* on 20 November¹.

“This is probably the clearest demonstration of the neural pathways responsible for

magnetic processing in any animal,” says Eric Warrant, a sensory biologist at Lund University in Sweden. Studies have suggested that various animals, including turtles, trout and robins, can sense the direction and strength of magnetic fields, although the evidence has sometimes been contested – and the mechanisms have remained controversial.

Bird-brained navigation

Two leading hypotheses have guided research into how birds sense magnetic fields. One is based on a quantum-physics effect in retinal cells in which birds ‘see’ magnetic fields. The other hypothesis is that microscopic iron oxide particles in the beak could act as tiny compass needles. However, it’s largely unknown where

News in focus

In the latest study, the team performed single-cell RNA sequencing in vestibular-system cells to search for molecules that are involved in detecting electric currents. They found a high prevalence of proteins that are sensitive to electromagnetic changes.

Hence, as a pigeon bobs its head, its inner-ear loops could provide its brain with information about the three *x*, *y* and *z* components of the magnetic field.

Finally, the team repeated the experiment by exposing pigeons to magnetic fields in the dark, and showed that light is not necessary for their brains to receive magnetic stimuli. This seems to contradict the retina-based model of magnetoreception, says Keays, although in principle, some animals could have more than one magnetoreception organ.

Ulrich Müller, a neuroscientist at Johns Hopkins University School of Medicine in Baltimore, Maryland, says that the study is “compelling”, but that it will be important to conduct genetic studies to validate it – such as using CRISPR technology to knock out the gene sequence that is central to Keays’ model to see if the effect disappears.

Warrant calls the paper “a spectacular contribution to our understanding of the mysterious magnetic sense”. “It took ten years to put this together,” Keays says.

1. Nordmann, G. C. *et al.* *Science* <https://doi.org/10.1126/science.aea6425> (2025).
2. Wu, L.-Q. & Dickman, J. D. *Curr. Biol.* **21**, 418–423 (2011).
3. Viguier, C. *Rev. Phil. France Etranger* **14**, 1–36 (1882).
4. Bellono, N. W., Leitch, D. B. & Julius, D. *Nature* **558**, 122–126 (2018).
5. Nimpf, S. *et al.* *Curr. Biol.* **29**, 4052–4059 (2019).

called Tmem81, stabilizes a complex of two other sperm proteins, creating a pocket for Bouncer to bind to (V. E. Deneke *et al.* *Cell* **187**, 7066–7078; 2024). Experiments backed up the tool’s predictions. AlphaFold “speeds up discovery”, says Pauli. “We use it for every project.”

Her team’s paper about this, published in 2024, is one of nearly 40,000 journal articles to cite the 2021 *Nature* paper describing AlphaFold2 (J. Jumper *et al.* *Nature* **596**, 583–589; 2021). Unlike many other highly cited life-sciences and biomedical papers from the same period, including seminal reports about the COVID-19 pandemic, interest in AlphaFold doesn’t seem to be slowing down (see ‘Peak citations’).

DeepMind’s John Jumper – who shared half of the 2024 Nobel Prize in Chemistry with chief executive Demis Hassabis for developing AlphaFold – says he is “deeply proud” of how useful the tool has been for scientists such as Pauli. “When will someone win one of these major awards because they used AlphaFold?” he wonders.

Part of AlphaFold2’s rapid impact is down to its accessibility, say researchers. Google DeepMind made the underlying code and other parameters freely available to scientists, and it quickly became possible for them to run the software themselves at scale: this is what Pauli’s team did.

Some 3.3 million users in more than 190 countries have accessed the AlphaFold database (AFDB), which is hosted by EMBL–EBI and contains more than 240 million structural predictions, encompassing most known proteins. More than one million AFDB users come from low- and middle-income countries, including China and India (see ‘Global appeal’).

Protein-structure revolution

The field in which AlphaFold seems to have made its biggest impact is structural biology. Researchers who used AlphaFold submitted around 50% more protein structures to a repository of experimental models, called the Protein Data Bank (PDB), than did a non-AlphaFold-using ‘baseline’ of structural-biology researchers, finds a Google-DeepMind-funded study of AlphaFold’s impacts released last month (see go.nature.com/3xgs92s). AlphaFold2 use was also associated with higher rates of PDB submissions than those of researchers using other ‘frontier’ methods in AI, structural biology and protein-structure prediction.

Jumper says he is especially gratified that AlphaFold2 – which was trained using PDB data – has proved so useful for deducing protein structures. The predicted structures can help researchers to make sense of raw data generated by X-ray crystallography and cryo-electron microscopy. “I love that it helps the people that gave us the data,” Jumper adds.

ALPHAFOLD IS FIVE — HERE’S HOW IT REVOLUTIONIZED SCIENCE

Since 2020, Google DeepMind’s AI tool has helped researchers to predict the 3D structures of proteins.

By Ewen Callaway

For nearly a decade, Andrea Pauli, a biochemist at the Research Institute of Molecular Pathology in Vienna, has been trying to work out how sperm and egg get together.

In 2018, her laboratory found a protein on the surface of zebrafish (*Danio rerio*) eggs, called Bouncer, that was essential for fertilization. But Pauli’s team and others struggled to show how Bouncer recognized sperm cells. Then a revolution happened.

Five years ago, in late November 2020, researchers at London-based Google DeepMind unveiled AlphaFold2. The artificial intelligence (AI) tool for predicting protein structures generated stunningly accurate 3D models that, in some cases, were indistinguishable from experimental maps, dominating a long-running structure-prediction challenge. The first version of AlphaFold was announced in 2018, but its predictions weren’t nearly as good as its successor, which limited its impact.

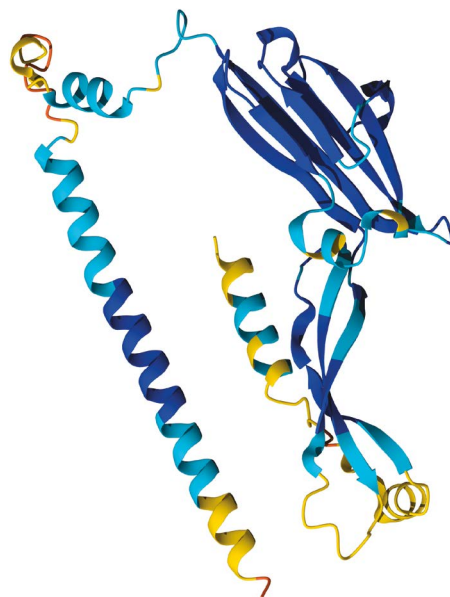
The 2021 release of AlphaFold2’s code and a database that has swelled to hundreds of millions of predicted structures mean that scientists can now get a reliable prediction for almost any protein.

“Having models for anything has had a huge impact,” says Janet Thornton, a bioinformatician at the European Bioinformatics Institute

in Hinxton, UK, part of the European Molecular Biology Laboratory (EMBL–EBI). “It’s like the second coming of structural biology.”

Rapid discovery

For Pauli’s team, the software shone a light on a path they might otherwise never have found. The model predicted that a protein,



An AlphaFold model of a Tmem81 protein.