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Research article

The undetectability of global biodiversity trends using local species richness

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Although species are being lost at alarming rates, previous research has provided conflicting results on the extent and even direction of global biodiversity change at the local scale. Here, we assessed the ability to detect global biodiversity trends using local species richness and how it is affected by the number of monitoring sites, sampling interval (i.e. time between original survey and re-survey of the site), measurement error (error of the measurement of the local species richness), spatial grain of monitoring (a proxy for the taxa mobility) and spatial sampling biases (i.e. site-selection biases). We use PREDICTS model-based estimates as a proxy for the real-world distribution of biodiversity and randomly selected monitoring sites to calculate local species richness trends. We found that while a monitoring network with hundreds of sites could detect global change in species richness within a 30-year period, the number of sites for detecting trends doubled for a decade, increased 10-fold within three years and yearly trends were undetectable. Measurement errors had a non-linear effect on statistical power, with a 1% error reducing statistical power by a slight margin and a 5% error drastically reducing the power to reliably detect any trend. The ability to detect global change in local species richness was also related to spatial grain, making it harder to detect trends for sites sampled at smaller plot sizes. Spatial sampling biases not only reduced the ability to detect negative global biodiversity trends but sometimes yielded positive trends. We conclude that detecting accurate global biodiversity trends using local richness may simply be unfeasible with current approaches. We suggest that monitoring a representative network of sites implemented at the national level, combined with models accounting for errors and biases, can help improve our understanding of global biodiversity change.

Keywords: bias, monitoring, PREDICTS, sampling, simulations, taxa mobility

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Introduction

Biodiversity is being lost at alarming rates and its decline is projected to continue well into the next century unless we achieve a transformational change in the global socio-economy (Pereira et al. 2010b, 2020, Pimm et al. 2014, Ceballos et al. 2015, Díaz et al. 2019). Measuring and identifying biodiversity trends is therefore an essential first step for effective conservation policy and management. However, biodiversity is multidimensional and scale-dependent, and quantifying biodiversity change is far from trivial (McGill et al. 2015, Chase et al. 2018). While it is clear that the number of species is declining at the global level, evidence for declines at national and smaller scales is mixed (Sax and Gaines 2003, Thomas 2013, Primack et al. 2018). Species richness at the local scale (α diversity) is one of the most ubiquitous measures of biodiversity (Hillebrand et al. 2018), but quantifying the extent and even direction to which local species richness is changing remains largely unresolved (Gonzalez et al. 2016, Cardinale et al. 2018). Even though local species richness is declining in many locations (Newbold et al. 2015), several studies indicate considerable global variation (Thomas 2013, Gonzalez et al. 2016, Cardinale et al. 2018), reporting little, or no net change in local species richness through time (Thomas 2013, Vellend et al. 2013, Dornelas et al. 2014, 2019, Blowes et al. 2019).

These conflicting results are not surprising, given the complex nature of biodiversity change, with heterogeneity of various biodiversity measures in space (Rodrigues et al. 2014, Keil et al. 2018, Blowes et al. 2019), time (Mihoub et al. 2017), taxa (Daskalova et al. 2020, Leung et al. 2020, Outhwaite et al. 2020) and habitats (van Klink et al. 2020, Staude et al. 2022). Human impacts can even increase species richness in some locations (Sax et al. 2002, McKinney 2008, Ellis et al. 2012), especially with species that thrive in human-dominated landscapes (Newbold et al. 2013, Aronson et al. 2014, Gerstner et al. 2017, Pyron 2018, Callaghan et al. 2019a, Dornelas et al. 2019, Valdez et al. 2021). Additionally, large losses in the abundance of species and communities do not always correlate with species richness change (Dornelas et al. 2014, Chase et al. 2018) because declining and rare species are often replaced by widespread, invasive or non-native species (Sax and Gaines 2003, Kortz and Magurran 2019, Staude et al. 2022) or because the declining species were the most abundant ones to start with (Schipper et al. 2016). Even when species are lost at the regional or biome level, high species turnover with additions matching or exceeding the rate of local species extinctions can result in little net change (Thomas 2013, Dornelas et al. 2019) or even a net gain in local species richness (Finderup Nielsen et al. 2019, Staude et al. 2020), despite regional homogenization of species composition. In addition, species richness trends may be calculated differently across studies with some analyses excluding non-native species (Alkemade et al. 2009), while others include all taxa.

Although monitoring local species richness is essential to the overall goal of tracking global biodiversity changes (Mihoub et al. 2017), accurate estimates rely on selecting sites that are representative of what is happening locally to species richness around the globe (Mentges et al. 2021). However, biases are pervasive in biodiversity data (Boakes et al. 2010, Trimble and van Aarde 2012, Mentges et al. 2021), and estimates confounded by spatial sampling biases are well-documented in biodiversity monitoring programs and citizen science data (Gonzalez et al. 2016, Callaghan et al. 2019b, Daskalova et al. 2021b). Biodiversity data is more likely to be derived from countries with a higher GDP (Callaghan et al. 2021), inside protected areas (Mihoub et al. 2017), densely populated areas (Mentges et al. 2021) or from regions with biodiversity hotspots (Sastre and Lobo 2009, Martin et al. 2012). Not surprisingly, there is an overall bias of biodiversity (Proença et al. 2017, Nuñez-Penichet et al. 2022) particularly monitoring sites towards North America and Europe (Pereira et al. 2010a, Simmons et al. 2019) and with forest biomes, particularly temperate broadleaf and mixed forests, studied more often than other biomes such as grasslands (Trimble and van Aarde 2012, Hughes et al. 2021). Spatial biases are therefore frequently prevalent in the data used to inform global mean indices of biodiversity change, influencing the results and interpretation of such findings (Simmons et al. 2019).

