The forecasted mean of 80 percent of wild populations and communities shows no change, and why

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Abstract

Broad-scale shifts in biodiversity demand a deeper understanding of both historical and future time trends across the Tree of Life. Retrospective analyses indicate that some groups, such as birds, fishes and insects, have experienced significant declines in recent decades. Broader investigations, on the other hand, reveal a more complex picture, with declines and increases roughly balanced. Here, we address the prospective task to statistically forecast biodiversity trends and assess our ability to do so based on available data. We analyzed approximately 43,000 population-level and 10,000 community-level time series from localities across the globe and covering taxa across the Tree of Life. Using unobserved components models and model selection, we found that only 23.5% of wild populations exhibit forecasted time trends (increasing and decreasing ones roughly balanced), while 76.5% show a forecasted constant mean. For communities (temporal α- and β-diversity), this figure rises to 84.0%. To explore the underlying reasons for the high prevalence of forecasted constant means, we used machine learning techniques (random forest models and SHAP analysis). We identified high variation in the rate of change (RoC) in the time series as the most important predictor of a forecasted constant mean. Further, life-history traits and locality accounted for 39.6% of the variation in the RoC variance of anmiotes, and sampling unit explained 44.4% of that variability for dicot plants. In summary, despite time trends being identifiable in ecological time-series data, parsimonious statistical models will very often suggest a forecasted constant mean. Our results offer a tempered perspective that can help realistically inform stakeholders and the general public, and guide the assessment of conservation action outcomes.

Keywords: biodiversity; machine learning; predictions; random forest models; SHAP analysis; state-space models; time series analysis.

Introduction

Since E. O. Wilson's seminal book "The Diversity of Life" (1992) – published the same year as the United Nations "Earth Summit" held in Rio de Janeiro – a growing body of research has chronicled an accelerating biodiversity crisis (e.g. Dirzo et al. 2014, and references therein). Numerous studies document alarming shifts in species' abundance and genetic diversity, in community composition, and in extinction rates. However, whether these trends amount to an impending or unfolding "sixth mass extinction" is contested. For example, Wiens and Saban (2025) show that, although contemporary losses are elevated relative to long-term baselines, they lack the catastrophic severity characteristic of past mass-extinction events.

Retrospective temporal analyses of recent biodiversity changes have shown that some taxonomic groups in particular have experienced large declines: examples come from birds (e.g. Rosenberg et al. 2019), fishes (e.g. UNEP-WCMC 2024) and insects (e.g. Hallmann et al. 2017). Broader studies, on the other hand, have found that the picture of biodiversity trends is more nuanced than a narrative of a pervasive decline implies, with no net change at local scales, and with declining and increasing trends roughly balanced (Dornelas et al. 2023, and references therein). At the same time, dozens of databases have been designed and made publicly available, which contain many thousands of time series at the population and community levels (also referred to as assemblages), spanning a wide range of taxa and localities globally (e.g. Johnson et al. 2024, and references therein). These data collections offer an unprecedented opportunity to investigate biodiversity changes at different temporal and spatial scales. Partly based on these databases, several authors have explored why reported biodiversity trends diverge so widely. One reason involves the diversity of definitions, methods, and approaches adopted (Boënnec et al. 2024). A second reason is methodological, such as the common neglect of correlation structures in the data (Johnson et al. 2024) and the presence of mathematical biases (Toszogyova et al. 2024) when computing summary trends. A third reason involves heterogeneity among the time series datasets. Although an impressive volume of records is now available for studies of biodiversity change, these data vary greatly in their temporal extent, reliability and the types of biodiversity attributes they measure (e.g. Toszogyova et al. 2024).

Prospective studies on expected biodiversity trends primarily focus on capturing the effect of human-caused drivers, including climate change, on future population and community states (e.g. Urban et al. 2016, Dietze et al. 2024). These prospective studies often rely on long-term scenario-based projections of environmental changes, for example projected climate change responses over the next several decades. Studies indicate that if current trends in human-caused stressors continue or worsen in the absence of significant conservation interventions, many systems might experience local biodiversity declines on the order of 10–20% over the next few decades (e.g. Newbold et al. 2015, IPBES 2019). In contrast to long-term projections, several authors have recently stressed the importance of near-term forecasts (i.e. a forecast horizon of at most a decade), not least to match the typical timescale of decision-making in biodiversity conservation management (Wood et al. 2018, Tulloch et al. 2020, Dietze et al. 2024). But despite this change of timescale to better and more actionably understand expected biodiversity trends, developing process-based approaches encompassing mechanistic links between stressors, populations and ecosystems remains a formidable task. We agree with Lasky et al. (2020) who question the usefulness to include processes from a multitude of fields (such as ecophysiology, evolutionary biology, demography): "We argue that answering this critical question is ultimately an empirical exercise requiring a substantial amount of data that have not been integrated for any system to date."

