open-minded, and warmly invite the devil's advocate into your intellectual life. If you're still not convinced, I recommend the book *Surrounded by Idiots* by Thomas Erikson for starters. It is funny 'cause it's true.

What do you think are the biggest problems science as a whole is facing today? The devaluation and disintegration of academia. Widespread polarization has created a hostile environment for academics, where rational discourse and critical thinking are now often spurned, punished and marginalized, even in universities (ironic, given the focus on diversity, equity and inclusivity). The delicate balance between politics and science has also tipped sharply towards a domineering overreach. Academic freedom, and the wider societal benefits it protects, is therefore under threat. It's no wonder that many brilliant minds are now running for the (silicon) hills. The books *The Coddling of the American Mind* by Greg Lukianoff and Jonathan Haidt and *The Madness of Crowds* by Douglas Murray sum up our times well, I think. As a psychologist, it's equally fascinating and dismaying to witness; history also shows that patience is a necessary virtue in these times. I was exceptionally lucky to have experienced an academic environment where information flowed freely, hierarchies were flat, rationale discourse was valued, and creativity was encouraged. I await patiently for its return.

What is your greatest research ambition? Cracking the code of human social communication. What do the specific face, body and voice cues mean? Why do they take their specific forms? And how do they orchestrate a unified system of communication? Seeing that knowledge animate artificial agents to enable them to communicate with humans would be the ultimate litmus (or, more appropriately, Turing) test. Maybe we'd even see one displayed in the Royal Museum of Scotland.

DECLARATION OF INTERESTS

The author declares no competing interests.

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Air-quality networks collect environmental DNA with the potential to measure biodiversity at continental scales

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One of the biggest planetary challenges is the accelerating loss of biodiversity threatening ecosystem functioning on a global scale. The WWF Living Planet Report (https://livingplanet.panda.org/) estimates a 69% decline in populations since 1970. The Convention on Biological Diversity and related international treaties ask countries to monitor shifts in community composition and assess rates of species decline to quantify extant biodiversity relative to global targets[1]. However, quantifying biodiversity is a challenge, and monitoring continual change is impossible at almost any scale due to a lack of standardized data and indicators[2,3]. A common problem is that the required infrastructure for such global monitoring does not exist. Here, we challenge this notion by analysing environmental DNA (eDNA) captured along with particulate matter by routine ambient air quality monitoring stations in the UK. In our samples, we identified eDNA from >180 vertebrate, arthropod, plant and fungal taxa representative of local biodiversity. We contend that air monitoring networks are in fact gathering eDNA data reflecting local biodiversity on a continental scale, as a result of their routine function. In some regions, air quality samples are stored for decades, presenting the potential for high resolution biodiversity time series. With minimal modification of current protocols, this material provides the best opportunity to date for detailed monitoring of terrestrial biodiversity using an existing, replicated transnational design and it is already in operation.

We test whether airborne eDNA[4], which contains information on plant, insect and animal life from the local landscape[5–9], is captured on filters (Figure 1A) as a by-product of the regular operation of air quality monitoring infrastructure. The UK heavy metals ambient air quality network (Figure 1B) is one of the UK's nationwide air quality monitoring networks. It collects PM_{10} particulate matter onto filters which are analysed for atmospheric pollutants on behalf of Defra and the Environment Agency (UK)[10]. Using a fixed location sampler in suburban south-west London adjacent to a 445 ha deer park, we took total suspended particulate matter (TSP) samples for one hour, one day and one week in triplicate (n = 9 samples). We compared these to historical PM_{10} samples from Scotland (n = 8) collected under normal operating procedures. A filter sampled air for seven days, and was then automatically exchanged for a new filter, but remained in the sampler for 28 days to generate four samples at a time (Supplemental information). The Scottish filters were stored for eight months at room temperature prior to eDNA analysis. We extracted eDNA and amplified and sequenced fragments of the 16S rRNA gene targeting vertebrates, COI gene targeting invertebrates and ITS region targeting plants and fungi following established protocols (Supplemental information).

We recovered eDNA which could be attributed to >180 different taxa of plant, fungus, insect, mammal, bird, fish, and amphibian, as well as traces of other phyla consistent with the local ecology (Figure 1C, Data S1). These taxa included charismatic species such as badgers, dormice, little owls and smooth newts, species of special conservation interest such as hedgehogs and songbirds, trees, including ash, linden, pine, willow and oak, plants like yarrows, mallows, daisy, nettles and grasses, arable crops, such as wheat, soybean and cabbage, and

pathogenic fungi like *Septoriella.* Of particular note were the 34 species of bird detected over the two locations. Longer sampling times detected increased vertebrate species richness (Figure 1D), possibly due to DNA accumulating on filters as more mammals and birds visited the area over a longer time period.

This finding has the potential to be game changing for our approach to biodiversity monitoring on land, because air pollution monitoring networks, often sampling daily or weekly at high density (Figure 1E–G), are likely to sample eDNA along with the particulate matter for which they were designed. These sites are concentrated in Central and North America, Europe and Asia but are also found in lower density in the global south.

