1 Temperature-related biodiversity change across temperate marine and

- 2 terrestrial systems
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Abstract

Climate change is reshaping global biodiversity as species respond to changing temperatures. However, the net effects of climate-driven species redistribution on local assemblage diversity remain unknown. Here, we relate trends in species richness and abundance from 21,500 terrestrial and marine assemblage time series across temperate regions (23.5-60.0° latitude) to changes in air or sea surface temperature. We find a strong coupling between biodiversity and temperature changes in the marine realm, where species richness mostly increases with warming. However, biodiversity responses are conditional on the baseline climate, such that in initially warmer locations richness increase is more pronounced, while abundance declines with warming. In contrast, we do not detect systematic temperature-related richness or abundance trends on land, despite a greater magnitude of warming. As the world is committed to further warming, significant challenges remain in maintaining local biodiversity amongst the non-uniform inflow and outflow of "climate migrants".

Temperature-driven community restructuring is especially evident in the ocean, whereas climatic debt may be accumulating on land.

Main text

Climate change is driving a reorganization of ecological communities as species track changes in air and ocean temperatures^{1–3}. However, global warming is not unfolding evenly across the planet, and this heterogeneity is layered over the uneven distribution of biodiversity. Populations of thermally restricted species may decline with warming, as individuals die, fail to reproduce or move to more suitable locations^{4–6}. Indeed, declines are typically expected for tropical species, since they have narrower thermal tolerances than

temperate species, and live closer to their upper thermal limits^{5,7–10}. In contrast, species benefiting from warming may exhibit abundance increases and expand their geographic ranges^{1-4,11}. Thus, mid- to high-latitudes undergoing warming may provide suitable habitat for species expanding their ranges poleward^{4,12}. As the tropics hold the majority of the world's species¹³, lower-latitude warming temperate regions may experience larger increases in species richness and abundance compared to temperate locations at higher latitudes, due to a larger source pool of climate immigrants (Fig. 1). Biodiversity change may further depend on the baseline climate, i.e. within latitudinal bands the effects of warming might differ between initially warmer versus colder regions^{3,5,12,14}. For instance, warmer temperate regions may offer greater habitat suitability for climate immigrants from lower latitudes. Warming-induced biodiversity change may also be stronger in the ocean than on land^{3,15,16}. Marine species are highly responsive to temperature change and can track changing isotherms with fewer barriers to dispersal, compared to terrestrial species^{3,14–19}. Moreover, the availability of thermal microrefugia is limited in the ocean, while in terrestrial ecosystems organisms can seek shade or burrow in soil to buffer the effects of warming ^{17,20} (Fig. 1). Therefore, biodiversity responses to temperature change are expected to be more immediate and directly detectable for marine ecosystems; this expectation is supported by a growing literature which has quantitatively compared individual species' responses to temperature change between marine and terrestrial realms^{3,14–16}. However, the net effects of temperaturerelated species' movements and abundance changes on assemblage-level diversity have not yet been systematically investigated across realms. Here, we quantify temperature-related species richness and total abundance change in marine and terrestrial assemblages across temperate regions of the planet (23.5°-60.0° absolute latitude; Fig. S1). Specifically, we test two predictions for the effects of temperature change on assemblage-level diversity: (1) species richness and total abundance will increase with

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warming, and such increases will be greatest across relatively warm regions that border the species-rich tropics; and (2) the coupling of assemblage and temperature change will be tighter in the ocean than on land. These predictions are informed by the interaction between the latitudinal gradients in species richness and warming tolerance, and the differences between realms regarding environmental heterogeneity and species distribution shifts (Fig. 1). We focus on local assemblage-level trends, rather than species-specific responses, and quantify changes in both total abundance and species richness. These two metrics can be decoupled from each other, and abundance is typically more responsive to environmental change than richness^{21,22}. We further disentangle richness change into species gains and losses to better understand the underlying dynamics of temperature-related biodiversity change. To test our expectations, we used the largest database of assemblage time series, BioTIME²³, which includes studies of plants, invertebrates, birds, mammals, and fish. These assemblages consist of co-occurring species systematically sampled through time. Since spatial extent varies among studies in BioTIME, we harmonized the biodiversity observations to a common spatial resolution to minimise the influence of variation in spatial extent on our results²⁴; this allowed us to quantify the effect of temperature change at a standardised resolution across regions and realms. We first estimated trends in biodiversity and temperature separately, and then quantified the relationships between the two. Specifically, for each study we allocated individual samples to 96 km² hexagonal grid cells based on their location (Methods; ²⁴); i.e., each sample was assigned to a specific combination of study ID and grid cell based on its latitude and longitude, resulting in equalextent assemblage time series with multiple samples across years. Each time series contained samples from only one study, thus the integrity of sampling methods within each study was maintained. We used these spatially harmonized assemblage time series in our analysis,