The number of studies making and reporting near-term statistical forecasts is rapidly growing (Lewis et al. 2022). Broad assessments across localities, realms and taxonomic groups, on the other hand, continue to be rare. Compared to retrospective biodiversity trend analyses, the currently available data collections have not yet been used extensively to construct a coarse forecasting baseline, against which more refined and system-specific approaches can be evaluated. Some of the studies focusing on forecasting have analyzed single taxonomic groups or realms (Harris et al. 2018, Olsson et al. 2025). Other studies have used several data collections to either assess the performance of forecasting models (Ward et al. 2014, Johnson et al. 2024) or to investigate the concept of predictability in ecology and conservation (Pennekamp et al. 2019, Bozzuto and Ives 2024). Predictability-related methods, however, are mainly insightful when analyzing time series spanning at least 20 years (Bozzuto and Ives 2024). A considerable fraction of currently available data collections, unfortunately, consists of (very) short time series. For example, in the widely used BioTIME database, only about 50% of the time series span more than seven years, and some only two years (Dornelas et al. 2025). We can expect that adapting approaches from climate change science will significantly improve our ability to predict expected biodiversity changes at different spatial and temporal scales using mechanistic models (Dietze et al. 2024). But for the

time being, we need answer a simple question: What do parsimonious, robust statistical models show about expected near-term biodiversity trends from typical ecological time series?

For this study we analyzed approximately 43,000 population-level and 10,000 community-level time series from 64 taxonomic classes nested within 6 kingdoms, with time series from throughout the world. We found that for the majority of populations and communities, parsimonious statistical models show a forecasted constant mean rather than a directional time trend. We then investigate important drivers of this result to determine what are the characteristics of typical ecological time-series data to this result. Our findings do not argue against the possibility of future biodiversity loss. They do, however, challenge the prevailing narrative that past trends are expected to "automatically" continue. We show that, based on data from high-profile databases, the most frequent parsimonious forecast is for no expected change, even though trends may be visible in the data.

Materials and methods

Time-series data

We used time-series data from ten different sources/databases (see Appendix S1: Table S1 for additional details, including access information): BioTIME (Dornelas et al. 2025), GBIF (Filippova et al. 2024), GPDD (Prendergast et al. 2010), LPI (Loh et al. 2005), LTER (Richter 2023), MASTREE+ (Hacket-Pain et al. 2022), RivFishTIME (Comte et al. 2021), TREAM (Welti et al. 2024), Swiss long-term phytoplankton data (Pomati et al. 2020), and Swiss long-term macrofungal data (Egli et al. 2006). To avoid the potential repeated inclusion of the same time series, we used each data collection for a specific taxonomic group and/or realm. Moreover, where possible we used a data collection for either population-level or community-level analyses. We achieved an almost global coverage for population-level data (Appendix S1: Figure S1; community-level: Appendix S1: Figure S2), and a broad population-level taxonomic coverage with 64 classes nested within six kingdoms (Appendix S1: Figure S3; community-level: Appendix S1: Figure S4).

We analyzed time series spanning at least 5 years. We allowed a proportion of missing values of at most 25% (of which at most 50% occurred consecutively), and we excluded binary data (e.g. presence-absence time series). We required the first and last time series value to be present (not missing) and non-zero (Toszogyova et al. 2024). Unless time series had already been transformed and contained negative values, we transformed the data using the inverse hyperbolic sine function. This transformation resembles the log-transformation for positive values, but can handle zeros. Finally, we z-transformed all resulting time series. In Appendix S2: Section S1 we provide additional details on data preprocessing.

At the community-level we considered two biodiversity metrics covering temporal α-diversity and temporal β-diversity. We only analyzed communities with at least 5 species (populations). To construct α-diversity time series, we computed year-specific Hill numbers (Dornelas et al. 2014). In particular, we used the ${}^{1}D$ metric which is the exponential of the Shannon entropy. To construct β-diversity time series, we compared each pair of temporally consecutive community compositions and quantified their similarity using Ruzicka's metric (Cha 2007). This metric is related to Jaccard's similarity metric, but additionally accounts for population abundances instead of identities alone. We then transformed these time series for further analysis as described above for populations.

Unobserved components models and model selection

Unobserved components models (UCMs) are univariate state-space models which are widely used in many fields of science, including ecology (e.g. Harvey et al. 1997, Durbin and Koopman 2012, Auger-Méthé et al. 2021) . They are flexible, explicitly separate measurement error from process error, can handle missing values, and accommodate nonstationary dynamics without the strict assumption of stationarity that is common in other time series frameworks. As a template for our four UCMs, we used the local linear trend model given by

$$y_t = m_t + \varepsilon_t, \qquad \varepsilon_t \sim N\left(0, \sigma_\varepsilon^2\right), \qquad \text{eq. 1a}$$

$$m_{t+1} = m_t + s_t + \xi_t, \qquad \xi_t \sim N\left(0, \sigma_\xi^2\right), \qquad \text{eq. 1b}$$

$$s_{t+1} = s_t + \zeta_t, \qquad \zeta_t \sim N\left(0, \sigma_\zeta^2\right). \qquad \text{eq. 1c}$$

Eq. 1a relates the unobserved true mean m_t to the data, y_t, with measurement error. The true mean (eq. 1b) evolves as a random walk and drifts due to a slope which also evolves as a random walk (eq. 1c). Depending on the variances included, many different UCMs can be constructed based on the local linear trend model. Preliminary investigations showed that the full local linear trend model (eq. 1a-c) almost never was selected as the best-fitting model for our collection of time series. Thus, for our analysis we selected the following four models.

