

LETTER

The predictability of a lake phytoplankton community, over time-scales of hours to years

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Abstract

Forecasting changes to ecological communities is one of the central challenges in ecology. However, nonlinear dependencies, biotic interactions and data limitations have limited our ability to assess how predictable communities are. Here, we used a machine learning approach and environmental monitoring data (biological, physical and chemical) to assess the predictability of phytoplankton cell density in one lake across an unprecedented range of time-scales. Communities were highly predictable over hours to months: model R^2 decreased from 0.89 at 4 hours to 0.74 at 1 month, and in a long-term dataset lacking fine spatial resolution, from 0.46 at 1 month to 0.32 at 10 years. When cyanobacterial and eukaryotic algal cell densities were examined separately, model-inferred environmental growth dependencies matched laboratory studies, and suggested novel trade-offs governing their competition. High-frequency monitoring and machine learning can set prediction targets for process-based models and help elucidate the mechanisms underlying ecological dynamics.

Keywords

Cyanobacteria, environmental monitoring, forecasting, machine learning, phytoplankton, prediction, time series.

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INTRODUCTION

Forecasting how environmental change will alter communities and ecosystems is perhaps the most important task facing ecologists today, and a tremendous challenge to our ecological understanding (Mouquet *et al.* 2015; Petchey *et al.* 2015; Houlahan *et al.* 2017). Nonlinear relationships (such as between temperature and most biological processes), stochasticity and sensitive dependence on initial conditions are sources of uncertainty that community ecology shares with other predictive disciplines, such as climate science. However, ecology additionally has to grapple with biotic interactions in complex food webs, evolutionary change and a paucity of data with which to assess predictive power and refine models (Magurran *et al.* 2010). Therefore, with few exceptions (notably in disease ecology, e.g. Axelsen *et al.* 2014), we do not know how predictable ecological communities are (i.e. how strong the association between present and future system states is, a proxy for forecast ability). Quantifying this would allow us to understand the time-scale over which we can provide actionable input for management and legislative decision-making, recently termed the *ecological forecast horizon* (Petchey *et al.* 2015).

To make accurate long-term forecasts, ecology needs to develop process-based forecasts akin to those prevalent in climate science. Correlational approaches based on present conditions and abundances are likely to make inaccurate forecasts over decadal time-scales because patterns of environmental

covariation will change in the future (Williams *et al.* 2007). Process-based models avoid this problem but are a challenge to design because of their complexity. This arises from a lack of knowledge of the functional forms (or shapes) relating population/community change to environmental factors, and a lack of data with which to parameterise them (Kremer *et al.* 2016). The scale of this challenge is highlighted by recent work showing that complex, highly nonlinear interactions between abiotic factors are a regular feature of physiological and ecological processes (Edwards *et al.* 2016; Zhu *et al.* 2016; Zimmer *et al.* 2016; Thomas *et al.* 2017). Designing process-based models using a traditional approach may require extensive experimental work examining high-dimensional interactions. High-throughput screening technologies are helping to address this problem. But in many cases, a traditional experimental approach to understanding interactions (i.e. through multidimensional factorial experiments) may not be realistic given present funding and experimental constraints.

Machine learning (ML) algorithms offer us an alternative path towards the creation of these process-based models. When faced with complex environmental datasets, ML allows us to avoid important constraints inherent in most traditional statistical approaches (*a priori* specification of functional forms, interactions and error distributions). Despite relying on underlying correlations, ML algorithms can improve substantially on traditional correlative analyses (Kehoe *et al.* 2012, 2015; Rivero-Calle *et al.* 2015). They can be used on

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complex datasets to assess associations (Rivero-Calle *et al.* 2015) and to quantify predictability in the absence of the knowledge needed for a process-based model (Ewers *et al.* 2017). Even more importantly, they can be used to *infer* the functional forms and interactions needed to develop process-based models. This approach will require large datasets, but as ecology enters the big data era, acquiring this is becoming feasible for many systems. As the cost of data acquisition continues to decrease, ML may prove a more efficient approach (relative to high-dimensional factorial experiments) to assessing community predictability and understanding the drivers of complex ecological dynamics.