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selecting data from temperate regions only (since these are the better sampled regions within BioTIME). We then selected time series with at least five years of sampling (mean=9.2 years), yielding 21,500 assemblage time series across both realms (19,875 marine and 1,625 terrestrial from 156 original studies; Figs. S1 and S2, Table S1). Because the number of samples can vary from year to year within each time series, we used sample-based rarefaction²⁵ to equalise sampling effort among years and then quantified trends in richness, total abundance, and number of species gained or lost. For the same locations and for the time spans matching the duration of the biodiversity monitoring periods, we extracted mean monthly temperature records from HadCRUT4^{26,27} and estimated the corresponding rates of sea surface or air temperature change per year. We then quantified the relationships between changes in biodiversity and changes in temperature with meta-analytical Bayesian hierarchical models, allowing responses to vary among taxonomic groups. To test our expectations, we included an interaction term between temperature change and long-term average temperature (i.e., baseline climate) or latitude in our models, fitted separately for the marine and terrestrial realms.

Results

Temperature trends were highly variable, with locations at similar latitudes exhibiting different directions and magnitudes of change (Fig. 2a). Yet, both sea surface and air temperatures increased on average across the locations and time periods of our study, even though the majority of our time series spanned less than 10 years (Fig. S2). The warming signal was more pronounced on land than in the ocean (Fig. 2b; the average mean temperature change rate was $0.022\,^{\circ}\text{C}$ year⁻¹ on land, *versus* $0.012\,^{\circ}\text{C}$ year⁻¹ in the ocean).

Biodiversity change was also highly variable among the assemblage time series (Fig. 2c). Yet, despite the variability in both temperature and biodiversity trends, coherent macroecological signals emerged in the marine realm (Fig. 3, Table S2). We found an overall positive relationship between warming and species richness, but conditional on the baseline climate. Species richness increases were more pronounced in initially warmer locations (as indicated by the positive interaction effect), and underpinned by higher rates of species gains, while there was no detectable signal for species losses (Figs. 3, 4 and S3). Additionally, warming coincided with losses of individuals in the warmest marine locations, whereas cooler locations tended to gain individuals with increasing temperature (Figs. 3, 4 and S3). In contrast, no systematic biodiversity responses emerged on land, where the 95% credible intervals overlapped zero for all the biodiversity metrics included (Fig. 3, Table S2). Our analysis highlights the fundamental role of climate baselines in modulating biodiversity responses in the ocean, given that latitude showed no or very weak interacting effects with temperature change (Fig. S4). Further tests revealed only a weak correlation between either baseline climate or latitude and temperature change (Spearman's rank correlation ρ = 0.063 and 0.098, respectively). As such, the correlation structure of our covariates is unlikely to bias our results towards a positive effect of temperature change when combined with baseline climate rather than latitude. Our results were highly robust to a number of further sensitivity tests addressing biases in the BioTIME dataset, differences amongst covariates, and model structure. We found similar responses in the marine realm when using subsets of the marine data that match the number of locations and latitudinal range of the terrestrial data, despite increased uncertainty in model estimates (Fig. S5). Our results were consistent across different baseline temperature variables (long-term annual and maximum temperature, and annual mean temperature of the first year) and between different temperature databases for quantifying climate baselines (Fig.

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S4; see Methods). Additionally, we did not detect any systematic effect of the number of years sampled, temporal duration or start year of the time series on the estimated rates of biodiversity change (Figs. S6 and S7). Finally, there was no evidence for systematic differences in biodiversity responses among the different taxonomic groups (as estimated via the random slope model components; Figs. S8 and S9; complete model outputs with posterior estimates are shown in Tables S3-S6).