To accurately quantify global change in local species richness, it is imperative to overcome the limitations of aggregating heterogeneous biodiversity data across space, time and taxa into global indices (Leclère et al. 2020). However, differences in the underlying statistical models and data selection to investigate biodiversity change can dramatically influence the results and their interpretation (Daskalova et al. 2021a, Desquilbet et al. 2021, Mentges et al. 2021). Even with unbiased spatial sampling, biodiversity estimates will still be strongly influenced by the number of sampling sites, sampling interval, spatial grain and species mobility (Pautasso 2007, Boakes et al. 2010, Chase and Knight 2013, Titley et al. 2017, Mentges et al. 2021). For example, the bias and precision of biodiversity estimators are highly sensitive to sample size, and statistical power increases precipitously with larger sample sizes for most biodiversity estimators (Gwinn et al. 2016). Additionally, trends estimated with shorter sampling intervals have lower statistical power and can result in incorrect conclusions or extreme estimates (Gonzalez et al. 2016), particularly when sample sizes are small (Daskalova et al. 2021a) or when the magnitude of the change is low and/or inter-annual variation is high (Stuble et al. 2021). Estimates of biodiversity change are also strongly scale-dependent and can even lead to differing conclusions based on the spatial grain (Pautasso 2007, Chase and Knight 2013, Chase et al. 2018, Mentges et al. 2021).

Although analytical approaches, such as stratified analyses or spatial weighting, can reduce bias and increase the precision and accuracy of biodiversity change (McRae et al. 2017, Cardinale et al. 2018, Hughes et al. 2021, Roswell et al. 2021), they have not been widely used. Additionally, these approaches do not always provide the best solution since they can have been found to sometimes weaken the detection

of biodiversity responses such as the change in species richness (Cao and Hawkins 2019). In any case, even if all these biases and issues are perfectly accounted for, measurement errors can still yield inaccurate estimates (Bonar et al. 2011, Daskalova et al. 2021a). Failure to consider any of these monitoring design issues can therefore lead to the misinterpretation of data and unwarranted extrapolations of trends.

In this study, we assess how well a network of sites monitoring local species richness would be able to detect the global pattern of biodiversity change at the local scale, or the mean trend of local species richness across the globe. We ask how this ability is affected by the number of monitoring sites, sampling interval (time between survey and re-survey), measurement error of species richness, spatial grain of the monitoring and spatial biases in site selection. We use outputs from a global model based on the PREDICTS database (Hill et al. 2018) as a proxy for the real-world trends of biodiversity, both in terms of magnitude, spatial distribution and temporal dynamics.

Methods

PREDICTS modelled outputs

As the global pattern of biodiversity change over time is not known, our strategy is to use a model-based estimate as a proxy of how local species richness has changed across the world. While previous studies have simulated biodiversity to measure the ability to detect change across various scenarios (Santini et al. 2017), purely theoretical simulations fail to capture realistic patterns of spatial heterogeneity and spatial autocorrelation. In addition, the speed of change of biodiversity would be completely hypothetical or ad-hoc in a simulation study. For a realistic representation of local species richness over time, we used modelled historical local species richness relative to a pristine baseline with a spatial resolution of 0.25 degrees from Hill et al. (2018), derived from the PREDICTS (Projecting Responses of Ecological Diversity in Changing Terrestrial Systems) database (Hudson et al. 2017).

The PREDICTS database is a spatially heterogeneous and globally comprehensive collation of site-level data from over 32 000 sites and over 51 000 species, covering a wide range of taxonomic groups across 767 studies (Hudson et al. 2017, Purvis et al. 2018). Estimates of terrestrial local within-sample species richness from 1900 to 2015 relative to a pristine baseline were modelled by Hill et al. (2018). Briefly, a linear mixed-effects model was used to model site-level species richness using the site-level data extracted from PREDICTS (Hudson et al. 2017), with historical land use and related pressures (land-use intensity, and human population density) as explanatory variables (Hurtt et al. 2020). The spatial pattern of the expected site-level species richness was then projected by combining the coefficients of this model with global raster data of these pressures for each focal year (Hill et al. 2018, Hurtt et al. 2020).

These models indicate that the average global rate of local species richness decline is driven by land-use change with marked geographic variation (Hill et al. 2018). While PREDICTS only estimates the impacts of land-use change, and the magnitude of real biodiversity change may be greater, land-use change is considered to have been the main impact on biodiversity in recent decades (Jaureguiberry et al. 2022). Additionally, like other most studies on local species richness (Sax and Gaines 2003, Vellend et al. 2013, Dornelas et al. 2014, Primack et al. 2018), PREDICTS does not distinguish between native and non-native species. Although the data used for PREDICTS has spatial and taxonomic biases, it still has been be more balanced across terrestrial ecoregions better than other multi-taxa biodiversity databases (e.g. Living Planet, BioTIME) (Daskalova et al. 2021b).

