on generic, self-organized physical processes before intrinsic developmental programs evolved[15]. Assessing the relative importance of programmed and self-organized processes in *C. perkinsii* development will be an exciting avenue for future research.

Could *C. perkinsii* be Haeckel's *Magosphaera*, finally rediscovered? Not quite: unlike *Magosphaera*, *C. perkinsii* does not perform ciliary swimming as a colony and lacks collective behaviour. The latter is observed instead in other relatives of animals such as choanoflagellates, the colonies of which can feed, move and undergo multicellular deformations evoking a developmental process called gastrulation[16]. This mosaic distribution of metazoan features across distinct unicellular cousins illustrates a general principle: many hallmarks of animal complexity are present in their holozoan relatives, but scattered across distinct lineages; only in animals are they all found together. To adapt a phrase from Leo Tolstoy's 1878 novel *Anna Karenina*, all animals are alike, but each non-animal fails to be an animal in its own way. Thus, integrating information from many lineages is necessary to understand animal origins. This work positions *C. perkinsii* as a powerful new model to investigate something that was hard to address until now: the origin of early embryogenesis.

An intriguing feature of animals is that they evolved only once: no other lineage across the whole diversity of organisms with a nucleus (eukaryotes) quite resembles them. This has been explained either by animals filling all ecological niches possible for potential competitors[17], or by the origin of animals having been an event contingent on exceptional circumstances or highly rare genetic innovations[18]. Although both explanations are possible (and the full explanation might include aspects of each of these two ideas), this study and others suggest that the genetic and cellular potential for animal complexity might be widespread across holozoans.

If all animals disappeared from Earth overnight, perhaps ichthyosporeans, choanoflagellates and filastereans would seize the chance to become larger and more complex, unburdened from competition with their overachieving relatives. Because such an experiment is unlikely to pass ethical review boards (never mind its feasibility), we shall for now content ourselves with beautiful studies such as this one.

Thibaut Brunet is in the Evolutionary Cell Biology and Evolution of Morphogenesis Unit, Pasteur Institute, Paris Cité University, CNRS UMR3691, 75015 Paris, France.
e-mail: thibaut.brunet@pasteur.fr

1. Olivetta, M., Bhickta, C., Chiaruttini, N., Burns, J. & Dudin, O. *Nature* **635**, 382–389 (2024).
2. Haeckel, E. *Biologische Studien. Erstes Heft: Studien über Moneren und andere Protisten* (Engelmann, 1870).
3. Brunet, T. & King, N. in *The Evolution of Multicellularity* (eds Herron, M. D., Conlin, P. L. & Ratcliff, W. C.) Ch. 13 (CRC Press, 2022).
4. Grau-Bové, X. *et al. eLife* **6**, e26036 (2017).
5. Sebé-Pedrós, A. *et al. eLife* **2**, e01287 (2013).
6. Ros-Rocher, N. *et al.* Preprint at bioRxiv https://doi.org/10.1101/2024.03.25.586565 (2024).
7. Fairclough, S. R., Dayel, M. J. & King, N. *Curr. Biol.* **20**, R875–R876 (2010).
8. Dudin, O. *et al. eLife* **8**, e49801 (2019).
9. Brunet, T. & King, N. *Dev. Cell* **43**, 124–140 (2017).
10. Shah, H. *et al. Nature* **630**, 116–122 (2024).
11. Laundon, D., Larson, B. T., McDonald, K., King, N. & Burkhardt, P. *PLoS Biol.* **17**, e3000226 (2019).
12. Tikhonenkov, D. V. *et al. BMC Biol.* **18**, 39 (2020).
13. Huldtgren, T. *et al. Science* **334**, 1696–1699 (2011).
14. Collinet, C. & Lecuit, T. *Nature Rev. Mol. Cell Biol.* **22**, 245–265 (2021).
15. Newman, S. A. & Müller, G. B. *J. Exp. Zool.* **288**, 304–317 (2000).
16. Brunet, T. *et al. Science* **366**, 326–334 (2019).
17. Stoy, K. S. *et al. Evol. J. Linn. Soc.* **3**, kzae008 (2024).
18. Ruiz-Trillo, I., Kin, K. & Casacuberta, E. *Annu. Rev. Microbiol.* **77**, 499–516 (2023).