We reveal striking differences in warming-related biodiversity change between marine and

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Discussion

terrestrial realms across temperate regions, with a much stronger signature of warming on marine assemblages. Our results are unlikely due to confounding factors, given that climate change is poorly spatially correlated with other anthropogenic drivers of change for both marine and terrestrial realms²⁸. Further, temperature is expected to be a strong driver of biodiversity change given its fundamental role in biological processes^{29–31}. The warming-related increase in local marine species richness is consistent with the expectation that as the Earth's climate warms, temperate regions undergoing warming will receive an influx of species tracking suitable temperatures, and increases in warm-affinity generalists^{2,6,7,18,29}. This warming-related increase in species richness is likely, in part, underpinned by species from lower latitudes shifting their ranges poleward to avoid exceeding their upper thermal limits^{4,12,14}. Indeed, projected rates of extirpation in response to recent and future warming are highest for tropical marine species^{7,32}, which in turn are better able to track changing isotherms¹⁴. Here, we find that species gains outpaced losses in the warmest temperate locations in the ocean where temperature has also increased. This finding is consistent with asymmetrical responses between species range edges, with faster

colonisations expected following climatic niche expansion, and with slower extirpations linked to delayed responses at species trailing edges^{3,4}. The prevailing influx of species with warming is likely to lead to novel biotic communities and interactions as species distributions are re-shuffled, with potentially far-reaching consequences for ecosystems functioning^{3,7,32,33}. Our results further highlight that loss of individuals can occur simultaneously with increases in richness, emphasizing that temperature-related changes in richness and abundance can be decoupled. Abundance declines may be occurring for more thermally restricted species, owing to reduced performance and population declines, as critical thermal thresholds are crossed^{4–6}, for instance related to the adverse effects of increasing temperatures on metabolic rates and primary production^{29,34}. Influxes of climate immigrants can also drive local declines in populations due to greater grazing and predation rates^{35,36}. The abundance declines across our warmest temperate locations in the ocean suggest warming-related destabilization of populations possibly reflecting reductions in the carrying capacity of marine ecosystems. We also find strong interacting effects of the baseline climate on both abundance and richness change in the ocean, which responded in different directions in our warmest temperate locations. This highlights that rising temperatures in locations that are already warm can lead to greater assemblage restructuring. Our findings may reflect the patchiness in temperature regimes across similar latitudes, for example due to altitudinal or depth gradients, proximity to the coast, or ocean currents, and may explain why latitude is a poor predictor for assemblage-level changes in our analysis. Specifically, within the scope of our data, baseline climate better captured context-dependent spatial patterns, and allowed us to detect biodiversity change across pockets of warmer and colder areas within latitudinal bands. Baseline climate therefore emerges as a major predictor of temperature-related biodiversity change in marine systems, as recently also found by others^{14,18}. Specifically, marine species track isotherms more readily in initially warm waters¹⁴, which may be due to tropical species

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overall living closer to their upper thermal limits, and thus more promptly responding to warming trends.

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Overall, and despite faster warming on land, we did not detect systematic responses in richness or abundance with temperature change for terrestrial assemblages. The stronger responses observed for marine assemblages are consistent with reported faster range shifts in the ocean and higher sensitivity of marine organisms to temperature change compared to terrestrial species^{3,12,14–16}. Our findings are also consistent with warming-related local extirpations being twice as common in the ocean as on land¹⁵. The lack of systematic assemblage-level change associated with temperature change on land might be due to greater thermoregulation capacity and wider thermal safety margins of terrestrial taxa^{8,15,16}. Additionally, compared to seascapes, higher landscape complexity enables terrestrial species to exploit thermal microhabitats, thus allowing for the persistence of local populations for longer periods^{8,20}. Indeed, access to thermal refugia was reported to be a fundamental factor underlying the relatively low vulnerability of terrestrial ectotherms to warming, and emphasizes the potential deleterious combined effects of warming and land-use changes¹⁵. Finally, a weaker link between assemblage responses and temperature change on land may be due to other factors, such as land-use change and moisture availability, posing stronger constraints on local biodiversity. Nonetheless, the smaller magnitude or slower responses of terrestrial species to temperature change 11,12,15,24,37,38, combined with the faster rates of warming on land, indicate a potentially higher accumulation of climatic debt (i.e. response lags) among terrestrial versus marine taxa^{3,12,14,19,37,39–41}. Additional research with higherresolution temperature data matching the scale of organisms' responses is needed to better quantify terrestrial assemblages' responses to temperature change, and these developments remain a major challenge for many different taxa.