Simulations of randomly selected monitoring networks

We sampled from the PREDICTS model outputs to build datasets of simulated biodiversity monitoring time series using various monitoring designs (Fig. 1). We simulated 1000 monitoring networks for each design scenario and for each size of the monitoring network, which ranged from 100 to 10 000 sites (Fig. 1). For each monitoring network, we randomly placed the sites in the different 0.25° grid cells of the terrestrial surface. For each site and sampling interval, we estimated the local relative species richness change as $(S_{2010} - S_i)/S_i$, where S_{2010} is the PREDICTS-based species richness for 2010, and S_i is the PREDICTS-based species richness at year i.

Testing for detection of local species richness trends

For each monitoring network, we tested whether the mean 'observed' local relative species richness change was significantly different from zero using a two-sided one-sample t-test. The simulated detection power (one minus the probability of a type II error) was determined by the proportion of monitoring networks for which the t-test or rejecting the null hypothesis of no trend would not be significant at $p \leq 1\%$. All analyses and figures were created in R ver. 4.0.5 (www.r-project.org).

Scenarios

Sampling interval
To test the effect of sampling intervals on detecting local species richness change, we explored 1, 3, 10 and 30-year sampling intervals between the first baseline survey (corresponding to the PREDICTS 2009, 2007, 2000 and 1980 model outputs, respectively) and the site resurvey (2010 PREDICTS model output, Fig. 1).

Measurement error
Errors that typically occur when sampling biodiversity include non-detection (i.e. not observing species that are
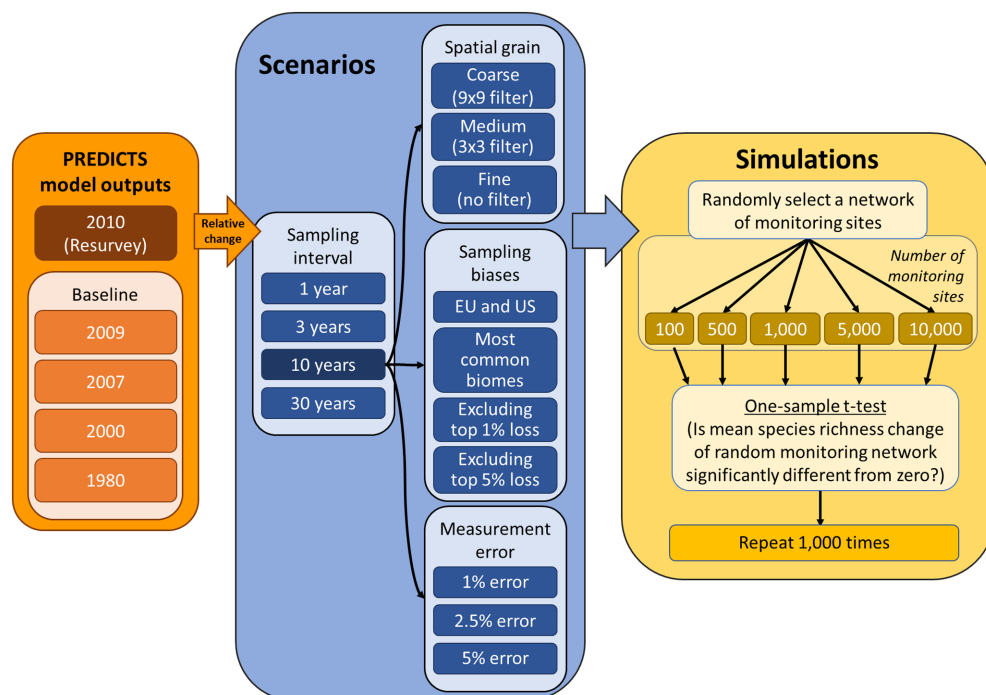
Figure 1. Diagram of the workflow used to build datasets of simulated time series of biodiversity monitoring across various sampling designs.

present) and misidentification (i.e. not correctly identifying species), resulting in lower and higher counts of species richness, respectively. Although difficult to measure, a literature review of these errors in plant surveys found that non-detection ranged between 10–30% and misidentification was between 5 and 10% (Morrison 2016). Other studies, found similar non-detection rates of 15.5–19.2% and misidentification between 2.3–5.9% at the species level and 0.9–1.9% at the genus level (Scott and Hallam 2003, Archaux et al. 2009). Although such errors would be expected to be much greater for more mobile and taxa with lower detectability, we assumed comprehensive and accurate monitoring of local sites and used a more conservative approach based on the lower limits of these misidentification errors. Therefore, to assess the effect of measurement error on observations of local species richness, we added uniformly distributed errors with lower and upper limits of ± 1, ± 2.5 and ± 5% to the PREDICTS historical species richness for the years 2000 and 2010 (sampling interval of one decade). These added errors were independent for each year and observed local relative biodiversity was then calculated as previously described (Fig. 1).