- *Deterministic constant*: This is the baseline model, with only eq. 1a included and where $m_t \equiv m$ is a constant. For this model, a single variance has to be estimated.
- *Deterministic trend*: This model includes both the measurement equation (eq. 1a) and the mean equation (1b), which however evolves deterministically. Therefore, $s_t \equiv s$ and $\sigma_\xi^2 = \sigma_\zeta^2 \equiv 0$, so that only one variance is estimated (eq. 1a).
- *Local level*: This model includes both the measurement equation (eq. 1a) and the mean equation (1b). The mean evolves stochastically as a random walk, but there is no stochastically changing slope. Therefore, $s_t = \sigma_\zeta^2 \equiv 0$, and two variances are estimated (eq. 1a-b).
- *Smooth trend*: This model includes all three equations (eq. 1a-c). However, the mean equation has no stochastic variation of its own. Therefore, $\sigma_\xi^2 \equiv 0$, and two variances are estimated (eq. 1a, 1c).

For each population or community time series, we fitted all four models and selected the best-fitting one using AIC corrected for small sample size (AICc).

Two of our models produce forecasts with no time trend (the deterministic constant model and the local level model), whereas the other two models will allow the forecasted mean to include a linear time trend. But whether the forecasted mean is constant or changes linearly, fitted UCMs can show a stochastic trend over the timespan of the data. To illustrate this, we analyzed the Eastern monarch butterfly population (Figure 1; Appendix 1: Section S1) (e.g. Zylstra et al. 2021). Each row shows a selected period of the whole time series (Figure 1a-b), and for each timespan we show all four model fits and include ΔAICc values, where a value of zero designates the best-fitting model. The left column in Figure 1 shows the two models with a forecasted constant mean, whereas the right column shows the two models with forecasted linear trends. We highlight three aspects. First, for the full time series (Figure 1a-b) and the one up to year 2018 (Figure 1c-d), the local level model is the best-fitting one. Here, the mean evolves stochastically and follows the data, including turns (2013, 2018). But because we can have no knowledge about future stochastic deviations (eq. 1b), the logical and robust consequence is a forecasted constant mean.

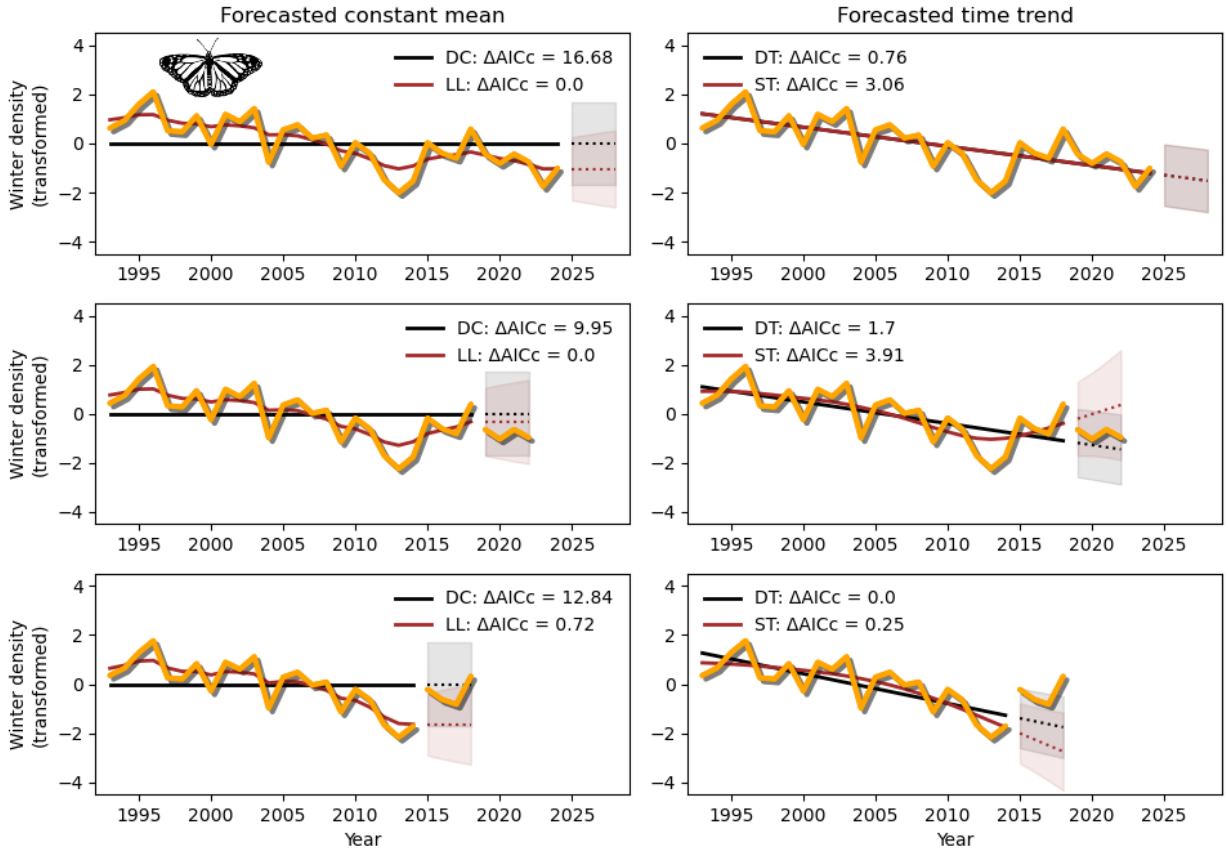

Figure 1. Eastern monarch butterfly population: dynamics and forecasts. Panels (a-b) show the complete time series (up to 2024), along with reconstructed mean trajectories and forecasts based on our four models. Panels (c-d) and (e-f) show the analogous results, however, assuming a shorter timespan (up to 2018 and 2014, respectively). The left column shows the fits of the two models exhibiting a constant forecasted mean: deterministic constant model (DC) and local level model (LL). The right column shows the fits of the two models exhibiting a forecasted linear time trend: deterministic trend model (DT) and smooth trend model (ST). All legends show model name abbreviations along with ΔAICc values, where a value of zero designates the best-fitting model. All forecasts are shown for 4 years ahead, including 90% confidence intervals. Icon: public domain (www.phylopic.org).