Our results warrant discussing some caveats. First, as commonly noted for biodiversity data, both taxonomic and geographic biases exist^{23,42}, with the majority of our data coming from the Northern Hemisphere, and disproportionately representing marine fish and terrestrial birds. Yet, we did not detect systematic differences in responses among the taxonomic groups in our data. Additionally, our ability to detect systematic trends on land may have been affected by the smaller number of terrestrial studies analysed, as illustrated by credible intervals often overlapping zero when using smaller subsets of marine data to estimate biodiversity change. The apparent inconsistency between our results and previous range shifts studies on land can be further reconciled by the different ecological levels at which such changes are being evaluated. As marine species track changing isotherms more closely than terrestrial species¹⁴, range shifts are more immediately translated at the assemblage-level in the ocean. On land, systematic effects on richness and abundance can be harder to detect given the general higher thermal tolerance and slower responses of terrestrial species. Our analyses represent a first step towards explaining divergent patterns of assemblage-level biodiversity change across the planet^{24,43}. Overall, our results provide strong support for the expectation that divergent biodiversity trajectories may arise as a consequence of global warming, with polar and temperate regions likely acting as "sinks", and tropical regions as "sources" 5,7,32. In turn, these responses could prompt a shift in the latitudinal diversity gradient towards higher latitudes, with faster rates of change in the ocean. While we focused here on temperate regions, tropical and polar biomes are predicted to undergo severe restructuring in response to temperature change, albeit along different trajectories^{5,7,12}. However, lack of sufficient biodiversity monitoring data for tropical and polar systems^{23,42} hampers a comprehensive assessment of assemblage-level responses to temperature change in these regions, which remains a key challenge for further research.

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Future global warming impacts on biodiversity are likely to exceed and potentially diverge from the changes revealed here^{7,32,34,44–46}. Indeed, initial increases in richness and abundance in response to warming may be followed by losses if warming continues^{6,47,48}. Declines in marine systems may affect food security and livelihoods of human populations that depend on the ocean^{6,49}. Additionally, while a consistent signal of temperature change was not evident on land, future impacts on terrestrial assemblages are expected from continuing rising temperatures, extreme heat events, fires, and lack of moisture^{34,45,50}. Because the Earth is committed to further warming, a systematic reduction of greenhouse gas emissions alongside efforts to further prevent habitat loss and improve habitat connectivity will be fundamental to allow species to track suitable climates across increasingly impacted land- and seascapes and to avoid severe biodiversity disruption and loss.

Methods

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Biodiversity data and trends 255 BioTIME²³ is currently the largest global database of assemblage time series, including 386 256 individual studies (Study ID; plus extended data sources) across different taxonomic groups, 257 258 holding over 12 million records of abundance for over 45,000 species. For this analysis, we 259 only included studies reporting counts of individuals per species in terrestrial and marine systems. We excluded freshwater studies as these are too few to confidently analyse 260 biodiversity trends across taxa and different regions. 261 Each study is comprised of distinct samples (i.e. individual plots, transects, tows, etc. 262 263 sampled at a given time), and the number of samples can vary among years within each study. As the spatial extent varies among studies, we gridded those studies that had large 264 extents and multiple sampling locations into hexagonal cells of ~96km²; many studies were 265 not partitioned because they were contained within a single cell²⁴. Specifically, each sample 266 was assigned to different combinations of study ID and grid cell based on its latitude and 267 268 longitude, resulting in new assemblage time series (each with multiple samples across years). These new time series were given a unique identifier that was the concatenation of the study 269 ID and the grid cell reference number, and thus contained samples from only one study -i.e. 270 271 the integrity of each study and each sample was maintained. This process allowed us to relate biodiversity and temperature trends at a standardized resolution. To minimise the effect of 272 unobserved species on estimates of biodiversity change, we calculated the abundance-based 273 274 coverage⁵¹ of each annual sample within each time series, and removed all samples with 275 coverage less than 0.85. To be able to reliably estimate biodiversity trends, we restricted our 276 analysis to time series sampled in at least five years (not necessarily consecutive). Because the number of samples can vary among years, we used sample-based rarefaction²⁵ to 277

standardise the number of samples among years for each time series before calculating the

