evolutionary origins of music — and language. I argue that understanding these deep origins will require more-inclusive and equitable collaborations across cultures and disciplines, weaving together Indigenous knowledge and the humanities with the natural and social sciences. This includes not only researchers and artists studying music and language in humans, but also biologists investigating the evolution of communication in other animals.

One influential but controversial theory links the origins of musical rhythm to auditory–motor connections in the brain that might have evolved through selection for vocal learning[12].

Although studies describing beat synchronization in sea lions and macaques have challenged this theory, they are hard to interpret in the absence of comprehensive data that compare vocal learning, beat synchronization and other relevant capabilities across species[1].

Combining such cross-species data with emerging information from neuroscience and genetic studies[17,18] holds great promise for finally settling long-standing debates about the evolution and universality of music. Even if music is not a universal language, it might hold the key to understanding the origins of language — and perhaps even what makes us human.

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1. Savage, P. E. *Comparative Musicology: Evolution, Universals, and the Science of the World's Music* (Oxford Univ. Press, 2026).
2. Savage. P. E. *et al*. Preprint at PsyArXiv https://doi.org/10.31234/osf.io/pv3m9_v3 (2025).
3. Rajendran, V. G., Prado, L., Marquez, J. P. & Merchant, H. *Science* **390**, 940–944 (2025).
4. McBride, J. M. *et al*. Preprint at PsyArXiv https://doi.org/10.31234/osf.io/y3rth_v2 (2026).
5. Lomax, A. *Folk Song Style and Culture* (Transaction, 1968).
6. Passmore, S. *et al*. *Nature Commun.* **15**, 3964 (2024).
7. Mehr, S. A. *et al*. *Science* **366**, eaax0868 (2019).
8. Savage, P. E., Brown, S., Sakai, E. & Currie, T. E. *Proc. Natl Acad. Sci. USA* **112**, 8987–8992 (2015).
9. Ozaki, Y. *et al*. *Sci. Adv.* **10**, adm9797 (2024).
10. Honing, H., ten Cate, C., Peretz, I. & Trehub, S. E. *Phil. Trans. R. Soc. B* **370**, 20140088 (2015).
11. Cook, P. F., Hood, C., Rouse, A. & Reichmuth, C. *Sci. Rep.* **15**, 12125 (2025).
12. Patel, A. D. *BMC Neurosci.* **25**, 65 (2024).
13. Dhariwal, P. *et al*. Preprint at arXiv https://doi.org/10.48550/arXiv.2005.00341 (2020).
14. Agostinelli, A. *et al*. Preprint at arXiv https://doi.org/10.48550/arXiv.2301.11325 (2023).
15. McDermott, J. H., Schultz, A. F., Undurraga, E. A. & Godoy, R. A. *Nature* **535**, 547–550 (2016).
16. Margulis, E. H., Wong, P. C. M., Turnbull, C., Kubit, B. M. & McAuley, J. D. *Proc. Natl Acad. Sci. USA* **119**, e2110406119 (2022).
17. Vuust, P., Heggli, O. A., Friston, K. J. & Kringelbach, M. L. *Nature Rev. Neurosci.* **23**, 287–305 (2022).
18. Wesseldijk, L. W., Ullén, F. & Mosing, M. A. *Neurosci. Biobehav. Rev.* **152**, 105302 (2023).

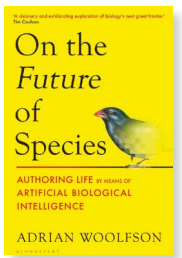
Will 'generative biology' transform life on Earth?

AI tools are helping scientists to build synthetic organisms from scratch. **By Kate Adamala**

Biology is undergoing a transformation. After centuries of studying life as it evolves naturally, researchers are now using a combination of computation and genome engineering to intervene, generating new proteins and even whole bacteria from scratch. The use of artificial-intelligence tools to design biological components, an approach known as generative biology, is set to turbocharge this area of research. Just last year, scientists used AI-assisted design to produce artificial genes that can be expressed in mammalian cells and, for the first time, an AI program was used to create an entirely synthetic virus.

This approach is much more than just a series of technical feats. It could transform how life on Earth develops, as biochemist Adrian Woolfson describes in his latest book. *On the Future of Species* provides a sweeping account of the history and science behind this transformational technology, from the first gene-sequencing efforts to the rise of AI-powered techniques. His vision of what biology is becoming gives the book a coherence that is sometimes lacking in broad surveys of synthetic biology, which often represent only the current science.

One of the central themes in Woolfson's book is that, thanks to computational tools, life's patterns (whether the order in which genes are arranged on chromosomes or the physical traits that are encoded by genes) are becoming increasingly predictable and manipulable. This is making it ever simpler for researchers to tinker with an organism's DNA to achieve a desired result — be it correcting a disease-causing mutation, designing proteins that have never existed in nature or engineering organisms that can clean up pollution.