The author declares no competing interests.
This article was published online on 6 November 2024.

Space physics

Space weather mapped by millions of smartphones

Juha Vierinen

Phone users around the world are enabling the creation of a space-weather monitor that will deepen our understanding of the physics governing Earth's ionized upper atmosphere and improve the accuracy of satellite positioning. **See p.365**

In February 2022, a solar storm caused the loss of 38 Starlink satellites when electrical currents in space increased the density of Earth's upper atmosphere, slowing the satellites down and ultimately causing them to come out of orbit[1]. This event highlights how crucial it is to monitor and predict the state of Earth's ionosphere — the region of the upper atmosphere in which some atoms and molecules are ionized by solar radiation and by energetic particles. Space weather can also obstruct telecommunications, disrupt the precise positioning services needed for navigation and induce harmful currents in power lines[2]. On page 365, Smith *et al.*[3] report a global sensor network that could help to solve these problems. If you have a smartphone, you might already be part of their solution.

Navigation satellites transmit signals that are picked up by receivers on Earth. By measuring the difference between the time a signal is received and the time it was broadcast, the distance from the receiver to the satellite can be estimated. Combining data from several satellites enables the location of the receiver to be determined (Fig. 1). However, the electromagnetic waves that encode the signals are affected by ionospheric electrons, which can slow down radio pulses. During the daytime, this disruption typically delays transmission by up to 150 nanoseconds (ref. 4) — a duration that is directly proportional to the total number of electrons between the receiver and the satellite. Transmitting signals at two or more frequencies allows the ionospheric electron content to be estimated. This can be used to improve the accuracy of position measurements — but it also contains valuable scientific information.

Earth's ionosphere is currently monitored using maps of electron density that are generated with data from a global network of navigation satellites and receivers[5,6]. However, there are considerable gaps in these data, particularly over the polar regions, the oceans, Africa, Russia, India and large parts of South America. Smith and colleagues' study is an attempt to fill these observational gaps using crowdsourcing and the multi-frequency satellite-navigation capabilities of modern smartphones. Each phone essentially acts as a receiver, increasing the coverage of the network.

Using millions of phones to map the ionosphere poses two key challenges: first, the data need to be retrieved from the phones; and second, the measurements are of low quality, with unknown observational biases. Smith *et al.* had a ready-made fix for the first problem: the authors are based at Google Research, so they had access to data collected by Android smartphones around the world. But the second issue was harder to address.

The standard deviation associated with phone-based measurements of electron density is more than 100 times that of science-grade satellite receivers. Phones move around with their users, and they save battery power by receiving signals only intermittently — so they don't track satellites

From the archive

A plea for researchers to get involved in shaping government science policy, and a book explores early studies of growth.

50 years ago

For years the last thing that most practising scientists wanted to know about was the machinery by which policy for science was evolved. After all the money generally could be relied on to roll in provided the proposal sounded plausible enough and dreary matters of policy could be left to those amiable and harmless civil servants in London, reinforced with sensible and central professors prepared to commute to endless committee meetings. We neither knew nor cared who they were, what they did in our name or how we were represented in international organisations because the funding was sufficiently pluralistic that if A regretfully couldn't provide, B probably would. And we were mercifully spared from Five Year Plans and the like ... [R]eal blows have come within the past two years when the budgets for science has been unable to keep up either with rising costs or with the ever increasing demands that scientists make on it ... To what extent are those who make and implement policy responsible to the scientist whose livelihood may be threatened? The short answer is not at all ... [O]ne would have greater confidence ... if there were more frequent occasions on which rank-and-file scientists could listen to their representatives explaining decisions and listening to opinions.