To understand the ecological value of this material future research needs to quantify the spatiotemporal nature of the signal. As a priority we must determine the useful range of these samplers, the degradation rate of airborne eDNA, the influence of sample size fraction (TSP vs. PM_{10} or $PM_{2.5}$) and the potential value of older stored filters. It also remains unclear why some taxa are more "detectable" than others, which has been observed previously[7,8] (Supplemental information). Our identification of eDNA relied on considerable coverage of UK taxa in reference collections (GenBank, BOLD) but will be challenging in understudied locations. While meteorological events impact particulate transport and thus detection distance, early experiments[9] suggest airborne eDNA signals are local. Some PM_{10} material can travel intercontinental distances, but larger particle sizes (e.g., upper range of PM_{10} or animal cells) likely travel much shorter distances. Our previous work[7] suggests short persistence and minimal travel of airborne eDNA. If this pattern is maintained, it should create a highly heterogeneous distribution of signals tied to the local ecology.

Air quality monitoring networks are a pre-existing infrastructure that may be taking readings of the local terrestrial ecology, using a standardised, highly controlled and repeatable sampling strategy, and

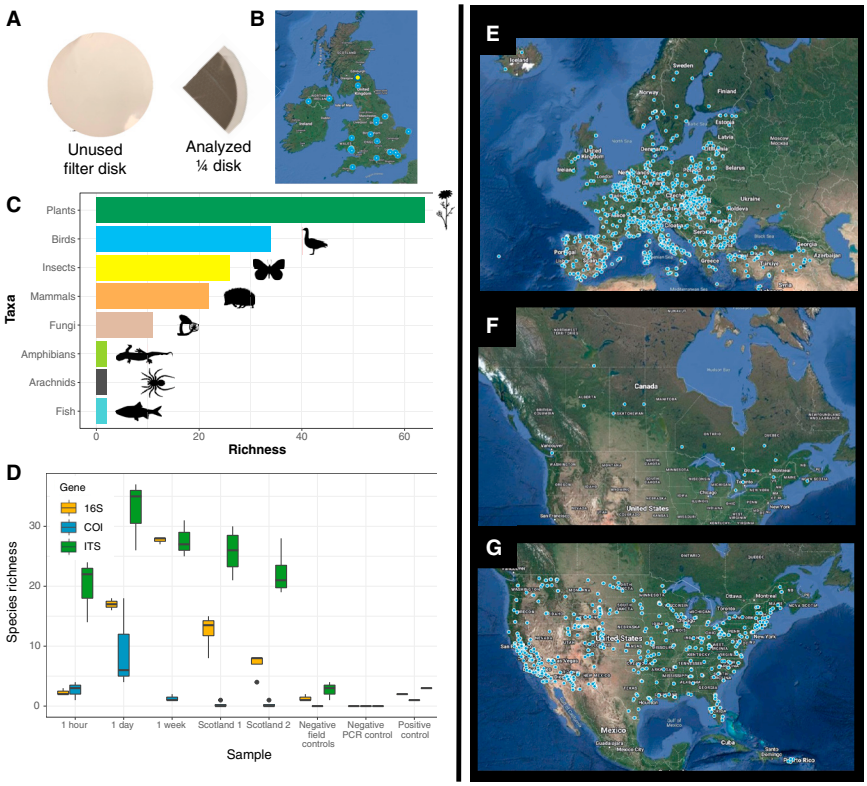

Figure 1. Biodiversity sampling by pollution monitoring networks.
Many air quality monitoring networks collect weekly PM_{10} samples for analysis. We analysed airborne eDNA from ¼ portions of filters (A) from a private TSP sampler outside London and a PM_{10} sampler in Scotland (yellow dot) used on the UK heavy metals network (B), and detected >180 mammals, birds, amphibians, trees, flowers, crop plants, insects and fungi from the local area (C). Detected taxonomic richness (D) was lowest in samples collected for only an hour and highest from filters collected for a full day (COI - arthropods and ITS - plants) or a week (16s - vertebrates) but remained surprisingly high even in samples collected for a week and then stored for months at room temperature (Scottish PM_{10} samples). Air quality monitoring networks are globally distributed and those specifically sampling particulate matter can be found in high density, for example operated across Europe by AirBase (E), in Canada by CAPMoN (F) and in the USA by the EPA (G). While many may not be compatible with eDNA collection in their current form, more investigation needs to be done to assess the variety of sampling approaches used for compatibility. The potential of regular, high-density sampling of environmental DNA representative of the local ecology as a by-product of existing monitoring programs using already established infrastructure is potentially game changing for the detection, monitoring and management of global biodiversity.

new sites could be established in key areas for biodiversity monitoring. The distribution and operation of these stations varies by country, and the variety of designs will make some easier to use than others. However, in locations like the UK, minimal modification of current collection and storage protocols will make the samples ideal for genetic analysis. The viability of the Scottish samples stored in ambient conditions suggests that, once collected, DNA on the filters is surprisingly stable. This approach may provide the best opportunity to date to measure terrestrial biodiversity in a semi-automated, highly controlled system and it is already deployed on national scales. Because of the rapid and repeated sampling, these networks also provide the elusive opportunity to monitor change over time.

These systems have been collecting material for decades but, until now, we have not realized their potential for biodiversity monitoring. With urgency, we must immediately investigate their utility, begin preserving these data and engage in a programme of analysis to determine their full value.

SUPPLEMENTAL INFORMATION

Supplemental information includes Supplemental experimental procedures and one datafile and can be found with this article online at https://doi.org/10.1016/j.cub.2023.04.036.

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