Spatial grain
To examine the effect of the spatial grain of monitoring, which is also related to taxa mobility (below), we decreased the resolution of the PREDICTS-based species richness for the years 2000 and 2010 (Fig. 1). This was done by applying a low-pass, or averaging, filter over the raster by calculating the mean value for all neighboring pixels using a moving focal window. We used two focal windows of 3 × 3 pixels (medium spatial

grain) and a 9 × 9 (coarse spatial grain), with the original 0.25° data considered to be 'fine spatial grain'. This replicates the case where we are unable to observe the exact values at each cell but instead observed the local spatial average of the species richness trend (e.g. by taking sub-samples in a wider area than the focal cell size). This spatial averaging can also happen when taxa are mobile and measurements of that taxa are affected not only by land use in the cell but also in neighbor cells. In contrast, sessile taxa (e.g. plants) observed at a site may not be affected if all the neighbor cells had been converted to degraded habitats but the focal cell habitat was preserved.

Sampling biases
To assess the effect of spatial sampling biases in the monitoring network we carried out four tests (Fig. 1). First, we used the Terrestrial Ecoregions of the World (TEOW) map (Olson et al. 2001) and tested the effect of constraining the distribution of monitoring sites to the four most common biomes in ecological research in our analysis (temperate broadleaf and mixed forests; Mediterranean forests, woodlands and scrub; temperate conifer forests; and tropical and subtropical moist broadleaf forest; Trimble and van Aarde (2014)). In other simulations, we constrained the monitoring network to the two most studied regions, i.e. USA and Europe (the European Union and UK). Lastly, areas undergoing the highest rates of species loss are also typically the less accessible and less studied, which means a high number of species are lost before they can even be identified in any baseline sampling that may eventually occur. To represent this scenario, cells with the largest 1% and 5% losses in species richness were excluded from the placement of monitoring sites.

Results

Sampling interval

The global mean across all cells of the local species richness change in the PREDICTS model outputs was −0.00056, −0.045, −0.17 and −0.49%, for the 1, 3, 10 and 30-year sampling intervals, respectively. The likelihood of detecting global biodiversity trends in a network of monitoring sites was therefore dependent on the interval between sampling events, with shorter sampling intervals requiring more samples to detect a trend (Fig. 2). Sampling intervals of thirty years required just 500 randomly-selected sites to (correctly) reject the null hypothesis of no trend, but the necessary size of the monitoring network doubled for a decade and increased 10-fold when the interval was only three years (Fig. 2). However, even very large monitoring networks did not detect global trends when sampled within one year (Fig. 2).

Measurement error

Adding measurement errors to the observed species richness estimates in each site reduced the probability of detecting the declining trend (Fig. 3). A sampling error of 1% only slightly reduced the simulated power to detect global biodiversity trends (Fig. 3). However, a 2.5% error would require at least 5 times more sites to nearly always detect a trend, while a 5% error drastically reduces the ability to detect global trends resulting in very low statistical power even with many thousands of sites (Fig. 3).

Spatial grain

Compared to finer spatial grains, a coarser spatial grain, representative of larger sampling areas, increased the ability to detect global changes (Supporting information). This is because simulated samples with this coarser grain resulted in fewer sites with values of extreme biodiversity loss or gains, and more sites that showed a slightly negative biodiversity change, as values of a monitoring site are the average across several neighbor cells (Fig. 4a). While the mean relative change stays relatively similar between the spatial grains (−0.00165, −0.00165 and −0.00164; for fine, medium and coarse spatial grain, respectively; Fig. 4b), the standard deviation is reduced as the spatial grain decreases from fine (0.011), to medium (0.0095) and coarse (0.0081). Additionally, the range of values also decreases as the spatial grain becomes coarser (Fig. 4b).

Sampling biases

Spatial sampling bias changed not only the number of sites required to detect global trends but also the direction of change inferred. Excluding areas with the top 1% losses only slightly reduced the ability to detect global biodiversity loss (Fig. 5). However, excluding areas with the top 5% losses resulted in failing to detect any trend even with large monitoring networks (Fig. 5). The areas with the largest losses represented sites that were located mostly in southern and central South America and central and eastern Africa, southeast Asia and Australia; while areas with the highest gains were mostly from North America, Europe, South Africa and parts of Russia (Supporting information). Therefore, trends
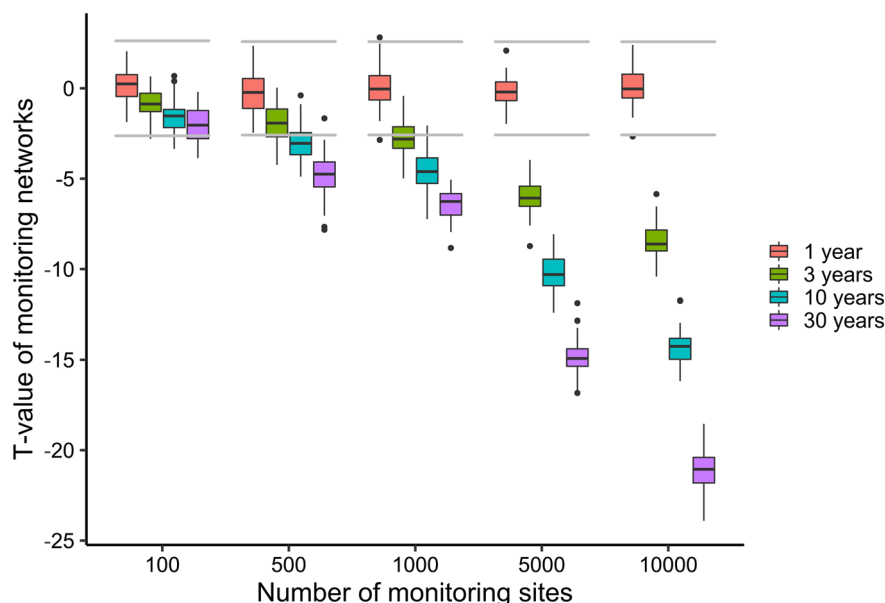

