nature

Why did *Nature* publish AlphaFold3 without its code?

Criticism of the journal's decision raises important questions. We welcome readers' views.

The latest iteration of the protein-structure-prediction algorithm AlphaFold has generated a great deal of interest since its release, accompanied by a paper in *Nature*, earlier this month[1]. Unlike its predecessor AlphaFold2, AlphaFold3 can predict not just the structures of protein complexes, but also when proteins interact with other kinds of molecule, including DNA and RNA. The artificial intelligence tool will be important in both fundamental research and drug discovery.

But its release has also prompted questions, and criticism, of both the AlphaFold team at Google DeepMind in London and *Nature*. When AlphaFold2 was published[2], the full underlying code was made accessible to all researchers. But AlphaFold3 comes with 'pseudocode' — a detailed description of what the code can do and how it works.

This was not a decision we took lightly, and this editorial briefly explains our reasoning. We think that research, regardless of the sector that does it, should be evaluated through peer review and published for the benefit of society and science. At the same time, we have no wish for this to be the final word. This is an opportunity for an important conversation among all research stakeholders at a time when the majority of global research is privately funded.

The basics of how the community can use the new version of AlphaFold remain the same: anyone with a Google account can use the tool for free, for non-commercial applications. But there are important differences between the latest iteration and previous ones. Notably, for AlphaFold2, the DeepMind team worked with the European Molecular Biology Laboratory's European Bioinformatics Institute, an intergovernmental (and publicly funded) research organization based in Cambridge, UK. DeepMind researchers have trained their software on thousands of published records of protein structures and their known shapes.

Now, DeepMind has partnered with Isomorphic Labs, a London-based drug-development company owned by Google's parent, Alphabet. In addition to the non-availability of the full code, there are other restrictions on the use of the tool — for example, in drug development. There are also daily limits on the numbers of predictions that individual researchers can perform.

Many researchers are disappointed by these constraints. In an open letter to *Nature* (see go.nature.com/3k9acav), its authors point out that the lack of an open-source code

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limits verification and reproducibility efforts. The letter has had an impact. Shortly after it was published, DeepMind's vice-president of research, Pushmeet Kohli, posted on the social-media platform X that the team is "working on releasing the AF3 model (incl weights) for academic use" within six months. This is an important step, and *Nature* will update the published paper once the code is released.

But why allow the complete data and code to be restricted at the time of publication? *Nature*'s editorial policies have been developed to support open science and state: "Authors are required to make materials, data, code, and associated protocols promptly available to readers without undue qualifications." One way we enable researchers to do so is through a partnership with Code Ocean, a computational-science platform that makes the information reproducible and traceable. But our policies also acknowledge that there can be restrictions, which "must be disclosed to the editors at the time of submission" and agreed with editors. The policy also states: "Any reason that would preclude the need for code or algorithm sharing will be evaluated by the editors who reserve the right to decline the paper if important code is unavailable."

Reasons for restrictions include a lack of discipline-wide data-reporting standards or of the technological infrastructure necessary for depositing data openly and in structured repositories. In other cases, confidentiality might have to be protected, or data might be withheld for safety, security or legal reasons. Similar principles apply to the availability of code, which is why *Nature*'s policies include an option for releasing the training model and pseudocode or limited code, as attested by examples of studies we have published in chemistry[3], climate change[4] and virology[5].

The private sector funds most global research and development, and many of the results of such work are not published in peer-reviewed journals. We at *Nature* think it's important that journals engage with the private sector and work with its scientists so they can submit their research for peer review and publication. This promotes the sharing of knowledge, verification of the research and the reproducibility researchers strive for. It also benefits product safety and efficacy. Progress needs more, not less, open data and code — something *Nature* will continue to support.

But this goal will not be achieved in a single step. It will require a process. And that requires engagement and dialogue between all stakeholders. To reiterate: we don't want our opinion to be the final word, but rather the start of a conversation. What further steps can we take to ensure openness from all parties in the research ecosystem? We would like to hear from all stakeholders — not just from researchers at universities and private companies, but from policymakers, non-governmental organizations and publishers, too. Write to us at correspondence@nature.com. We will use these pages to update readers.

1. Abramson, J. *et al.* *Nature* https://doi.org/10.1038/s41586-024-07487-w (2024).
2. Jumper, J. *et al.* *Nature* **596**, 583–589 (2021).
3. Mikulak-Klucznik, B. *et al.* *Nature* **588**, 83–88 (2020).
4. Bi, K. *et al.* *Nature* **619**, 533–538 (2023).
5. Desautels, T. A. *et al.* *Nature* https://doi.org/10.1038/s41586-024-07385-1 (2024).