Natural communities of microbes such as phytoplankton are vital parts of most biogeochemical cycles and food webs (Falkowski *et al.* 1998; Field *et al.* 1998), and so assessing their predictability is especially important. Phytoplankton have generation times on the order of a day, and respond extremely rapidly to environmental change: shifts on time-scales of minutes to hours are sufficient to elicit physiological and ecological changes (Goldman & Glibert 1982; Demers *et al.* 1991; Hemme *et al.* 2014). Despite this sensitivity to environmental conditions, we do not know the time-scales over which phytoplankton community dynamics may be predicted.

Historically, most plankton-monitoring campaigns have measured the community at coarse time-scales of once to twice a month (Jochimsen *et al.* 2013), or on the order of once per 10 generations. These efforts have helped us understand broad changes driven by eutrophication and environmental warming (Pomati *et al.* 2012; Jochimsen *et al.* 2013), helping to make the case for policies limiting further changes. However, with rare exceptions (notably Hunter-Cevera *et al.* 2014, 2016), plankton-monitoring efforts have not captured the data needed to accurately assess community predictability across time-scales. High-frequency monitoring campaigns that sample communities and environmental drivers on sub-daily time-scales can partly address this (Pomati *et al.* 2011, 2013; Hunter-Cevera *et al.* 2014, 2016), filling in pieces of the picture that coarser long-term datasets have hinted at. They also provide us with the quantity of data needed to profitably employ ML tools.

We quantified the predictability of phytoplankton cell density over time-scales ranging from 4 hours to 10 years, or approximately 10^{-1} to 10^3 generations. Cell density, or the number of phytoplankton cells per unit volume, is the most important parameter characterising a phytoplankton community. It is a strong proxy for phytoplankton biomass (including in our system, Fig. S1) and for primary productivity, an important ecosystem property. We characterised predictability of cell density in Greifensee, a meso-eutrophic peri-alpine lake in Switzerland. The Greifensee plankton community, chemistry and physics have been monitored for > 30 years. In this period, there have been dramatic changes in biological and chemical parameters as a result of eutrophication and re-oligotrophication (Bürge *et al.* 2003). We make use of two complementary datasets examining the Greifensee phytoplankton community:

(1) High-frequency time series from monitoring campaigns carried out in the summer and autumn of 2014 and 2015. Cell density was measured every 4 hours at six different depths

(Fig. 1) using scanning flow cytometry (SFCM), and environmental data were also collected (Table S1).

(2) A long-term time series created from monthly measurements of depth-integrated phytoplankton measurements (Fig. 1), as well as associated environmental data (Table S2).

Although the datasets differ in methodology and size, they measure substantially similar biological, physical and chemical factors (Tables S1 and S2). Given the length of the two datasets and their sampling frequency and location, we are able to directly compare predictability in the two datasets at a time lag of 1 month.

In addition to community density, ecology aims to predict the dynamics of functional groups and taxa. Especially because toxic cyanobacterial blooms are a major health concern (Chorus & Bartram 1999; Paerl & Huisman 2009; Paerl *et al.* 2011), we also assessed the predictability of cyanobacterial cell density over these time-scales, and the drivers of competitive dynamics between cyanobacteria and eukaryotic phytoplankton (Fig. 2). Eukaryotic densities have remained relatively stable in Greifensee since the 1980s, while average cyanobacterial densities first increased 100-fold during eutrophication and then decreased by a similar amount over this time period as a result of re-oligotrophication (Fig. 2). Understanding the drivers of growth and competition between these two broad phytoplankton groups can help us refine process-based models of water quality, with important implications for the management of aquatic ecosystem services.

METHODS

Overview

Greifensee is an 8.45 km² peri-alpine lake in Switzerland (47.35 °N, 8.68 °E) with a documented history of eutrophication and re-oligotrophication (Bürge *et al.* 2003). The lake is currently meso-eutrophic, 32 m deep at its deepest point and just over 20 m deep at the sampling locations used for both datasets.

We use two datasets in this study: a high-frequency dataset consisting of measurements every 4 h during the summer and autumn of 2014 and 2015 using the automated monitoring station Aquaprobe (Pomati *et al.* 2011), and a long-term dataset consisting of monthly measurements from March 1984 to June 2016. In both cases, important environmental data (both abiotic and biotic) was collected simultaneously near the middle of the lake, allowing similar analyses to be conducted and thereby enabling comparisons. However, the datasets differ in important ways:

(1) The high-frequency dataset involved measurements by SFCM, while the long-term dataset involved microscopy measurements. Therefore, sampling effort and density assessment methods differ.