biodiversity metrics. Specifically, we identified the minimum number of samples taken in each year within each assemblage time series; this minimum was then used to randomly sample each year down to that number of samples. Finally, given the paucity of data representing polar and tropical regions, we excluded these regions (based on absolute latitudinal cut-offs at 60° and 23.5°, respectively). This process yielded 21,500 assemblage time series representing 156 original studies (Fig. S1; Table S1) between 1900 and 2016, across 19,875 marine and 1,625 terrestrial locations. The average number of years sampled across the time series was 9.2 years, with the longest time series spanning 97 years (Fig. S2). To quantify rates of biodiversity change, we calculated linear trends over time for species richness (logS), total abundance (logN), number of species gains and species losses. Counts of gains and losses retained species identity information, and were quantified based on comparison with the first year sampled in each time series. For losses, a positive slope means the number of species lost from a location is increasing through time; negative slopes represent time series where the magnitude in species losses decreased over time. We repeated the sample-based rarefaction process described above 199 times for each time series, recorded the values and took the median for each biodiversity metric in each year, in order to reduce the effect of any outlier samples on our estimates. We used ordinary least squares regression because we were interested in the long-term direction and magnitude of the biodiversity trends, and to allow us to compare the rates of change among locations, realms and metrics. We retained the estimated slope and standard error for each time series for use in our second-stage meta-analytical models.

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We focus on temperature as a climate variable because of its influence on every level of
biological organization, from individual metabolic rates to biological communities' dynamics
and structure ^{29–31} . We extracted temperature records from HadCRUT4 ^{26,27} , specifically the
HadSST3 data for marine Sea Surface Temperature (SST) on a 1° resolution, and the
CRUTEM4 data for air temperature on land on a 0.5° resolution. We did not harmonize the
spatial resolution between the two data sources because we wanted to use the best available
data in each realm. For the location of each biodiversity time series, we extracted monthly
mean temperature records for the duration of the biodiversity monitoring period
(Year _{start} :Year _{end}), and estimated mean temperature trends using generalized additive models
(GAM), including a temporally autocorrelated error structure (package mgcv ⁵²). This also
allowed us to assess if accounting for seasonality within years would improve model
performance. We used AIC to compare models with and without "month", selecting the best
model for each time series. We extracted the linear slope from the model, which summarises
the trend for mean annual temperature change.
To test if biodiversity responses to temperature change were modulated by the baseline
climate at any given location, we extracted annual mean temperature data from the
WorldClim ⁵³ database for terrestrial time series, and from the Bio-ORACLE database ^{54,55} for
marine time series (on a resolution of 0.01° for terrestrial and of 0.1° for marine systems,
respectively). For each realm, we standardized the long-term annual mean temperature across
all the locations by subtracting the mean and dividing by the standard deviation.

Meta-analysis

Having estimated the trends for biodiversity and temperature independently for each individual
time series, we assessed the effect of temperature change on the rates of change of each
biodiversity metric in a second-stage analysis. We employed a meta-analytical Bayesian
framework using the package brms ^{56,57} (version 2.6.0), and fitted generalized linear models to
each realm separately, having initially evaluated that there was an effect of realm when fitting
a full model. All models were created using the Stan computational framework (http://mc-
stan.org/) accessed via brms. To determine whether the baseline climate modulated the
biodiversity responses, models were fit with an interaction term between temperature change
and the long-term average temperature at each location. Additionally, we fitted similar models
using latitude. We used two random effect terms: one allowing for different slopes per
taxonomic group (Taxon), and another allowing for different intercepts per study ID nested
within Taxon. This allowed us to account for: 1) potentially different responses to temperature
change among taxa; 2) differences in species richness among taxa, as well as different
assemblage time series originating from the same study, and different studies monitoring the
same taxonomic groups across the BioTIME database, respectively; and 3) spatial
autocorrelation. The different taxonomic groups were informed by the original data sources
metadata, and were: "Amphibians", "Benthos", "Birds", "Fish", "Mammals", "Marine
invertebrates", "Terrestrial invertebrates", "Terrestrial plants", and "Multiple taxa". "Multiple
taxa" refers to Study IDs where the sampling methodology captured multiple taxa
simultaneously. Additionally, taxonomic groups with only very few studies in BioTIME (e.g.
reptiles) were included in this group for practical reasons; we note this category represented
only 9% of the original studies and 5% of the standardised time series.

The overall model structure implemented for each realm was:

 Δ Biodiversity ~ 0 + Δ Temperature * Long-term average temperature +

 $(0 + \Delta \text{ Temperature} \mid \text{Taxon}) + (1 \mid \text{Taxon/StudyID}).$

The meta-analytical framework implemented allows the response variables to be weighted by their uncertainty; specifically we included the estimated standard errors for the biodiversity trends using the function se() when specifying the formula for the models, using the brms syntax 56,57 : Δ Biodiversity | se(Δ Biodiversity, sigma = TRUE). Additionally, a global intercept equal to zero was specified to reflect a scenario where there is no biodiversity change when all the independent variables are zero; i.e., the model assumes that no change in temperature would correspond to no change in the assemblage metrics for the average baseline climate (i.e. at the mean value across our data).