Figure 2. Observed t-values of two-sided tests for the mean local species richness change being different from zero in a network of monitoring sites with a given sample size, for sampling intervals of 1, 3, 10 and 30 years. Box plots represent the t-values of 1000 random networks per sample size (median, interquartile range, minimum, maximum and outliers). Grey horizontal lines indicate the critical values for rejecting the null hypothesis of no change in species richness at a 1% significance level.
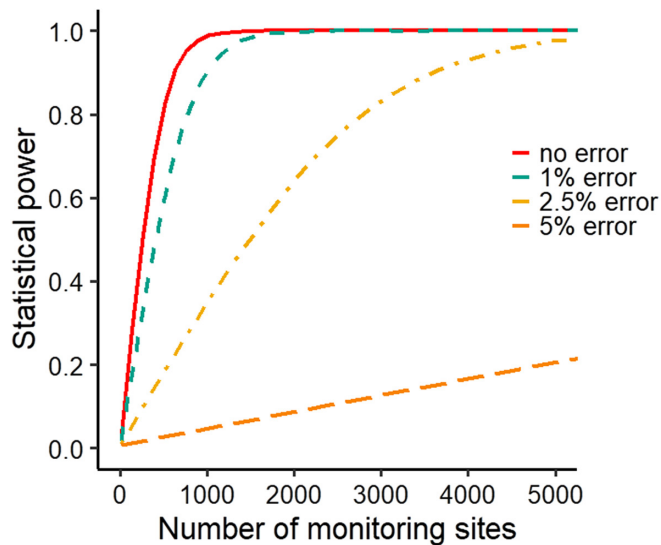
Figure 3. The statistical power of a network of monitoring sites in detecting a change in local species richness within a decade as a function of the number of sites. Lines represent sites with no measurement error (red), 1% uniformly distributed measurement error (green with a short dash), 2.5% uniformly distributed error (yellow with dash and dot) and 5% uniformly distributed error (orange with a long dash).

could not be detected reliably when sampling only the most frequently studied biomes (Fig. 5). Meanwhile, sampling only the USA and Europe resulted in positive trends, even with a very small sample size (Fig. 5).

Discussion

Our study suggests that aggregating local estimates of species richness change are unlikely to provide estimates of global trends of local species richness that are accurate enough to be practical or useful for policy. We found that detecting global trends in local species richness reliably over short sampling intervals required a large number of monitoring sites. While only 500 sites had to be sampled with no errors to detect trends in species richness over thirty years, at least a thousand sites were needed to detect trends within a decade, five times more sites were required to detect trends within three years, whereas annual global changes could not be detected at all. The importance of long sampling intervals for achieving sufficient statistical power to reliably detect biodiversity trends has been well demonstrated (Jennions and Møller 2003, Gonzalez et al. 2016, Seibold et al. 2021). However, we show that, even with perfect measurement of local species richness at an unbiased set of locations, it may not be feasible to detect global trends over short time intervals. This is because the
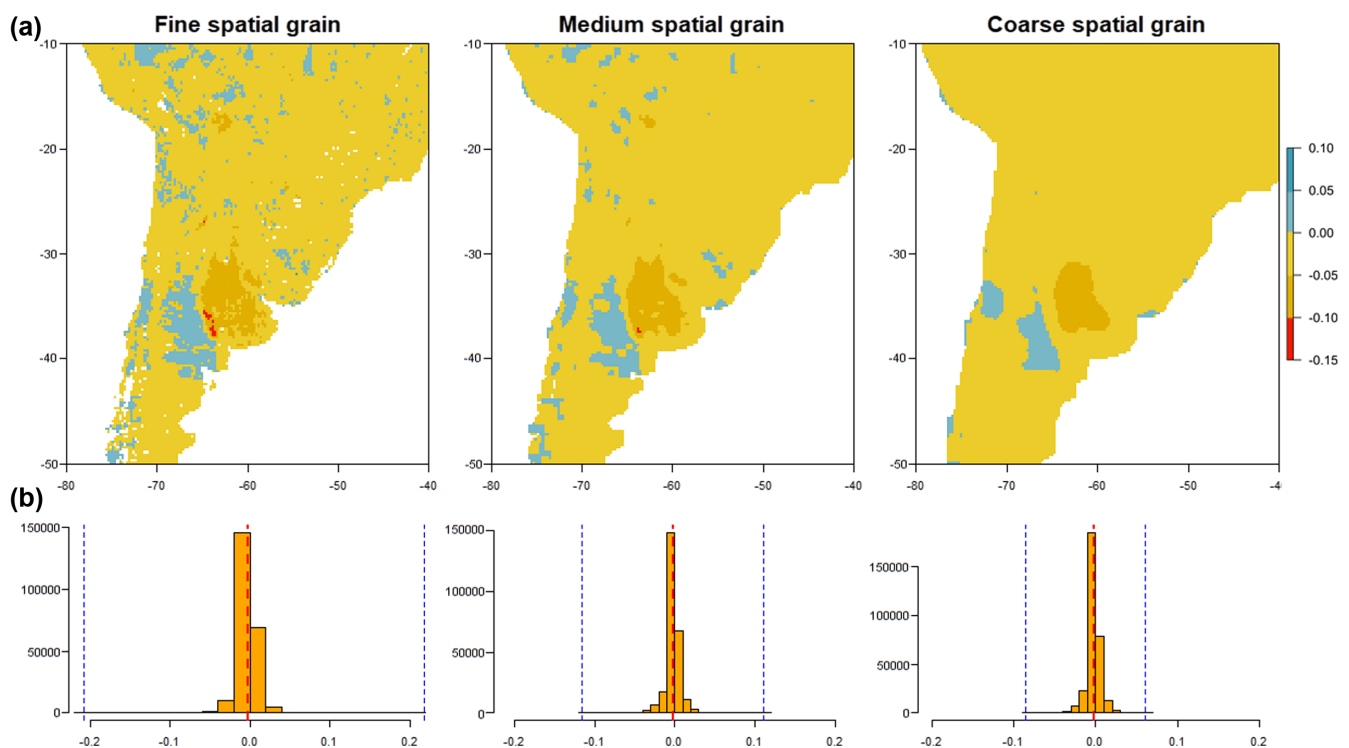

