YSSP Report
Young Scientists Summer Program

Assessing the predictability of time-series of population abundance

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30/05/2022

This research was funded by IIASA and its National Member Organizations in Africa, the Americas, Asia, and Europe.

ZVR 524808900

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Abstract

Biodiversity is declining fast so we need robust tools to predict how biodiversity will respond to changes in land-use and climate. Available global biodiversity indicators, such as the Living Planet Index, help us prioritise conservation resources and evaluate the effectiveness of conservation and policy interventions and show progress towards environmental targets. But is it possible to accurately extrapolate these indicators spatially and/or project them into the future? And if so, how far can we reliably project them and when do predictions become too inaccurate to be useful? To assess the predictability of biodiversity trends, we apply a set of models to predict inter-annual change within time-series of vertebrate population abundance based on historical land use and climate data and assess their performance against withheld data. For this, we used a hindcasting validation approach. For a time series of length t we stepwise removed *x* years (ranging from 1-10) a) at the tail end of the time series, b) at the beginning of the time series and c) randomly in the middle of the time series creating gaps of maximum length x. The removed data points in each time-series represented our test set and the remaining data points the training set. We then applied random forest and linear mixed effects models to the training data, with relative population change and Relative Percent Difference (RPD) between years as response variables. As this analysis is in progress, we present a sample of results for random forest models, and discuss how we plan to progress the work in order to provide a complete assessment of predictability of vertebrate population trends. Being able to accurately predict population trends is important as population declines can be a prelude to extinction and – if we get them right - predicted trends could be used to determine a species' extinction risk via IUCN criterion A.

Acknowledgments

I am grateful to my IIASA and PhD supervisors for their support and ideas on this project, and particularly to Martin Jung for his guidance during the YSSP. I thank my colleagues in the Living Planet Index team who curate the data I have used for my analysis and all the people who provide data to large databases thus making global-scale analyses possible. I acknowledge the financial support from the Daisy Balogh fund, which made possible for me to visit IIASA in person during the YSSP.

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Valentina Marconi is a PhD student at University College London. Her PhD topic revolves around the use of machine learning to support the development of global biodiversity indicators. Alongside her PhD, Valentina is also a Postgraduate Research Assistant at the Zoological Society of London working on the Living Planet Index.
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Introduction

As global biodiversity continues to decline it is critical that we have robust tools to rapidly assess drivers of wildlife abundance trends across biodiversity dimensions. Explanatory models help identify what traits and ecological factors are good at predicting population trends of species we know about, and at testing potentially theoretically important predictors. Abundance trends in birds and mammals are associated with body mass, rates of climate warming, and conversion to anthropogenic land use (Spooner, Pearson and Freeman, 2018). Past environmental change also strongly correlates with abundance trends (Cornford *et al.*, Manuscript under revision) and with biodiversity responses more generally (Kuussaari *et al.*, 2009; Semper-Pascual *et al.*, 2021). However, we also need models to accurately predict future biodiversity trends from past data, a process known as forecasting. This is important for conservation and management decision-making, particularly in the context of future environmental change. If sufficiently accurate, this process would allow us to estimate the rate of biodiversity loss in data-poor regions (Yates *et al.*, 2018), improve our ability to predict biodiversity trends under different scenarios (Nicholson *et al.*, 2012; Visconti *et al.*, 2016; Powers and Jetz, 2019; Leclère *et al.*, 2020) and help us gauge which actions are needed to achieve targets (Visconti *et al.*, 2016; Nicholson *et al.*, 2019).

If models are used to make predictions to inform conservation policy at different scales, their outputs need to be evaluated carefully, their limitations known and their accuracy specified and communicated (Mouquet *et al.*, 2015). It is important to understand what aspects of ecological systems are predictable, and to quantify the uncertainty around these predictions or forecasts (Pennekamp *et al.*, 2017), especially in the near-term (Dietze *et al.*, 2018). Predictions should be calculated over a range of dimensions, such as space, time, and phylogeny (Petchey *et al.*, 2015) and evaluated in terms of their accuracy (Harris, Taylor and White, 2018). However, knowledge about how far into the future (or along other dimensions) we can accurately predict is limited in ecology. A recent study (Cornford *et al.*, Manuscript under revision) suggests that the linear mixed effects models developed so far to predict average population trends, such as Spooner, Pearson and Freeman (2018), have high explanatory power, but do not perform well in out-of-sample predictions. Here, we apply random forest and linear mixed effects models to predict change in population abundance of vertebrate species. We test our models' ability to accurately predict existing values withheld from the models during training. This is known as hindcasting, a term borrowed from meteorology (Jolliffe and Stephenson, 2011). With this work, we hope to establish a forecasting horizon for predictions of vertebrate population trends. Population declines are a sensitive indicator of biodiversity loss as they can be a prelude to extinction. Our outputs could ultimately also be used to inform the IUCN Red List criteria, particularly via criterion A, which is based on population declines (IUCN, 2012).