Models were run using four chains, each with 8,000 iterations, with a warm up of 4,000 and non-informative flat priors. Stan implements Hamiltonian Monte Carlo and its extension, the No-U-Turn Sampler (NUTS) algorithms, which converge quickly⁵⁷. Convergence was assessed by visually examining trace plots and using Rhat values (the ratio of the effective sample size to the overall number of iterations, with values close to one indicating convergence)⁵⁷. All the analyses were run in R version 4.3.1⁵⁸.

Sensitivity analysis

To evaluate the robustness of potential interactions with the baseline climate, we additionally ran our models with two alternative baseline temperature variables. To that end, we extracted the variables "Mean Temperature of Warmest Quarter" from WorldClim and "Long-term maximum sea surface temperature" from Bio-ORACLE, as well as the average temperature

in the first year sampled for each biodiversity time series from the same dataset that was used to quantify the trends (i.e. the spatially less resolved HadCRUT4 dataset).

To evaluate whether uneven sampling could be driving the observed differences between the marine and terrestrial realms, we fitted models to subsets of the marine data that matched both the number of locations (1,625 time series) and the latitudinal range of the terrestrial data. We did not attempt to control for temperature change differences between realms because this is part of the signal to be modelled. We fitted the meta-analytical models to 100 random subsamples for each biodiversity metric, illustrating that the estimates for the marine realm are robust (Fig. S5). This analysis also illustrated that a smaller sample size may have affected our ability to detect systematic biodiversity changes on land, given that confidence intervals overlapping zero occurred for several of the meta-analytical models fit to subsets of the marine data matching the number of terrestrial time series. We further evaluated that biodiversity responses did not show any clear pattern as a function of the number of years sampled, duration and start year of the time series. Although shorter time series tend to show higher rates of biodiversity change, these also tend to have higher standard errors, which are in turn accounted for within the meta-analytical framework. We further note there were no notable differences in the estimated rates of biodiversity change as a function of number of sampled years between marine and terrestrial time series. Thus, we believe the temporal heterogeneity of sampling in our data is very unlikely to drive our findings (Figs. S6 and S7).

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392	Author contributions
393	M.D. and A.M.S. conceived the idea, and all authors contributed to design the project. L.H.A
394	analysed the data in close consultation with S.A.B., A.E.B., M.D. and A.M.S L.H.A. wrote
395	the first draft of the manuscript. L.H.A., A.E.B., M.D., A.M.S., S.A.B., C.W., S.R.S. and
396	A.E.M. all contributed to manuscript completion and revision. M.D. and A.M.S. are shared
397	senior authors.
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400	Data Availability
401	All the data can be accessed through the BioTIME database on Zenodo
402	(https://doi.org/10.5281/zenodo.1211105) or through the BioTIME website (http://biotime.st
403	andrews.ac.uk/).
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406	Code Availability
407	Code to reproduce the analysis is available on GitHub
408	(https://github.com/lauraantao/Temp_Biodiv_Change) and in an online archive at Zenodo ⁵⁹ .
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411	Competing interests
412	The authors declare no conflict of interest.
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Acknowledgements

We are grateful to all the scientists, data collectors and their funders for making data publicly available. We thank the University of St Andrews Bioinformatics Unit (Wellcome Trust ISSF grant 105621/Z/14/Z). L.H.A. acknowledges funding from PBL Netherlands Environmental Assessment Agency, as part of the GLOBIO project (www.globio.info), and from the Jane and Aatos Erkko foundation. A.E.B. was supported by the Canada Research Chairs Programme. S.A.B. acknowledges the support of the German Centre of Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig (funded by the German Research Foundation; FZT 118). C.W. was supported by the Natural Environmental Research Council (grant number 563 NE/L002531/1). M.D. is funded by a Leverhulme Fellowship and by the John Templeton Foundation (grant #60501 "Putting the Extended Evolutionary Synthesis to the Test"). The BioTIME database was created using funding from the European Research Council (AdG BioTIME (250198) and PoC BioCHANGE (727440) granted to A.E.M.), and we also acknowledge funding from the Leverhulme Centre for Anthropocene Biodiversity. We thank Gergana Daskalova for valuable input on an early draft of the manuscript and suggestions for the figures. The two icons in the figures are from the Noun Project under CCBY license: *land* by Alexander Skowalsky, and *wave* by B. Farias.