From *Nature* 15 November 1974

100 years ago

Growth. By G. R. de Beer — The experimental study of tissue growth is a comparatively recent branch of biological research ... It is always a matter for regret that science should guard her treasures from the general public by a bristling array of formidable technicalities, and Mr. de Beer is therefore to be congratulated on reducing our knowledge of one of the most important, and at the same time one of the most difficult subjects in biology, to a form in which it can be appreciated by the man in the street.

From *Nature* 15 November 1924

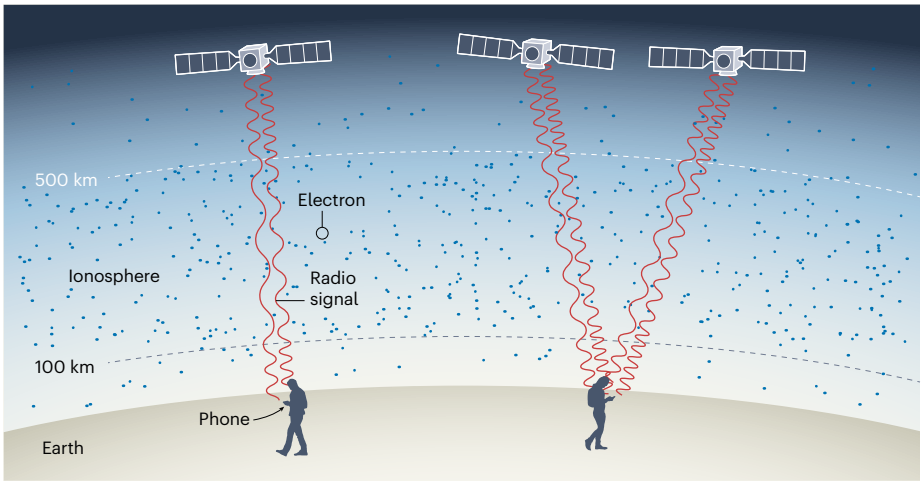


Figure 1 | Crowdsourcing a space-weather monitor. Satellite signals can be used to map the electron content of the ionosphere, the part of Earth's upper atmosphere in which some atoms and molecules become ionized. This is possible because radio waves are slowed by these electrons, and the duration of the delay is directly proportional to the total number of electrons between the receiver and the satellite. By transmitting signals at two or more frequencies, the total number of ionospheric electrons along a signal's path can be calculated. Smith *et al.*[3] used millions of smartphones as receivers for satellite signals to map the ionosphere in this way. In doing so, they filled observational gaps created by the sparse placement of stationary receivers.

continuously. And because users are often in built-up environments, the signals can bounce off objects (such as buildings) and reach the phone receiver along multiple paths. This can cause the frequency-dependent delay to change relatively quickly over time, which means that phones need to be calibrated regularly to obtain an unbiased estimate of the delay caused by ionospheric electrons.

It is therefore remarkable that Smith *et al.* succeeded in producing ionospheric electron-density maps using phone-based receivers. To do so, they used averages of the phone measurements, to reduce uncertainty and bias to a level at which they could obtain high-quality observations of ionospheric structure.

The study's statistical data processing relies on the assumption that the ionosphere is the same along paths between satellites and different phones, as long as these paths are sufficiently close together. When many receivers detect signals along a similar path, averaging over their independent measurements reduces the error considerably, making it possible to determine the electron density along that path. The authors' approach to the problem is similar to that used to determine receiver biases for stationary satellite receivers[7], but this method has never before been scaled up from thousands to millions of receivers.

Although a comprehensive characterization of the data produced by the phone-based network is yet to be completed, the results presented in the study are extremely encouraging. One of the ionospheric maps reveals low-density bubbles of plasma (ionized gas) near the equator over Africa and India, imaged with unprecedented clarity. These structures have not previously been observed with high fidelity, owing to insufficient receiver coverage in these regions. However, monitoring such bubbles is crucial, because they are linked with disruptions in satellite communications and positioning systems[8].