Figure 4. A regional example of the local species richness changes in (a) southern South America between 2000 and 2010 for a fine (1 × 1 pixel), medium (3 × 3 pixel) and coarse (9 × 9 pixel) spatial grain. Light to dark yellow represents areas with small and large biodiversity losses, respectively; light to dark blue represents areas with small and large biodiversity gains, respectively. Red indicates areas with the greatest biodiversity loss. The (b) respective histogram for the frequency (y-axis) of all values (x-axis) of each spatial grain within the selected region. The dotted red line represents the mean and the dotted blue lines represent the minimum and maximum values.
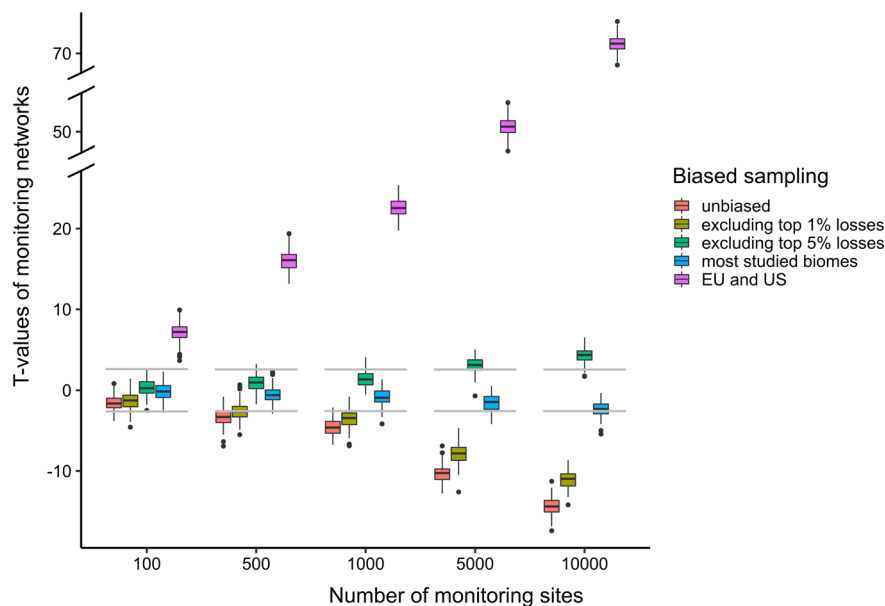
Figure 5. Observed t-values of two-sided tests for the mean local species richness change being zero in a network of monitoring sites with a given sample size, for different types of spatial sampling biases. Sampling spatial bias towards only the top 99 and 95 percentile (removing sites with extreme 1 and 5% losses, respectively), the most studied biomes and only the USA and European regions. Box plots represent the t-values of 1000 random networks per sample size (median, interquartile range, minimum, maximum and outliers). Grey horizontal lines indicate the critical values for rejecting the null hypothesis of no change in species richness at a 1% significance level.

change in local species richness is not only highly variable but mostly centered around zero, particularly with shorter sampling intervals. Additionally, measurement errors are inherent in species richness data, and we found that even a relatively small measurement error of up to 5% can severely reduce statistical power and prevent reliable trend detection. This measurement error is not only considerably lower than what previous studies have observed for plants (Scott and Hallam 2003, Archaux et al. 2009, Morrison 2016) but would be expected to be much larger for more mobile and harder-to-detect taxonomic groups and species. Overall, these results call into question whether we can effectively estimate the global change in local species richness with currently available biodiversity datasets.