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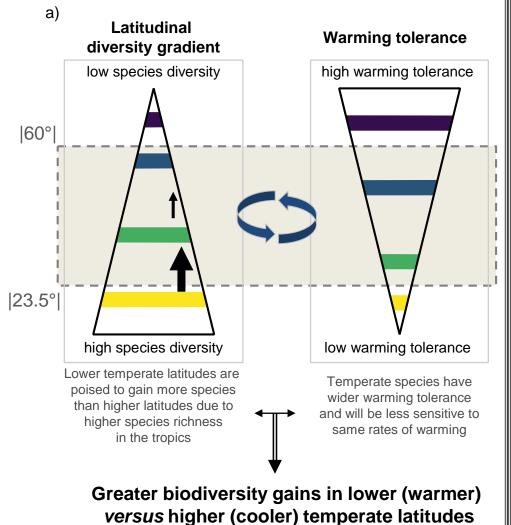
Figure Legends

Figure 1. Conceptual figure of the mechanisms underlying our hypotheses for how temperature-related biodiversity change may unfold unevenly across the planet, stemming from the (a) latitudinal gradients in species diversity (decrease with latitude) and species thermal tolerances breadths or thermal safety margins (TSM; increase with latitude); and (b) differences between marine and terrestrial realms in terms of environmental heterogeneity and geographical range shifts. Note this is a schematic simplified representation of these large-scale mechanisms and patterns (for instance, TSMs are not necessarily linear with latitude 15, and heat tolerance declines more steeply with latitude for marine ectotherms 60).

Figure 2. Variation in temperature and local biodiversity trends across the time series (marine in blue, n= 19,875; terrestrial in green, n= 1,625). (a) Each dot indicates the rate of temperature change (°C year-1) for a specific time series, coloured according to the long-term average temperature. There was no clear latitudinal pattern in temperature change: while the majority of locations in both realms experienced warming, and more so for terrestrial locations (b), many locations underwent cooling during the period examined. Local biodiversity change estimates (rate year-1) also exhibited wide variability (c) (note the different scales for the different metrics; x-axes were truncated to improve clarity). Tick dashed vertical lines indicate the overall mean per realm in all the density plots. The biodiversity time series locations cover numerous habitats and biomes, and sample a large range of the planet's long-term average temperature gradient (although most data originate from the Northern Hemisphere; Fig. S1).

Figure 3. Biodiversity responses to temperature change and its interaction with long-term average temperature (i.e. baseline climate). Marine locations (blue) exhibited stronger responses compared to terrestrial locations (green), while baseline climate modulated these responses in divergent directions. The main effects of baseline climate were negligible, and are not shown. Bars represent the estimated parameters and whiskers indicate the 95% credible intervals from the Bayesian meta-analysis (note the different scales for the different metrics); estimated parameters were considered to represent signals in the responses when the credible intervals did not include zero (Table S2; see Tables S3-S6 for complete model outputs).

Figure 4. Biodiversity responses to the combined effect of temperature change and baseline climate. Each panel depicts the rate and direction of biodiversity change depending on the temperature change experienced (cooling *versus* warming) and on the long-term average temperature (colder *versus* warmer), where red indicates positive slopes for the biodiversity response, and blue indicates negative slopes (note the different scales across the different metrics), for marine (top row) and terrestrial realms (bottom row). Grey dots represent the distribution of data along the two axes. Stars indicate when the 95% credible intervals for the interaction term from the meta-analytical models did not overlap zero (Fig. 3, Table S2).



b) Geographic range shifts and Landscape versus seascape heterogeneity terrestrial marine Temperature Arrows indicate New range asymmetrical Old range edge shifts Greater microclimate variation Greater connectivity (less and higher availability of barriers) in seascapes thermal microrefugia in versus landscapes landscapes versus seascapes