Second, AICc as a selection metric covers all aspects of the fit, and it might not always confirm our "visual intuition". Despite the smooth trend model and its increasing forecast seem to confirm that after the monarch population hit its bottom in 2013/14 and increased again afterwards (Figure 1d), the local level model is the better model to explain the data up to 2018, and thus delivers the most parsimonious forecast. In fact (and unfortunately), the increasing period ended in 2018. Third, forecasting is not

foreseeing: when only analyzing data up to year 2014, the best-fitting model is the deterministic trend model with a forecasted mean continuing to decline. Needless to say, nobody could have anticipated the sharp increase in 2015. Here, even if the local level model (as second-best model) suggests a forecasted constant mean, its forecasted variance equally well (or better) captures the unforeseeable turn in dynamics. In sum, selecting the best-fitting model can lead to a forecasted constant mean, despite stochastic increases or decreases in the data.

Analyzing the high prevalence of forecasted constant means

To investigate what best explains the unbalanced proportion of populations with forecasted constant mean vs. linear trend (see the *Results* section), we used a random forest classifier (Breiman 2001, Cutler et al. 2007). Two main advantages over similar methods like a logistic regression are that the algorithm automatically considers nonlinear effects and interaction effects among predictors (henceforth called features). We analyzed population-level and community-level results separately. For each set, we split all analyzed instances into a training and a test set, the latter one used for out-of-sample predictions. Because the target data were already imbalanced, we refrained from splitting the time-trend instances into declining vs. increasing categories – doing so would have further skewed the class balance and reduced sample support in each group.

Our selected features cover different aspects of the populations, communities and the analyzed data. To roughly summarize the time series dynamics, we first computed first-differences of the transformed time series; from eq. 1a, these are the differences $y_t - y_{t-1}$. Based on these differences (rates of change, RoC), we computed the mean(RoC) and the var(RoC) and included these two metrics as features. To capture "data quality", we included three features: time series length (henceforth 'length'), proportion of non-missing values (henceforth 'p(data)'), and proportion of unique (non-missing) values (henceforth 'p(unique)'). Furthermore, we included locality (coordinates) and taxonomic information. We matched all taxonomic data with the GBIF backbone taxonomy (https://doi.org/10.15468/39omei), and we then used the first four components from a PCA, based on one-hot-encoded taxonomic data. In Appendix S2: Section S2 we provide more details on data preprocessing and feature selection.

Subsequently we used the trained random forest classifier to investigate feature importance in terms of predicting a constand vs. linearly changing forecasted mean. Hereto, we computed SHAP values (Shapley Additive ExPlanations values), a meanwhile widespread approach to explain machine learning models (Lundberg et al. 2020, Molnar 2025). Simply put, for each instance (e.g. a population) the respective prediction is compared to the overall average prediction, and based on game-theoretic methods

the influence of each feature is computed to best explain the difference between the instance-specific prediction and overal average prediction. Advantages over alternative ways to compute feature importance include the additive nature of SHAP values (for example to group features), their consistency (features that add more value to a prediction yield higher SHAP contributions), and their local reliability, that is, providing instance-level insights that aggregate to global interpretations (Molnar 2025). SHAP values have the same units as the target variables: for a classification, they are measured in log-odds. In our analysis, the sign and magnitude of the SHAP values jointly influence the predictions: positive values push predictions towards a forecasted constant mean, and negative values towards a forecasted time trend.

Understanding the drivers of important features

The SHAP analysis allows ranking features based on their importance, and var(RoC) emerged as the most important driver of the type of forecasted mean (see the *Results* section). As a further step, we investigated interaction effects among features, and we used random forest regressors to investigate important predictors of var(RoC). A random forest regressor offers the same advantages as a classifier (see preceding subsection), with the target variable now being continuous instead of binary. We fit two different regressors with features we anticipated would affect var(RoC). First, sampling unit: we compared time series of reproductive output (e.g. pine cone counts) versus time series of, for example, counts of individual adults. We expected sampling unit to affect the amount of fluctuations in the data, in turn affecting var(RoC). Based on auxiliary data we could find, we analyzed population-level time series from the taxonomic class Magnoliopsida (dicots; n = 4,268), with reproductive output data stemming from MASTREE+ (Hacket-Pain et al. 2022), and all other time series from BioTIME (Dornelas et al. 2025) (Appendix S1: Table S1). Second, life history characteristics and locality: we expected population fluctuations to be associated with life history traits and locality (Albaladejo-Robles et al. 2023, and references therein), and consequently affecting var(RoC). Based on available auxiliary data, we restricted our analysis to amniote populations (birds, mammals, and reptiles; n = 6,916). In addition to the populations' locality, we included four life-history traits (Myhrvold et al. 2015): age at maturity, maximum lifespan, body mass, and yearly reproductive output. In Appendix S2: Section S3 we provide more details on the auxilliary data and data preprocessing.

