

What does the supply of caffeine have to do with this week's special issue of *Nature* that discusses biodiversity, the extinction of species and how to conserve them? Everything. For, as some biologists argue, too much current thinking on conservation agrees with *Time Out*. The standard definition of biodiversity focuses too heavily on counting the number of different species, when perhaps it should concentrate on what each of those species contributes to the ecosystem.

Carry your coffee to drink at the rocky seashore, for example. Within a square metre or so you might find four species — a mussel and three different species of barnacle. A bit farther along, in another square metre, you find another four species, but this time the mussel is joined by a starfish, an anemone and a seagrass (see [go.nature.com/2qmbfah](http://go.nature.com/2qmbfah)). Under current conservation measures, each community has equal biodiversity and deserves equal attention. That's because a thatched barnacle is considered to be as different from an acorn barnacle as it is from the seagrass. Just as a barista who remembers your name is as different from a forgetful one as he or she is from a librarian.

To see and designate the second seashore community as different from the first, some biologists argue that we should consider what these species do, individually and collectively. The idea is called functional diversity, and it's catching on. Many biologists have felt for decades that the starfish, anemone and seagrass make up a more diverse community than the barnacle trio. But as a News Feature explores (page 22), the concept is gaining ground in policy circles. And it's being used to set priorities and to determine how conservation resources are allocated.

Intuition is not evidence, and there are already concerns that proponents of functional diversity are trying to run before they have worked out if they want to walk. Which functional traits should be considered and how can they be compared? How can biologists ensure that all functions of a species are accounted for, and not just those that are the most obvious? Do we have sufficient data to link diversity of traits to the health of an ecosystem? What if table service at a coffee shop is the only reason that a rich couple visit, and spend money in other shops while there?

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To consider the utility of creatures in a habitat and not just their number can certainly throw up counter-intuitive findings. Some measures of functional diversity, for example, judge degraded post-logging secondary forests in the tropics to be as healthy as the primary forests they replace (see C. A. Sayer *et al. Biol. Conserv.* **211** (A), 1–9; 2017). (That is not an argument to stop protecting primary forest, but it might be a reason to give the degraded areas equal status.)

What is clear — and laid out in much detail in a series of other articles this week (see page 47) — is that existing attitudes and measures are failing to halt the global loss of habitats, species and ecosystems. To address the decline and stem the damage to the natural world, new approaches and new thinking are needed. Functional diversity, properly applied, could be a pragmatic and necessary step. All species are equal. But perhaps some are more equal than others. ■

## ANNOUNCEMENT

## Towards greater reproducibility

Since 2013, *Nature* and the Nature research journals have asked authors of papers in the life sciences to complete a checklist when they submit a paper. This extra step — prompting authors to disclose important elements of experimental design and analysis — was part of a broader effort to improve the quality of reporting in our life-sciences articles.

This week we go further. Alongside every life-sciences manuscript, we will publish a new reporting-summary document, to which authors will now be expected to add details of experimental design, reagents and analysis. This is another step in encouraging transparency, in ensuring that papers contain sufficient methodological detail, and in improving statistics reviewing and reporting.

We expect that the new reporting summary will assist reviewers and editors in assessing experimental quality and help readers to locate crucial details on data collection and analysis. Those familiar with the original checklist will find similar elements in the new reporting summary. The summary also has a strong focus on points that are known to be sources of experimental variability and that tend to be poorly reported in the literature.

*Nature* has long been interested in promoting the reproducibility of published results (see [go.nature.com/huhbyr](http://go.nature.com/huhbyr)). Although the issues that give rise to the 'reproducibility crisis' are multifaceted, and come into play long before a paper is submitted, our responsibility is to ensure that the research we publish is well planned, well executed and well reported.

It is not possible to capture the diversity of work across the life sciences in a single document. So this new general-reporting summary will be accompanied by more-specific and more-detailed accessory reporting summaries. These can cover

greater experimental detail for papers based on chromatin immunoprecipitation sequencing, flow cytometry and magnetic resonance imaging. Although our physical-sciences papers will not use a standard reporting summary, we are launching accessory summaries on lasers and solar cells to elevate reporting standards in these areas. In future, we will expand this set to cover other techniques. Like the core reporting summary, these accessory summaries will be published with the relevant paper.

We are happy for other journals and institutions to use the same approach, and so we have made all the reporting-summary templates available for use or adaptation under a CC-BY licence.

As with the initial checklist, these documents aim to improve reporting, rather than to enforce a defined set of standards. They should make apparent the details of how a study was designed, performed and analysed, to allow reviewers and readers to interpret the results and understand any limitations. There are, of course, separate experimental standards that must be met to comply with our editorial policies, and these are captured in our new editorial-policy checklist (see [go.nature.com/2rdnfbh](http://go.nature.com/2rdnfbh)).

As a complement to these new documents, we will now mandate greater transparency in data presentation. We will ask authors, where possible, not to use bar graphs, and instead to use approaches that present full data distribution. We've also expanded our data-deposition mandates to include proteomics data, and our policy on reporting of cell-line authentication is being extended to all papers with data from cell lines. And we have added a reporting table for cryo-electron microscopy, which joins those for nuclear magnetic resonance imaging and X-ray crystallography.

With these and other steps, we will continue to work to ensure the rigour of the work we publish, and to promote the ability of the community to build on this research. But journals can only do so much. Institutions must invest greater resources in training scientists in scientific rigour and statistics. Funders must enforce appropriate experimental design from the earliest stages of scientific projects. And the community must appreciate the importance of transparency and replication. Only by working together can we all improve research reproducibility. ■