The one challenge that remains unsolved for crowdsourced, phone-based measurements relates to the phase of the satellite signal, which is the fraction of the waveform that has elapsed at any given time. To make accurate measurements of ionospheric perturbations, this phase needs to be tracked continuously over long periods of time, which is difficult to achieve with many receivers that are constantly coming on- and offline. Satellite receivers that are always switched on and are mounted on fixed pedestals with a clear view of the sky will probably still be needed in the future to obtain the best possible accuracy for such measurements.

Although the study was conducted on a huge scale, there is scope to scale it up further. Smith *et al.* used only a small fraction of all the phones in the world that are equipped with multi-frequency satellite receivers, and only two of the six types of navigation satellite. The authors also collected data exclusively during the daytime. Future results that encompass other types of phone and satellite, and that use night-time data, could be even more impressive than those reported here.

It should be noted that, although the data were crowdsourced, Smith *et al.* took care to ensure that no phone users could be identified or tracked. There could well be further discussion about the most ethically sound

way of collecting such data, but the hope is that the authors' approach offers sufficient anonymity, and that ionospheric maps similar to those reported can be generated routinely and published for scientific use. Smith and colleagues' study was conducted with the goal of improving location-service accuracy, but the data will also be invaluable to space physicists studying Earth's ionosphere.

Juha Vierinen is in the Department of Physics and Technology, UiT The Arctic University of Norway, N-9037 Tromsø, Norway.
e-mail: juha-pekka.vierinen@uit.no

1. Fang, T.-W. *et al. Space Weather* **20**, e2022SW003193 (2022).
2. Buonsanto, M. J. & Fuller-Rowell, T. J. *Eos Trans. Am. Geophys. Union* **78**, 1–4 (1997).
3. Smith, J. *et al. Nature* **635**, 365–369 (2024).
4. Klobuchar, J. A. *IEEE Trans. Aerosp. Electron. Syst.* **3**, 325–331 (1987).
5. Wilson, B. D., Mannucci, A. J. & Edwards, C. D. *Radio Sci.* **30**, 639–648 (1995).
6. Rideout, W. & Coster, A. *GPS Sol.* **10**, 219–228 (2006).
7. Vierinen, J., Coster, A. J., Rideout, W. C., Erickson, P. J. & Norberg, J. *Atmos. Meas. Tech.* **9**, 1303–1312 (2016).
8. Aarons, J. *Space Sci. Rev.* **63**, 209–243 (1993).

The author declares no competing interests.

Structural biology

Mechanisms of odour discrimination revealed

Rafaella G. Naressi & Bettina Malnic

How do odorant receptors in the human nose recognize a wide variety of scent molecules? The structures of engineered versions of these receptors finally provide much-needed answers to this fundamental question. **See p.499**

Humans can distinguish a multitude of odorant molecules that have a wide variety of chemical structures. To understand how distinct smells are discriminated between, we need to understand how odorant receptors (ORs) in the olfactory neurons of the nose[1] interact with the various odorants. However, efforts to determine 3D structures of these receptors using cryogenic electron microscopy (cryo-EM) have been hampered by the fact that these receptors are poorly expressed in model cell lines. On page 499, de March *et al.*[2] report a strategy that circumvents this problem and enables the determination of cryo-EM structures for engineered human ORs — providing fundamental insights into how these receptors detect an enormous variety of odorants.

ORs are members of the superfamily of membrane-bound proteins known as G-protein-coupled receptors (GPCRs), which typically respond to a stimulus in a cell's environment by engaging with G proteins inside the cell. Humans express around 400 ORs, used in combination to distinguish odorants[3]. Members of the OR family are divided into two classes and have diverse amino-acid sequences: the sequence identities (the percentages of exactly matching amino-acid residues) of members range between 24% and 99.7% (ref. 4). Class I ORs generally recognize water-soluble odorants, such as carboxylic acids, whereas Class II ORs, which account for more than 80% of all ORs, recognize more-hydrophobic molecules.