Results

Forecasted dynamics of populations and communities

After fitting the unobserved components models and retaining time series with no missing attributes for the subsequent classification (next subsection), we grouped time series according to the type of forecasted mean of the respective best-fitting model: forecasted time trend (deterministic trend model and smooth trend model) vs. forecasted constant mean (deterministic constant model and local level model). We found that only 23.5% of populations had forecasted time trends (increasing and decreasing ones roughly 12% each), while 76.5% had a forecasted constant mean (Table 1). For communities, this figure rises to 84.0%, with a negligible difference between temporal α- and β-diversity time series. The simple baseline model (deterministic constant model) with a forecasted constant mean was selected as best-fitting model for 51.2% of the population-level and 69.6% of the community-level time series (Table 1).

Table 1. **Overview of forecasted mean results**. The columns give: *n*, number of time series; *p*(constant mean), the percentage of time series with a forecasted constant mean; *p*(time trend), the percentage of time series with a forecasted linear trend; *p*(baseline), the percentage of time series in which the baseline model (deterministic constant model) is the best-fitting model.

	n	*p*(constant mean)	*p*(time trend)	*p*(baseline)
Populations	43,403	76.5 %	23.5 %	51.2 %
Communities				
total	10,409	84.0 %	16.0 %	69.6 %
α-diversity	5,098	84.6 %	15.4 %	64.6 %
β-diversity	5,311	83.4 %	16.6 %	74.7 %

Explaining why forecasted constant means are most common

To investigate what biological and data-related characteristics drive the dominance of a forecasted constant mean, we first fit a random forest classifier with the type of forecasted mean as the dependent variable, followed by a SHAP analysis. The trained random forest classifier achieved good predictive ability, with a weighted average f1-score of 0.82 (Appendix S1: Table S2). The model, however, was much better at predicting forecasted constant means (class 1; f1-score: 0.88) than forecasted time trends (class 0; f1-score: 0.65), despite explicitly accounting for class imbalance (76.5% vs. 23.5%; Table 1).

28.7% of the actual time series with forecasted time trend were misclassified as having a forecasted constant mean, while 14.9% of the time series classified as having a forecasted time trend were actually constant-mean cases. One reason might be the diffuse boundaries of feature values between the two classes (Appendix S1: Figure S5). A second reason might be the limited support for time series with forecasted time trends, due to class imbalance (Appendix S1: Table S1). A third reason might be that the features used here are less suited to explain forecasted time trends (see the *Discussion)*.

The SHAP analysis at the population-level showed that the most important feature driving a predicted forecasted constant mean vs. time trend is the variation in the rate of change in the data, var(RoC), followed by mean(RoC) and time series length (Figure 2). The results at the community-level are very similar (Figure 2). For these importance rankings, we computed the mean absolute SHAP value per feature. In Appendix S1 we show the detailed SHAP value results: their distribution per feature (Figure S6); as a function of the respective feature values (Figures S7-S8; non-aggregated features); visualizations for aggregated features (taxonomy: Figures S9-S10; locality: Figures S11-S12).

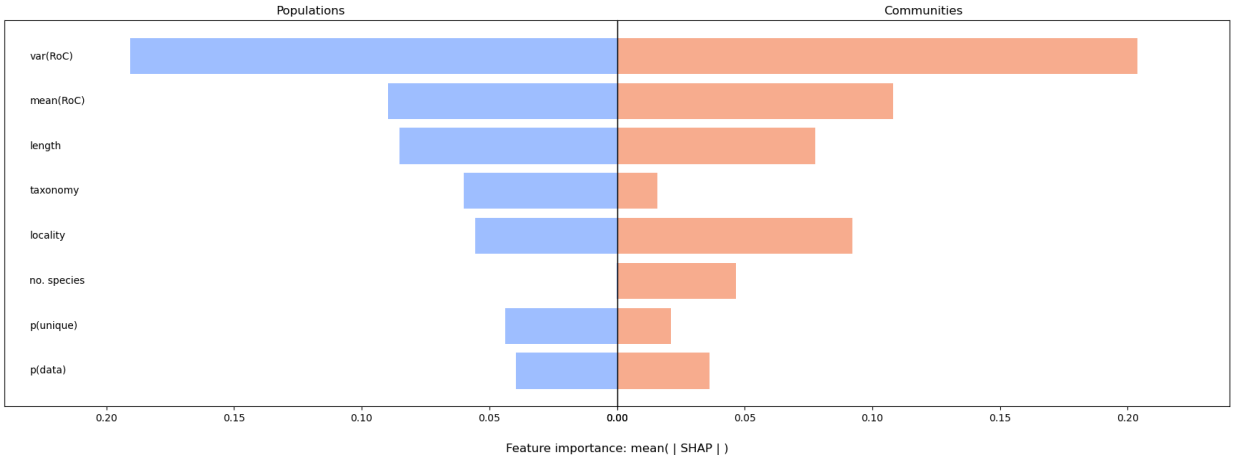

Figure 2. **Feature importance values from the random forest classifiers**. For each feature in the model, the mean absolute SHAP value is shown separately for population-level and community-level predictions. Note that the features 'locality' and 'taxonomy' are aggregated (i.e. summed effects): 'locality' represents coordinates, and 'taxonomy' comprises four PCA components.

Both metrics var(RoC) and mean(RoC) – roughly capturing the dynamics in the time-series data – account for approximately 50% of the total importance. Time series with high yearly fluctuations are more likely to be associated with a forecasted constant mean (Figure 3a), and we find the same association for (very) low-magnitude mean(RoC) values, as well as high-magnitude mean(RoC) values

(Figure 3d). As for time series length (Appendix S1: Figure S7-S8), short time series tend to be identified as having forecasted means containing time trends, while longer time series have an increased probability of a forecasted constant mean. Despite other data characteristics playing a less important role on their own (Figure 2), they partly contribute – via interactions – to the importance of var(RoC) and mean(RoC).