Although our results indicate that just a few thousand randomly selected and perfectly measured sites would probably yield accurate global trends in species richness in a somewhat reasonable time period, such data currently does not exist. In general, biodiversity data is rarely random: geographic and taxonomic biases in biodiversity datasets is the rule rather than the exception (Boakes et al. 2010, Gonzalez et al. 2016, Hughes et al. 2021, Mentges et al. 2021). Global synthesis and meta-analysis where data on biodiversity times series is collected from disparate parts of the world into large databases such as BioTIME, or the repeated vegetation survey dataset (Vellend et al. 2013), are vulnerable to these biases. Although these datasets represent the best state-of-the-art (at the time of publication) aggregation of biodiversity data, they are based on an opportunistic collection of studies that typically do not meet the requirements of standardized, long-term quantitative sampling of local species richness. Similar biases

have been reported for other global biodiversity datasets that use alternative metrics, such as the living planet index which is based on population abundance times series (Collen et al. 2009, Murali et al. 2022).

Our results show that, if sites are biased, the true global trend of local species richness will be inaccurate or difficult to detect at all. For example, positive biodiversity trends in local species richness may be detected when sampling only in the USA and Europe, the regions that are most overrepresented in biodiversity databases (Trimble and van Aarde 2012, Gonzalez et al. 2016). This is because these regions display some of the highest biodiversity gains in the PREDICTS model outputs, mostly due to land abandonment. Similarly, if only the most studied biomes are sampled, it is very difficult to detect a trend even with extremely large sample sizes. This is important because, despite the highest losses occurring in tropical forest biomes, particularly in Africa, Asia and South America, these remain under-sampled compared to temperate biomes (Trimble and van Aarde 2012, Hughes et al. 2021). The positive trends in the most studied regions cancel out the negative trends documented in the tropical areas of the Global South, further constraining the accurate detection of global trends.

In addition, there is what is sometimes referred to as the 'parking lot' problem, where biodiversity surveys are no longer carried out from locations that have been highly degraded or undergone complete habitat loss due to development or urbanization (e.g. there are likely not too many biodiversity surveys in parking lots, shopping malls, etc.). Such areas with a high loss of species would therefore not be included in most, if any, biodiversity time series. Here, we show that if

the top 1% of species losses are not included in the sampling network, it slightly reduces statistical power to detect a trend, whereas not sampling the top 5% will mostly result in the conclusion that there is no net change in local species richness. A striking example of how even small sampling biases can completely change the outcome of global biodiversity assessments was presented by Leung et al. (2020) who demonstrated that removing less than 2% of clusters of extreme declines from the Living Planet Index (LPI) fundamentally altered the interpretation of global vertebrate abundance trends. Although this analysis and its interpretation have been debated (Loreau et al. 2022, Mehrabi and Naidoo 2022, Murali et al. 2022, Puurtinen et al. 2022), they demonstrate that it can be problematic to extrapolate the results of a non-representative set of sites to global trends.

Another important and largely unexplored factor that may influence our interpretation of trends is the spatial grain of the monitoring. This is often associated with taxa mobility, with more mobile taxonomic groups requiring larger areas to be sampled. Since more mobile groups are affected by land-use changes over larger areas, a sample at any given site is influenced by the spatial configuration of the landscape at larger scales (Fahrig 2013), resulting in mobile organisms effectively acting as spatial 'averagers'. Here, we show that global change in local richness derived from fine grain monitoring was more difficult to detect than when monitoring at coarser spatial grains. This is because the spatial averaging associated with the larger spatial grains results in a smaller range and standard deviation of per-grid-cell values of relative change, which means fewer sites are required to reject the null hypothesis. An alternative way of understanding this phenomenon is that at finer spatial grains (smaller plot areas), it is necessary to sample exactly the cells where biodiversity change has occurred. Neighboring cells are not affected and would therefore provide no trend signal to a monitoring network. In the case that site sub-samples are taken over a larger area, either because the observation method samples a larger area or because the taxa being studied are more mobile, then it is easier to pick up the response of biodiversity to land-use change.

With biodiversity rapidly declining from anthropogenic pressures (Díaz et al. 2019), and with the CBD post-2020 framework set to include action targets to be evaluated in 2030, it will be imperative to consistently monitor a representative set of sites to measure those targets. However, we demonstrate that an unfeasibly large number of sampling sites could be required, and we may simply have to accept that is currently impossible to reliably monitor global biodiversity trends in local species richness over such short periods. Considering the magnitude of wildlife population declines over the past decades (Almond et al. 2020), even with thousands of perfectly sampled sites, many species will likely go extinct before we can adequately detect any meaningful global biodiversity change. More importantly, given the considerable spatial variation and patterns of biodiversity, the question is whether it is even useful to estimate the global average of local species richness change.

Even if we could detect the global change in species richness at the local scale, very little is revealed about the change in species composition and biotic homogenization (Dornelas et al. 2014, Hillebrand et al. 2018, Primack et al. 2018). Moreover, trends at the local scale are unbalanced, with the addition of just one individual of a newly observed species resulting in a net gain, while the complete loss of all individuals from an already occupying species would be required for a net loss (Vellend et al. 2013, Chase et al. 2019, Jandt et al. 2022). The question of the correct biodiversity metric and interpretation of local species richness change has been ongoing for over two decades, with intense debates between the various scientific communities (Vellend 2017, Cardinale et al. 2018, Primack et al. 2018).