Methods

We applied random forest and linear mixed effects models to predict interannual change in population abundance of vertebrate species. We used data from one of the most comprehensive abundance databases available and aligned to best practices for making and evaluating ecological forecasts (Harris, Taylor and White, 2018). We used a broad range of predictors, including environmental and trait data. We then assessed the temporal predictability of population trends by testing model results against data already available at the time when the predictions were made, but that were withheld from the model during training. The withheld values were removed from different sections of the time series (at the beginning, at the end and in the middle). Two different error metrics were calculated to evaluate the gap between predicted and observed values. A schematic representation of the modelling process and validation steps is provided in Figure 1.

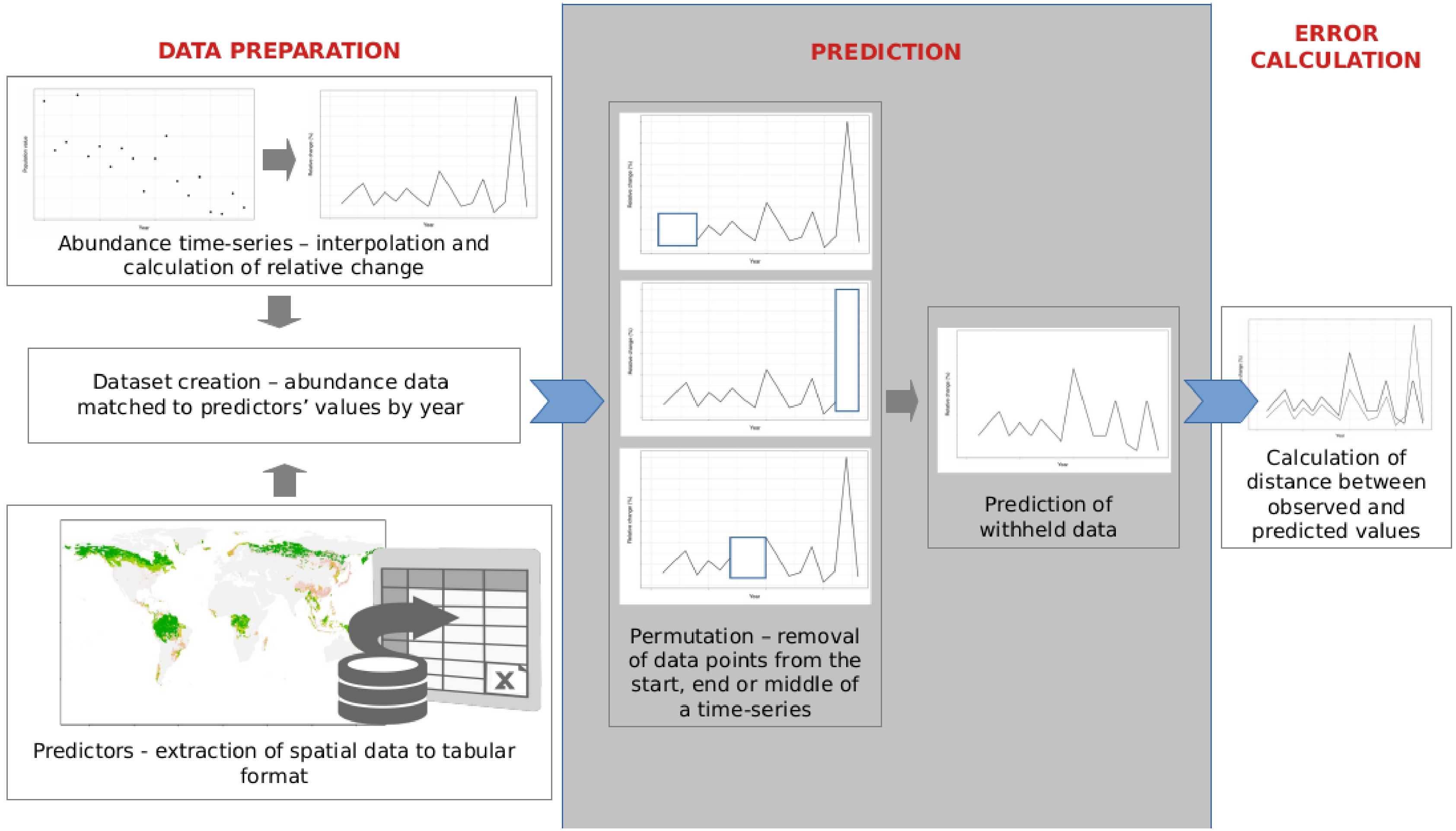

Figure 1 Illustration of the modelling process and validation steps with hypothetical data.

Data preparation

Population data

Population abundance data were gathered from the Living Planet Index (LPI) database (https://www.livingplanetindex.org). The LPI database contains time series of population estimates for over 27,000 vertebrate populations monitored across the globe during the period 1950–2019. Time series are collated from the scientific literature, online databases and gray literature. To be included in the database, data must meet three conditions (Loh *et al.*, 2005). The data source must be referenced and traceable. Data must have been collected using comparable methods for at least two years for the same population. Units must be of population size, either a direct measure such as population counts, densities, or indices, or a reliable proxy such as breeding pairs, nests, tracks, capture per unit effort or measures of biomass. We further filtered the data to include only populations that met the following additional criteria: a) data was covering terrestrial and freshwater tetrapod species, b) populations were monitored in specific locations with accurate coordinates (therefore excluding many of the LPI population trends that are aggregated over large areas and thus cannot be spatially linked to environmental data), c) time-series spanned a period of at least 4 years, d) the time-series had at least 3 data points.

Missing values between the start and end point of a time series were interpolated using moving weighted exponential average with +/-4 window size. Relative percentage change and relative percent difference (RPD) were then calculated on the imputed dataset between consecutive years. Relative percentage change was calculated as the difference between the population value at time t and the value at t-1, divided by the value at t-1, multiplied by 100:

$$\frac{x_t - x_{t-1}}{x_{t-1}} * 100$$

Relative population change varies between -100% and infinite, but positive change was capped at 10000%. We thus retained very large values, but capped their extent to an arbitrary threshold for changes deemed biologically realistic. RPD between X and Y is defined as follows:

$$d_1\,(x,y)\ = \frac{x\ - y}{(|x|\ + |y|)/2}\ =\ 2\frac{x\ - y}{|x|\ + |y|}$$

RPD values always lie between -2 and 2 and they are positive when x exceeds y and negative when y exceeds x.

Species characteristic, climate and environmental data

Geographical range size data was sourced from Birdlife (2021) for birds and IUCN (2021) for all other species. Only the portions of the range where the species is "extant" or "possibly extant" were taken into account. Body mass for each species was sourced from a recent study on threats to vertebrate populations (Noviello *et al.*, 2020). We extracted mean values of 21 environmental and anthropogenic pressure variables (Table 1) across an azimuthal equidistant projection 25km^2 buffer centered around the midpoint of each population's location as per Spooner et al. (2018) to take into account changes at landscape level around each population. Mean accessibility and elevation were extracted as static variables (one data point only) due to data availability. All other variables were extracted in the form of time-series, as per best practices recommendations for producing and evaluating ecological forecasts (Tredennick *et al.*, 2016; Harris, Taylor and White, 2018). The number of records within the buffered zone available for each species in the Global Biodiversity Information Facility (GBIF) (*GBIF: The Global Biodiversity Information Facility*, 2021) was included to test for the presence of site-selection bias (Palmer, 1993; Fournier, White and Heard, 2019). These extracted variables were filtered to include only the years for which population estimates were available (with a lag of 1 year, so that relative change in population abundance between e.g. 1970 and 1971 is associated with predictors for the year 1970). When variables were available as daily or monthly values, an average value was calculated for each year. As Jung, Scharlemann and Rowhani (2020) showed that incorporating lagged environmental change into models increases prediction accuracy, historical land use was included in the models as the average across the 30 years prior to the start of the time-series.