What drives var(RoC)?

A multitude of factors can influence the extent of yearly fluctuations of populations and communities, ranging from life-history characteristics to environmental drivers like climatic conditions, harvesting and land-use change, and community-specific species fluctuations, just to name a few. From a more technical perspective, one source contributing to var(RoC) in driving the type of forecasted trend are interaction effects with other features. These interactions can be visualized by plotting SHAP values for var(RoC) and mean(RoC) while coloring points according to the values of other features (Figure 3). These visualizations reveal, first, that short time series increase the likelihood of a forecasted time trend for a given low var(RoC). Moreover, short time series increase the likelihood of a forecasted constant mean for a given high var(RoC). For mean(RoC) short time series make up the bulk of high-magnitude trends in the data and push predictions towards a forecasted time trend. Second, the proportion of non-missing data – despite being of secondary importance overall (Figure 2) – tends to affect predictions in two ways via interaction effects. For high var(RoC) values, missing values in the data decrease the likelihood of a forecasted constant mean. For mean(RoC), on the other hand, missing data make up the bulk of high-magnitude trends in the data and tend to push predictions towards a forecasted constant mean.

An additional interaction with var(RoC) stems from taxonomy. The overall importance of taxonomy to explain predictions is moderate (Figure 2), although some insightful patterns in the Tree of Life are already revealed (Figure 4a), like the higher proportion of forecated time trends in vertebrates compared to invertebrate phyla. In terms of an interaction effect, in Figure 4b we show how population-level var(RoC) values are associated with all taxonomy-related data, resolved at the taxonomic rank of class. In both panels of Figure 4 we only show classes with at least 10 populations (41 out of 64 classes; *cf*. Appendix S1: Figure S3), for better mean values. The differences in var(RoC) at the kingdom level are minimal, but differences build up markedly towards classes. Already at the phylum level var(RoC) differs markedly between invertebrate and vertebrate animals or between mosses (*sensu latu*) and vascular plants.

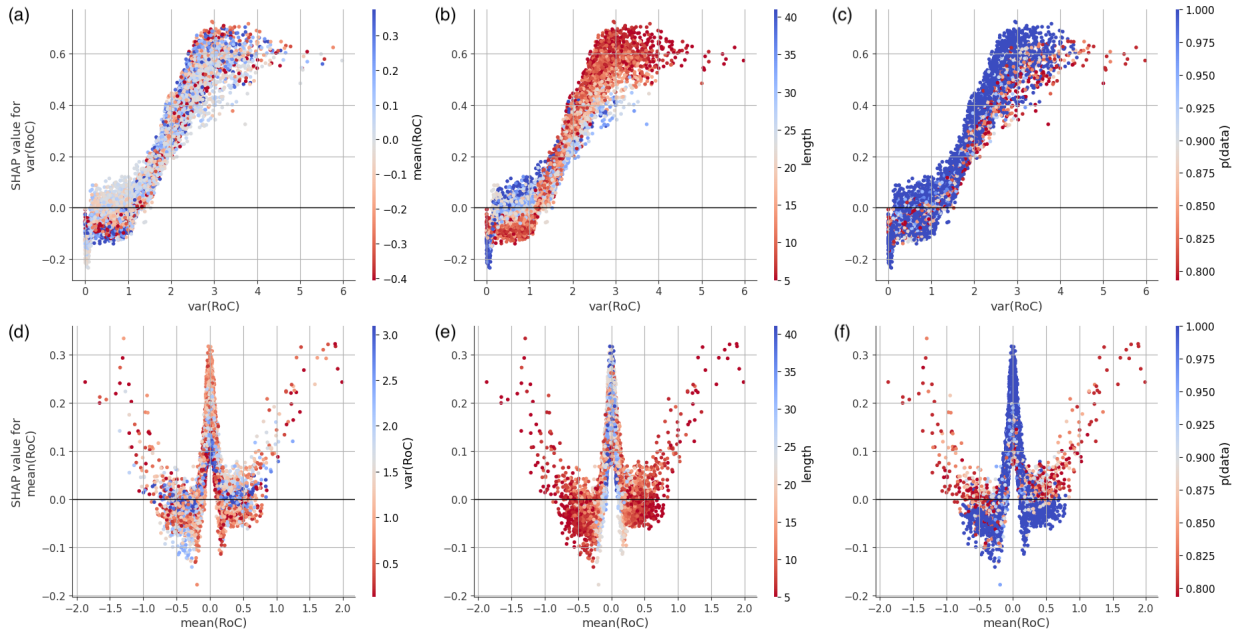

Figure 3. **SHAP values and feature interactions**. For the population-level time series, panels (a-c) show SHAP values of var(RoC) plotted against its values, and panels (d-f) show SHAP values of mean(RoC) plotted against its values. In addition, the data in each panel are colored based on the values of a different feature (colorbar labels) to visualize interactions among features.