Tighter coupling of assemblage and temperature change in the ocean than on land

Figure 2

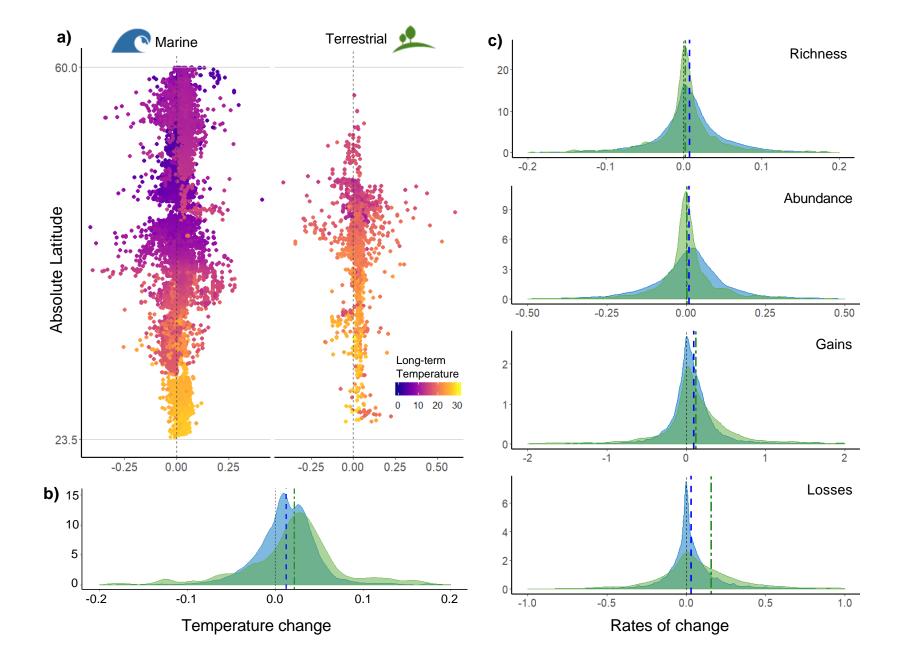


Figure 3

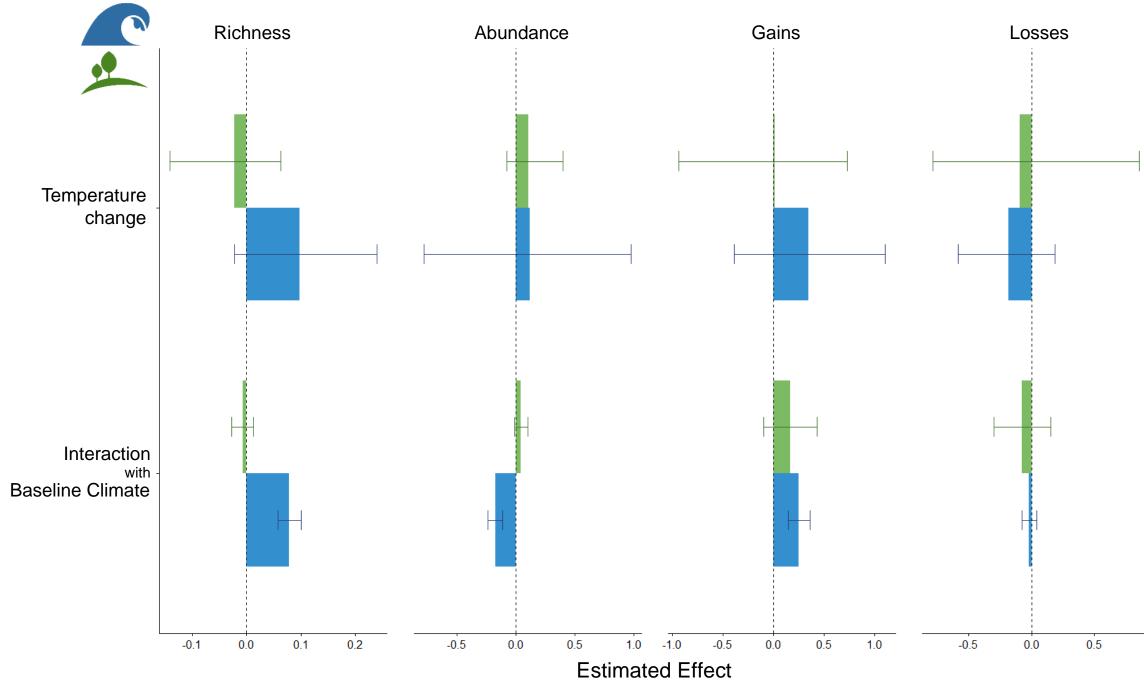


Figure 4