Dataset creation and software used

Time-series of population abundance and predictors were combined to generate the final datasets, comprising over 65,000 data points from 4,675 time-series of 1,262 species. If ecological forecasts are to be improved, it is important to continue making them available for future assessment (Dietze *et al.*, 2018). We plan to make most of the data and the code to replicate the analysis publicly available. LPI data are publicly available except for the time series that have been provided to the LPI team under the agreement they would be kept confidential, usually because of sensitivity around the species location. The final code to replicate the analysis and the non-confidential data will be available on GitHub.

Data extraction and preparation were carried out using Google Earth Engine (Gorelick *et al.*, 2017) and R (R Core Team, no date). The dplyr (Wickham *et al.*, 2019), ggplot2 (Wickham *et al.*, 2021), data.table (Dowle *et al.*, 2021), reshape 2 (Wickham, 2020), lubridate (Spinu *et al.*, 2021),zoo (Zeileis *et al.*, 2021), xts (Ryan *et al.*, 2020) and imputeTS (Moritz, Gatscha and Wang, 2021) packages were used to format the population trend data. The raster (Hijmans *et al.*, 2022) and reshape2 (Wickham, 2020) packages were used to extract and format the environmental data. The packages lme4 (Bates *et al.*, 2015), mgcv (Wood, 2011), MuMIn (Bartoń, 2022), caret (Kuhn *et al.*, 2021) and ranger (Wright, Wager and Probst, 2021) were used to model and predict population trends.

Table 1 Variables included in the models as predictors.

Class	**Variable**	**URL**	**Source**	**Unit**	**Static/ Time span**	**Resolution**
Trait data	Body mass	https://doi.org/10.1101/2020.12.17.423192	Noviello *et al.* (2020)	g	Static	
Range	Range size	https://www.iucnredlist.org/resources/spatial-data-download, http://datazone.birdlife.org/species/requestdis	Birdlife (2021); IUCN (2021)	km2	Static	
Environmental	Elevation	https://srtm.csi.cgiar.org	Jarvis *et al.*, (2008)	m	Static	90m
Environmental	Precipitation, temperature, soil temperature, snow cover, evaporation	https://cds.climate.copernicus.eu/cdsapp#!/dataset/10.24381/cds.68d2bb30?tab=overview	Copernicus Climate Change Service, (2019)	Multiple units	1981-2019	0.1◦
Environmental	Normalized Difference Vegetation Index (NDVI)	https://climatedataguide.ucar.edu/climate-data/ndvi-normalized-difference-vegetation-index-noaa-avhrr	Vermote et al., (2014)	Normalized difference vegetation index	1981-2018	0.05°
Human impact	Number of GBIF occurrence records	https://www.gbif.org/	The Global Biodiversity Information Facility, (2021)	number of records	1950-2019	Aggregated in 25km^2 buffer areas around

						population location
Human impact	Mean accessibility	https://figshare.com/articles/dataset/Travel_time_to_cities_and_ports_in_the_year_2015/7638134/3	Nelson *et al.*, (2019)	Travel time in minutes to nearest urban area with a population of over 50,000 people in 2015	Static (2015)	30 seconds
Human impact	Land use (primf: forested primary land, primn: non-forested primary land, secdf: potentially forested secondary land, secdn: potentially non-forested secondary land, pastr: managed pasture, range: rangeland, urban: urban land, c3ann: C3 annual crops, c3per: C3 perennial crops, c4ann: C4 annual crops, c4per: C4 perennial crops, c3nfx: C3 nitrogen-fixing crops	https://luh.umd.edu/data.shtml	Hurtt *et al.*, (2020)	Proportion of grid cell covered by land use type	850--2015	0.25◦×0.25◦

Research design

Cross validation

To evaluate predictability of local biodiversity change over time, we applied a hindcasting validation approach. For a time series of length t we stepwise removed *x* years (ranging from 1-10) a) at the tail end of the time series, b) at the beginning of the time series and c) randomly in the middle of the time series creating gaps of maximum length x (Figure 1). The removed data points in each time-series represented our test set and the remaining data points the training set.