At the low end of average var(RoC), vertebrate classes (phylum Chordata) stand out, exhibiting low to medium annual fluctuations. To explore what drives this variability within vertebrate populations, we fitted a random forest regressor using four life-history traits and locality as predictors. The model explained R^2 = 39.6% of the variation in var(RoC) (range-normalized RMSE: 16.1%). Appendix S1: Table S3 reports R^2 values when each predictor group is analyzed separately. Within the phylum Tracheophyta (vascular plants), we found pronounced differences in average var(RoC) values among classes (Figure 4b). We therefore fitted a second random forest regressor to assess the effect of sampling unit on var(RoC) of populations in the phylum Magnoliopsida (dicots), that is, comparing time series based on reproductive output to time series of individual plants or similar. The model explained R^2 = 44.4% of the variation in var(RoC) (range-normalized RMSE: 16.3%; Appendix S1: Table S3). This result also clarifies the variation within the vascular plants (Figure 4b): at the high end of average var(RoC), all but one Pinopsida (conifers) time series are based on some reproductive output as sampling unit; at the low end of var(RoC), only about 1% of Liliopsida (monocots) time series is based on reproductive output. Note that the two reported R^2 values are not directly comparable because of differences in data preprocessing (Appendix S2: Section S3).

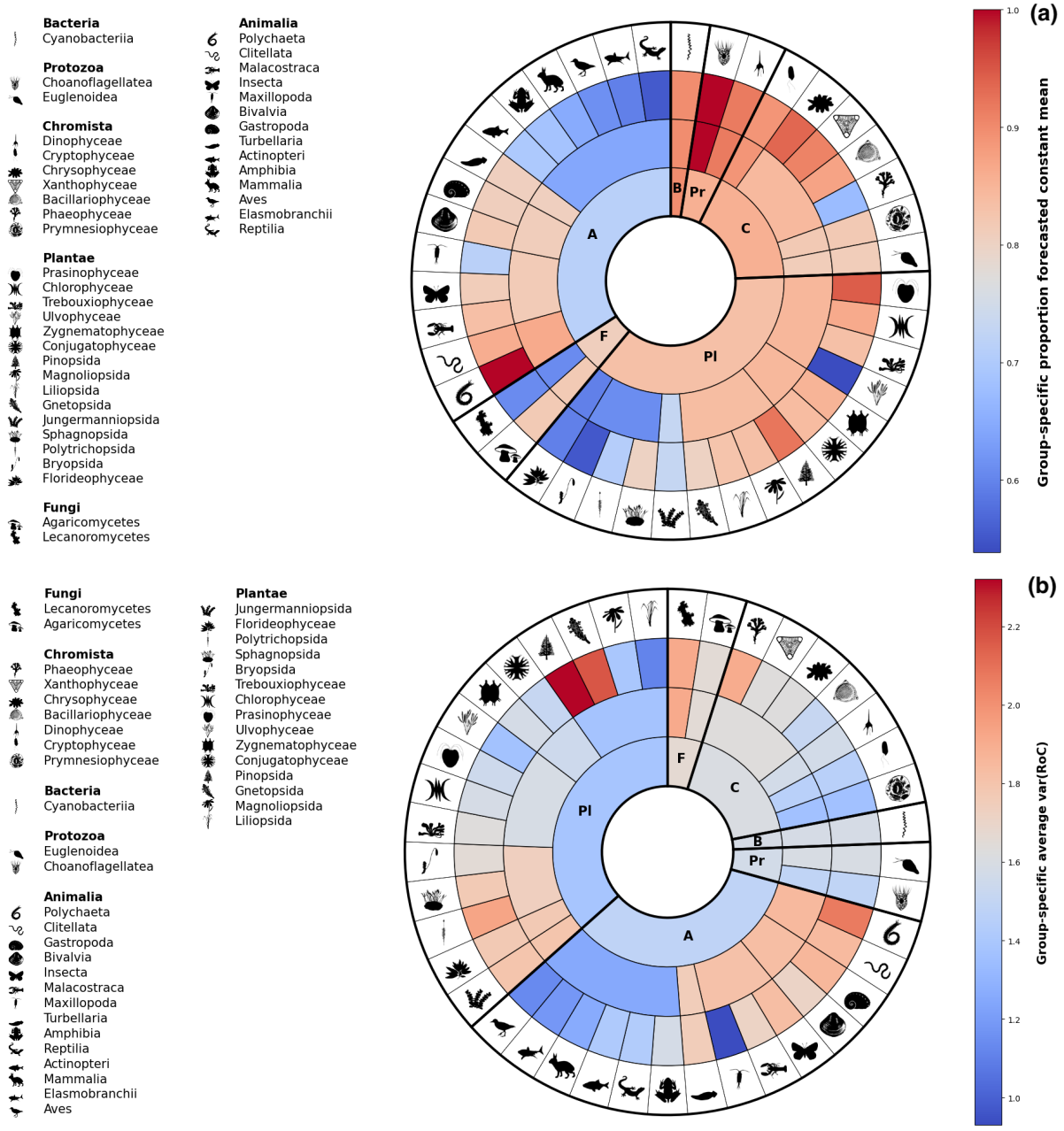

Figure 4. **Visualization of the taxonomy dependence of forecasted constant mean and var(RoC)**. For the population-level time series, the nested pie charts show (a) the proportion of forecasted constant means, and (b) the average var(RoC) values per taxon (ranks kingdom, phylum, class). Only classes with at least ten populations are shown (41 out of 64 classes: Appendix S1: Figure S3). Each ring stepping towards the center shows a higher taxonomic level. All taxa are ordered clockwise in descending order (classes and phyla within higher taxon). Kingdom abbreviations: F[ungi], C[hromista], B[acteria], Pr[otozoa], A[nimalia], Pl[antae]. Icons: public domain (www.phylopic.org).