On the Future of Species: Authoring Life by Means of Artificial Biological Intelligence
Adrian Woolfson
Bloomsbury (2026)

Brave new world

AI systems can redesign genomes *in silico* as if they were software, rearranging bases like code. These programs use modelling to predict how the sequence of a gene relates to the structure of the protein it encodes, and therefore the protein's function. They can also run simulations to test how a redesigned genome might behave.

One day, Woolfson theorizes, AI-assisted genome design might enable scientists to produce a computer system that he calls a

FRANCESCO RICCARDO IACOMINO/GETTY

Once extinct, the unique constellation of traits a species carries can never be replicated.

ILLUSTRATION: PETRA PETERFFY

species catalogue. This repository would contain all of the information needed to design a whole host of possible life forms. Such a catalogue would enable researchers to create organisms for a specific purpose, such as producing innovative drugs and making crops resistant to pests to eliminate the need for pesticides in agriculture.

Eventually, Woolfson notes, researchers hope to achieve what he refers to as artificial biological intelligence — models that can propose complete, working genomes from scratch. Yet there are many limitations that prevent current models from achieving this. For one thing, it is still frustratingly difficult to predict how the expression of each individual gene affects the expression of others. Furthermore, organismal development is context-dependent and is therefore hard to consolidate into a neat algorithm. Bee larvae can develop into workers or queens depending on nutrition, for example, and people learn to speak with the accent of their parents and peers. Neither of these characteristics can be predicted by computer models.

And then, of course, there are the challenges that come with actually building the organism in the laboratory. Just because it is possible to design a unicorn genome doesn't mean that people will get to ride one. The synthetic yeast genome project, which began in 2006, illustrates some of these difficulties. The genome is a modified version of a natural yeast, *Saccharomyces cerevisiae*, with tweaks to remove non-essential genetic regions and to make it easy to physically shuffle sections of the genome, among other things. But assembling the synthetic chromosomes has been labour-intensive, with the last few being completed in 2025. Moreover, DNA produced conventionally is condensed as it is created so that it fits into the nucleus; it is difficult to retrospectively stuff whole chromosomes into a cell. The researchers involved are still working on this last problem.

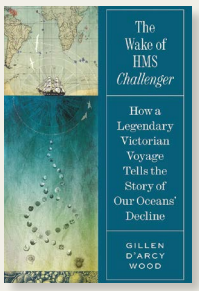
"Genome edits today could lock in irreversible biological futures."

Another complexity is how evolution limits the possible pathways down which an organism can develop, as a decades-long experiment highlights. Since 1988, researchers have tracked how cultures of *Escherichia coli* bacteria kept in identical conditions have evolved over many years. Most of the bacterial cultures have gradually accumulated genetic mutations to metabolize the glucose in their feedstock more efficiently. But in 2003, one culture surprised researchers by evolving to instead metabolize another molecule entirely: citrate. This shift required gene duplications and the rewiring of entire metabolic programs. It was probably written into the strain's destiny early in the experiment, when the first of these mutations occurred, sending this one strain down a distinct evolutionary path from the others.

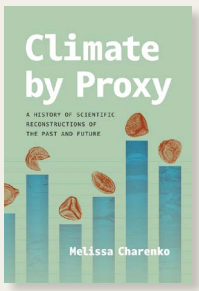
This shows, Woolfson warns, how small genome edits today could lock in irreversible biological futures. Some choices, once made, eliminate other options. If researchers want to freely design species, they need to watch out for these one-way streets. For example, if scientists edit out a biosynthesis pathway because they think that it isn't necessary, all future organisms from that lineage will lack it. Too much genome editing might create organisms that cannot evolve, or be evolved, in response to changing environments.

On the idea of redesigning human genomes, Woolfson resists wading into the ethical debate about making edits that might be passed down through generations, instead focusing on what's technologically possible now and what might be possible in the future. Small therapeutic edits made to just a few genes are already benefiting people with diabetes and sickle-cell disease. But eliminating more complex conditions such as

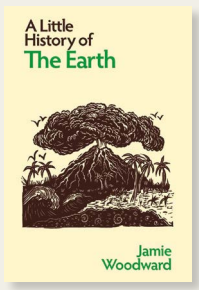
Books in brief



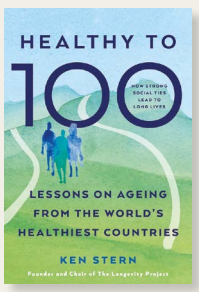
The Wake of HMS *Challenger*
Gillen D'Arcy Wood *Princeton Univ. Press* (2025)
Similar to the global voyage of naturalist Charles Darwin on the HMS *Beagle* in the 1830s, HMS *Challenger*'s 1872–76 oceanographic expedition left a vast scientific legacy — although one less familiar than its predecessor's. The HMS *Challenger*'s crew members are "long gone, but the ship's imprint is still on the world's oceans", concludes Gillen D'Arcy Wood, an environmental historian. Wood's book revives the importance of the expedition's "floating marine laboratory" and reveals its relevance to the challenges the oceans face today.