Modelling

To assess the predictability of population time series of population abundance, we applied two modelling approaches to the training data, with relative population change and Relative Percent Difference (RPD) between years as response variables. For the modelling, all numeric predictor variables were scaled by centering them to a mean of zero and dividing them by one standard deviation. As some variables had missing data, we excluded all observations that had missing data. We fitted random forest models to predict the withheld population abundance values based on the predictors included in the data set. We grew 500 random forest trees for each random forest iteration and calculated variable importance for each permutation. We also constructed linear mixed effects models with study ID and Binomial as random effects to take into account differences between monitoring methods, locations and individual species, as suggested by Harris et al. (2018) as a way to address unknown or unmeasured predictors. The number of records in GBIF, range size, body mass and the year the data had been collected in were included in all models as fixed effects. In addition to these, for each permutation (removing trailing and starting years and creating gaps) we selected the top 5 remaining variables of higher importance from the random forest models for that specific subgroup and added those to the models as additional fixed effects. The variables included in the models are summarised in Table 2. Using the dredge() function from the Mumin R package (Bartoń, 2022) we evaluated all models resulting from all possible combinations of the selected predictors and their pair interactions. The top models (where the cumulative sum of the AIC weights were ≤0.95) were used to generate predicted values for the test data. Predictions were obtained from each of the tops models and then averaged based on the respective coefficients (Burnham and Anderson, 2002; Anderson, 2008).

Table 2 Data included in the linear mixed effects models as fixed effects.

	Percentage change			**RPD**		
	START	**GAP**	**TRAIL**	**START**	**GAP**	**TRAIL**
Number of GBIF records	X	X	X	X	X	X
Range size	X	X	X	X	X	X
Body mass	X	X	X	X	X	X
Year	X	X	X	X	X	X
Historical C4 perennial crops coverage	X	X	X	X	X	X
Historical forested primary land coverage	X	X	X	X	X	X
Historical potentially forested secondary land coverage	X	X	X	X	X	X
C4 perennial crops coverage at year -1	X	X	X	X	X	X
Mean snow cover at year -1			X		X	X
Forested primary land coverage at year -1	X	X		X		

Evaluation of predictability

Our work differs from previous studies that have used a summary metric averaged across time as a response variable (Spooner, Pearson and Freeman, 2018; Cornford *et al.*, Manuscript under revision). We chose to predict interannual change as we are ultimately interested in establishing a forecasting horizon for the predictions (Petchey *et al.*, 2015). Forecast proficiency is defined by Petchey et al. (2015) as "a measure of how useful a forecast is, usually some function of accuracy and precision". To measure it, we calculated three error metrics: Root Mean Square Error (RMSE), Mean Square Error (MSE), and Mean Absolute Error (MAE) for all time-series that had 3 or more data points left after removal of data points.

Results

As these analyses are ongoing, we are limited in terms of the conclusion we can draw from the data at this stage. Here we show initial results using RPD as the response variable and RMSE as the error metric for random forest models. RMSE has the advantage of being expressed in the same unit of measurement as the data. As the number of years removed from the time-series increases, the RMSE also increases (Figure 2). For percentage change, the error for predictions of years removed at the beginning and in the middle of a time-series follow similar trajectories. The error for predictions of years removed at the end of a time-series initially trails behind, but becomes greater than the other two around the five year mark (Figure 2). This might suggest that five year could represent the forecasting horizon for predicting into the future. For RPD, the error relative to predictions of years removed in the middle of a time-series appears to increase more slowly, and it remains below the other two lines up to the five year mark. Predictions for years removed at the start and at the end of a time series initially follow a similar trajectory to then diverge in the last five years (Figure 2).