Discussion

Using unobserved components models designed to forecast near-term population and community trends, we investigated the forecasts for approximately 43,000 population and 10,000 community-level time series across the globe and the Tree of Life. We then investigated what biological and data-related characteristics of the time series best explain the high prevalence of forecasted constant means.

In contrast to the prevailing narrative of pervasive biodiversity decline (Dornelas et al. 2023, and references therein), our results show that approximately 80% of population and community-level time series have a forecasted constant mean (Table 1); when a time trend is forecast, increasing trends are as common as decreasing trends, mirroring findings from retrospective analyses. Furthermore, the deterministic constant model that assumes fluctuations around a constant mean (Figure 1) was selected as best-fitting model for ~50% of the population and ~70% of the community-level time series. This result echoes previous findings for bird-specific forecasts (Harris et al. 2018). As illustrated with the Eastern monarch butterfly population (Figure 1), we emphasize that the visual appearance of a trend in the data is often not upheld by a statistical model that correctly accounts for variation and consequently forecasts no future change in the mean.

From a methodological perspective, unobserved components models in state-space form are robust statistical tools with high statistical power to identify trends (e.g. Harvey et al. 1997), and therefore our results are not the consequence of inadequate methods. Moreover, random forest models in conjunction with SHAP analysis give a sensible and robust approach to investigate complex data such as the drivers of patterns identified by the unobserved components models (e.g. Molnar 2025). Nonetheless, our time-series analyses have not addressed spatial and taxonomic correlation among the time series (Johnson et al. 2024), which would become important for example when computing an overall expected trend for a specific taxonomic group (e.g. WWF 2024). In general, however, accounting for spatial and taxonomic correlation will decrease the likelihood of identifying significant trends (Ives 2022), leading to the categorization of even more forecasted constant means. Further, we analyzed each time series without including covariates, because it would be impractical to try to assemble appropriate covariate time series for the large number of time series we analyzed. While including covariates in the time-series analyses may have revealed interesting patterns, we do not think that this would change our finding of few time series with forecasted time trends, because the simplest model of a constant mean was most often the best-fitting model (see also Lasky et al. 2020).

We also addressed the relevance of time series length. Many studies call for longer time series (e.g. White 2019, Cusser et al. 2021). Our results at first sight seem to go against it: time series shorter than 15 years are more likely associated with forecasted time trends (Appendix S1: Figure S6-S7), but this is mainly due to spurious trends in the short time series (Figure 3d). Beyond 15 years, the likelihood of a forecasted constant mean increases, and mean(RoC) often approaches zero. Longer time series are always preferable, both for narrowing the uncertainty in mean(RoC) and var(RoC) and for ensuring robust analyses (Figure 3). However, this will often result in a forecasted constant mean for the best-fitting models. This observation mirrors retrospective trend analyses, which indicate that steady means are common (Dornelas et al. 2023, and references therein). We should be wary of short time series because their forecasted trends more often than not may be spurious.

What do our findings imply for near-term biodiversity forecasts? First, low variation in the rate of change, var(RoC) – the strongest predictor of a forecasted time trend (Figure 2) – is the exception, not the rule in typical ecological data (Figure 3). While knowledge about biological and environmental drivers of var(RoC) is increasing (see also the *Results*), this variation will remain characteristic for ecological data, thus favoring forecasted constant means. Second, the profile of data attributes in current ecological data collections is unlikely to change soon. Constraints on time-series length, sampling unit and frequency, among many other attributes, will continue to drive uncertainty about the true state of populations and communities, hindering our ability to confidently detect and forecast true underlying time trends. Third, it is true that certain groups, like vertebrates, are more likely to have low var(RoC): depending on the forecasting scope, taxon-specific analyses could reveal true expected changes (Figure 4). Obviously, vertebrates represent only one phylum among many in the Tree of Life, and relying on their trends is misleading for taxonomic generalizations. This is especially important when managing or restoring whole ecosystems: data permitting, the entire taxonomic breadth should be used to produce forecasts to gauge expected near-term changes in composition and function. Here, however, not only population-level analyses across the Tree of Life, but even more so community-level analyses will often lead to a forecasted constant mean (Table 1). Finally, our finding of roughly 80% of populations and communities showing a forecasted constant mean echoes retrospective analyses (Dornelas et al. 2023, and references therein), and it implies we cannot rule out that directional long-term trends might be uncommon across the Tree of Life.

The ongoing biodiversity crisis demands both retrospective and forward-looking trend analyses. Working with typical ecological time-series data can be challenging, but overall a nuanced picture is emerging with respect to the details and extent of population-level and community-level changes. Near-term statistical forecasts are critical to inform stakeholders, as well as devising and monitoring

conservation actions. Despite their simplicity, we believe parsimonious forecasting approaches continue to offer valuable, robust, and actionable insights, to address the challenges posed by a changing natural world.

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Data availability: Most of the data that support the findings of this study are publicly available online and are referenced in the main text. See Appendix S1: Table S1 for further details.

Code availability: Code (Python), along with raw results files, will be uploaded to the zenodo repository after acceptance.

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Author contributions: **C.B.** Conceptualization, Methodology, Formal analysis, Data Curation, Writing - Original Draft, Writing - Review & Editing, Visualization. **A.R.I.** Methodology, Formal analysis, Writing - Review & Editing.

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