In this study, we based our analysis on species richness trends since the key research studies triggering the net change debate have all used this as the main metric of analysis (Vellend et al. 2013, Dornelas et al. 2014). However, we acknowledge that analyses of other biodiversity metrics can lead to different conclusions. Species diversity metrics that use abundance (e.g. Shannon or Simpson indices) can be more sensitive to change than species richness (Van Strien et al. 2012), while purely abundance-based metrics such as the geometric mean abundance (used in LPI and the Common Bird Indicators in Europe) may in some cases provide earlier detection of trends (Van Strien et al. 2012, Santini et al. 2017). While this study focused on only one biodiversity metric, the problems from sampling biases, measurement errors and spatial heterogeneity similarly apply to other biodiversity metrics.

Although measuring the global state of local species richness trends may not be feasible, conservation policies and responses are coordinated and acted out, not globally, but at local and national scales. Measuring and quantifying biodiversity trends at the regional and national level is not only more viable but critically important to understand the drivers and impacts of biodiversity loss. Arguably, we need a representative network of sampling sites that provides unbiased, integrated and regularly updated biodiversity data. This requires long-term and large-scale monitoring programs at the national and regional levels designed to measure relevant biodiversity trends and assess policy-relevant targets (Lindenmayer et al. 2022). Designing effective national and regional biodiversity surveys can be accomplished by selecting sampling sites that cover the full array of different environmental and geographical conditions to improve the effectiveness of biodiversity inventories (Nuñez-Penichet et al. 2022). To do this, a stratified approach or randomized subsampling of monitored sites that are more representative of the entire gradient of the impact of drivers on biodiversity loss (Bowler et al. 2020) can help balance the uneven data and reduce the number of sites required. Additionally, models can optimize currently existing biodiversity observation efforts and monitoring data (Akçakaya et al. 2016, Honrado et al. 2016, Ferrier et al. 2017), with model uncertainty, spatial biases and measurement errors being dealt with within the modeling workflow (Akçakaya et al. 2016).

Effective monitoring, therefore, requires a coordinated effort and appropriate sampling designs to overcome the limitations of detecting biodiversity change across time. One approach is to establish a sustained, user-driven, locally operated, harmonized and scalable biodiversity observation network (BON) as developed by the Group on Earth Observations Biodiversity Observation Network (GEO BON) (Navarro et al. 2018). Such a BON is currently being undertaken and showing promising results in the European Union with the EuropaBON project (Moersberger et al. 2022, Pereira et al. 2022). This initiative also applies the framework of essential biodiversity variables (EBVs), which identifies a comprehensive set of biodiversity variables to be monitored (Pereira et al. 2013, 2017, Geijzendorffer et al. 2016, Proença et al. 2017, Kissling et al. 2018). EBVs allow for the integration of biodiversity data which can be harmonized across multiple dimensions of biodiversity change across space and time to produce more robust assessments of global change (Kim et al. 2018). Using an EBV approach can also help identify existing biases and further prioritize data mobilization and modelling efforts (Geijzendorffer et al. 2016, Navarro et al. 2018).

Conclusion

Predicting future biodiversity change and its consequences is an urgent scientific challenge and will be an essential component for the next stage of IPBES global biodiversity assessments and the global biodiversity indicators for the Post-2020 Global Biodiversity Framework. However, we question not only if quantifying global change of local species richness is feasible but whether it is even useful for effective and responsive biodiversity conservation. Biodiversity is unquestionably declining at the global level, but conservation policies and responses are implemented at the local and national scales. We should begin to focus less of our resources and efforts on attempting to quantify local species richness at the global level and instead on portraying an accurate picture of biodiversity change across multiple metrics at national and regional levels. By implementing harmonized monitoring of a representative network of sites sampling taxa at the appropriate spatial grains, leveraged through models accounting for measurement errors and spatial biases, we can improve our understanding of global biodiversity trends of local species richness.

Author contributions

Jose W. Valdez: Conceptualization (supporting); Formal analysis (lead); Investigation (lead); Methodology (equal); Visualization (lead); Writing – original draft (lead); Writing – review and editing (lead). **Corey T. Callaghan**: Conceptualization (equal); Formal analysis (supporting); Methodology (supporting); Visualization (supporting); Writing – original draft (supporting); Writing – review and editing (equal). **Jessica Junker**: Visualization (supporting); Writing – review and editing (equal). **Andy Purvis**: Data curation (equal); Resources (equal); Writing – review and editing (equal). **Samantha L. L. Hill**: Data curation (equal); Resources (equal). **Henrique M. Pereira**: Conceptualization (lead); Data curation (equal); Formal analysis (supporting); Investigation (lead); Methodology (equal); Project administration (lead); Resources (lead); Supervision (lead); Validation (lead); Visualization (equal); Writing – original draft (equal); Writing – review and editing (equal).

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Data availability statement

Code and data are available from the Dryad Digital Repository: https://doi.org/10.5061/dryad.n5tb2rc0d (Valdez et al. 2022). Modelled outputs also available from the EBV Data Portal: https://doi.org/10.25829/e3cwb2.

Supporting information

The Supporting information associated with this article is available with the online version.

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