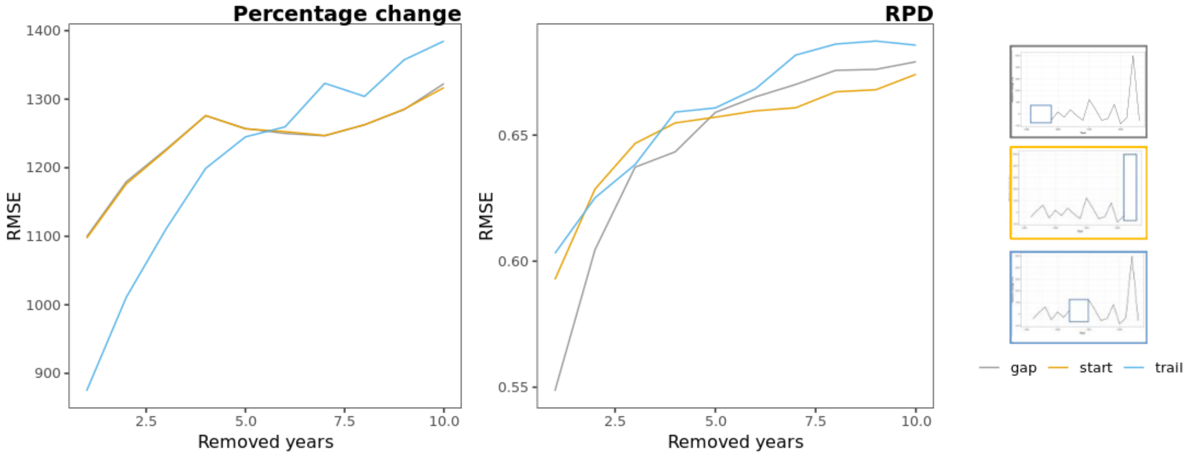

Figure 2 Changes in the precision metric RMSE (Y-axis) against the number of years removed from the tail (blue line) or start (yellow line) end of a time-series, and the length of the gap removed from the middle of a time-series (gray line) (X-axis) for both percentage change (left) and RPD (right) calculated from random forest models outputs.

Even though we are not using these models within an explanatory framework, we note that for random forest models, the number of GBIF records, range-size, mean snow cover, C4 perennial crops coverage and forested primary land coverage are among the variables of higher importance alongside historical C4 perennial crops coverage, historical forested primary land coverage and historical potentially forested secondary land coverage. All these predictors have high importance across permutations and irrespective of the response variable, except for mean snow cover and range size, which only appear in the model predicting RPD when data have been removed from the end of a time-series.

The analysis applying linear mixed effects models is in progress. However, our ability to compare the two modelling techniques (random forest and linear mixed effects models) is limited. This is primarily because due to methodological constraints it wasn't possible to run the linear mixed effects models using all predictors as in the random forest models. Some predictors had to be selected or excluded a priori (Table 2), thus making it difficult to compare results at this stage.

Discussion and next steps

Research with a primarily predictive goal is a relatively recent feature in ecology (Tredennick *et al.*, 2021), but the number of studies aimed at and advocating for predicting and forecasting ecological phenomena has increased in recent years (Petchey *et al.*, 2015; Houlahan *et al.*, 2017; Dietze *et al.*, 2018; Harris, Taylor and White, 2018). Fields with a successful forecasting culture, such as meteorology, can provide useful insight on how to improve forecasts (Dietze *et al.*, 2018). Based on this, we outline here what our next steps are to provide a complete assessment of predictability of time-series of population abundance.

We have gathered additional data from the BIOTIME database (Dornelas *et al.*, 2018), which we plan to use to expand our sample size. We also plan to test additional predictors and to test the use of alternative climate and land use maps. It has been shown that population trends projections are dependent on the land use data chosen for the analysis (Cornford *et al.*, Manuscript under revision). We also intend to expand the dataset by imputing environmental and climate time-series as done for time-series of population abundance to create a larger (imputed) dataset.

We will expand the set of models used to generate predictions in order to compare predictive performance across models. In particular, we aim to apply a Generalised Additive Modelling (GAM) framework and a Gradient Boosting framework to prediction population trends. This will help us establish which approach performs better - comparatively - in the task of predicting annual population change. Particularly as - due to the a priori selection of predictors - the two approaches tested so far cannot be directly compared. It is also important to compare the chosen modelling approaches to simple baselines models, as done by Harris et al. (2018). This will allow us to establish if the forecasts obtained are more accurate than models based on naive assumptions (Jolliffe and Stephenson, 2011; Perretti, Munch and Sugihara, 2013). We plan to construct two baseline models, based on one of the following assumptions; a) that future values of the parameter of interest are not going to deviate from the average across the time-series and b) that future values will be similar to the last observed value.

In order to make the models useful for actual long- and short-term predictions, we plan to make predictions from the whole dataset (without splitting it into training and prediction set) as done by Harris et al. (Harris, Taylor and White, 2018). This will allow future researchers to assess the performance of our models on longer time horizons as more years of data become available.

In terms of testing the robustness of our results, we will use error measurements to inform the data preparation stage. In this first iteration, we have interpolated all time-series of population abundance using moving weighted exponential averages. We have not set a threshold for the maximum length of gaps we want to interpolate over. The trajectory of error over time across models could suggest a suitable threshold. We would then re-run the models having only interpolated time-series with gaps lower than the threshold. This would also serve as a sensitivity analysis to gauge how robust our results are to changes in the initial dataset (exclusion of time-series with long gaps). We also intend to test additional cross-validation techniques, by removing entire time-series (Leave One Out Cross Validation) from the training set or removing data in blocks based on population location or taxonomic groupings.

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