Until now, the only available 3D structure of a native (not engineered) human OR has been that of OR51E2, a Class I receptor that is unusually highly expressed in cell lines[5]. To obtain structures of Class II ORs, de March *et al.* used an established strategy[6,7] in which the amino-acid sequences of the members of a subfamily of proteins are aligned to determine the residues most commonly found at each position in the sequence; these evolutionarily conserved residues are then used to construct a 'consensus' protein. Because conserved residues are important for the thermal stability and biological function of proteins, consensus proteins can be used as stable models of unstable native proteins in structural studies.

The authors first made a consensus protein of the human OR51 subfamily, which belongs to Class I and contains OR51E2. The constructed protein, named consOR51, was highly expressed in cell lines. This enabled de March *et al.* to isolate it and to obtain a cryo-EM structure of the receptor in a complex with its G protein. The authors observed that the overall architecture of consOR51 is highly similar to that of native OR51E2 — suggesting that consensus proteins of other OR subfamilies would also be useful structural models of native ORs.

Next, de March *et al.* constructed consensus proteins for three Class II OR subfamilies (OR1, OR2 and OR4) and solved the structures of these proteins bound to their respective odorants. They also produced molecular dynamics simulations of the consensus proteins, and produced mutant versions of the constructs to work out which residues in the odorant-binding pocket are most important for binding. Taken together, these studies show that Class I and Class II ORs have highly similar architectures, but different mechanisms of odorant binding.

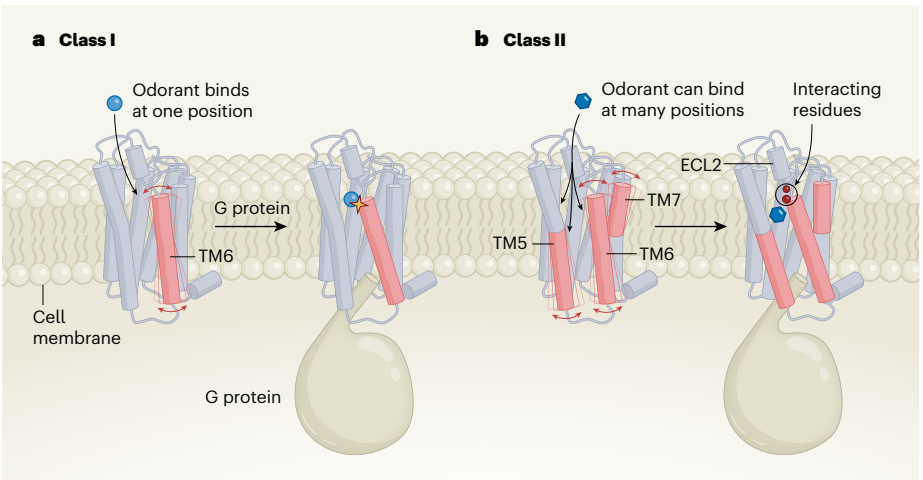


Figure 1 | Activation mechanisms of odorant receptors (ORs). ORs in the nose can distinguish a vast range of odorant molecules. de March *et al.*[2] studied engineered human Class I and Class II ORs to investigate how the receptors are activated by odorants. **a**, In Class I ORs, the transmembrane α-helix TM6 is flexible (red arrows) when no odorant is bound. Odorant binding fixes TM6 into a conformation that enables the binding of a G protein, triggering signalling to the brain. Conformational fixing occurs because odorants bind at one position in the OR's binding pocket, where they interact with an amino-acid residue in TM6; star symbol indicates the interaction site. **b**, In Class II ORs, α-helices TM5, TM6 and TM7 are initially flexible. Odorants can access many positions in the binding pocket, which only partly constrains the helices. The helices become fully constrained and activated by binding of the G protein and by an interaction between two residues — one in an extracellular loop (ECL2) of the OR and the other in TM6. (Adapted from Fig. 6 of ref. 2.)