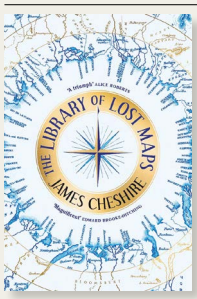
Climate by Proxy
Melissa Charenko *Univ. Chicago Press* (2025)
"Climate defies easy definition," writes historian Melissa Charenko in her complex yet accessible book on the scientific study of the climate during the twentieth century. This research relied on climate proxies, which fall into two types. Physical proxies include fossilized pollen, tree rings and stalagmites. Meanwhile, historical records such as diaries, photographs and ship logs can contain information about cloud cover and harvest dates. Today's challenge, Charenko argues, is to combine data from many proxies using modern computers.



A Little History of the Earth
Jamie Woodward *Yale Univ. Press* (2025)
One of the many vivid details in geographer Jamie Woodward's brief history of Earth is palaeontologist Stephen Gould's demonstration of the planet's 4.5-billion-year lifespan during his lectures. Using his outstretched arm, Gould's shoulder marks Earth's formation, life appears at the elbow and the last millimetre of his middle fingernail represents the history of humans. Even so, Woodward's lively book devotes about one-quarter of its space to humans, while also addressing the "five great spheres of the Earth system".



Healthy to 100
Ken Stern *PublicAffairs* (2025)
In 2024, businessman Ken Stern visited "five of the most successful aging countries in the world" — Japan, South Korea, Spain, Italy and Singapore — which define his thought-provoking book about ageing and health. Although these nations do not rank at the top of global indicators that are conventionally associated with health and life expectancy, such as gross domestic product, he reveals that they all share strong social-support networks, which encourage "lifelong learning, intergenerational relationships, and volunteerism".



The Library of Lost Maps
James Cheshire *Bloomsbury* (2025)
The finest maps combine art, science and history — as shown by the success of the British Library's 2010 Magnificent Maps exhibition in London. So why are "no major museums or galleries" devoted to maps, asks geographer James Cheshire. Inspired by a map library at University College London, his detailed study ranges from a US army map of Hiroshima in Japan before the atomic bomb was dropped on the city to Marie Tharp's map of the mid-Atlantic Ridge, which helped to confirm the theory of continental drift. **Andrew Robinson**

autoimmune diseases would require rewiring complicated genetic programs that are still only partially understood, a capability that scientists are still years away from.

A library of life

Woolfson is at his most compelling when discussing the second central theme of the book, biodiversity. He frames ecosystems and species as vast archives of evolutionary knowledge: a giant library of possible forms, functions and solutions to the challenges of life. Every organism has developed its own strategies to optimize thermodynamics, metabolism, reproduction and more.

Researchers could draw on this library when redesigning organisms. But no individual scientist or algorithm could fully reconstruct these unique and hugely complex adaptations if a species were to become extinct. Even if researchers had a complete genome sequence, a separate species, with a different gestational environment, would have to carry the pregnancy, and epigenetic information (molecular marks on DNA that modulate gene expression) would be lost. Thus, Woolfson argues, biodiversity is not simply aesthetically valuable or ethically important. It is also the foundation on which predictive biology and genome construction ultimately depend.

On the Future of Species manages to articulate the connections between molecular biology, systems biology, computation and evolution, without reducing any of these disciplines to caricatures. Woolfson's attention to detail is excellent, with precise explanations that are accessible to non-specialists while offering enough depth to engage experts.

However, at times, Woolfson's optimism about future modelling capabilities exceeds current theoretical frameworks. In my view, his confidence that we will eventually be able to predict the relationships between genes and the traits that they encode perfectly might underestimate the role of stochastic variation in biology. But this could be a biased criticism from an experimentalist who worries about her job being made obsolete by comprehensive genomic simulations.

In closing, Woolfson delivers a warning. Creating genomes from scratch is not inherently dangerous, but we are acquiring tools powerful enough to remake life while lacking the theoretical understanding needed to control the consequences. Redesigned organisms might cause unintentional harm. For example, bacteria engineered to be resistant to antibiotics could, if they escape the lab, cause the spread of resistance in wild bacterial populations. Care is needed to ensure that our new tools are used safely and responsibly.

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