(2) The high-frequency dataset consists of measurements at six specific depths (1.0, 2.5, 4.0, 5.5, 7.0 and 8.5 m). Abiotic environmental data were also estimated at the same depth as the collected sample. In contrast, the long-term dataset consists of integrated phytoplankton measurements across the top 20 m of the lake. Abiotic measurements were not integrated,

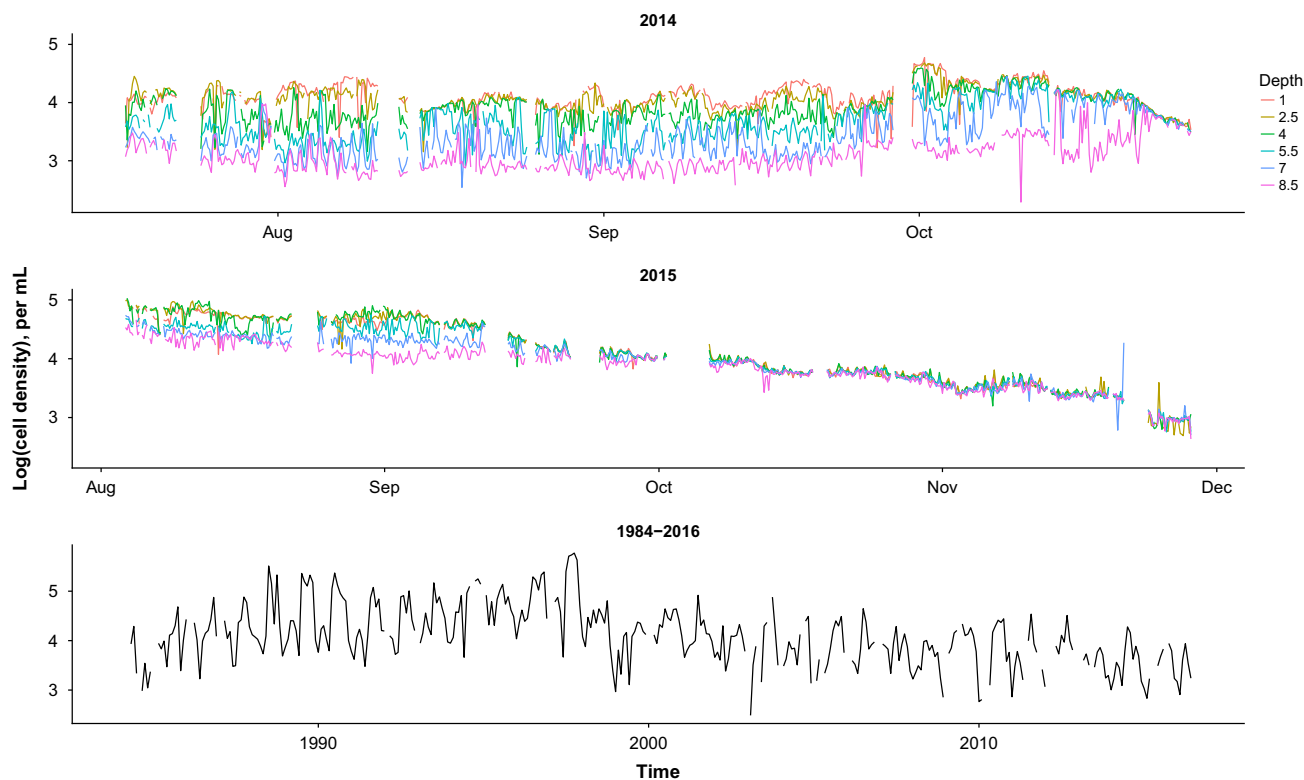


Figure 1 Dynamics of cell density of the total phytoplankton community, in both the high-frequency and long-term datasets from Greifensee. High-frequency measurements were made every 4 h in summer–fall 2014 and 2015, at six depths. Long-term measurements were made monthly from 1984 to 2016 and were integrated over the top 20 m. Note that X-axes are on different scales in each panel. Y-axes are identical for the top two panels but differ for the third.

but collected at specific depths (except for light, which is a surface estimate), and so we calculated the maximum and minimum value of each abiotic factor in the top 20 m for use as predictors.

(3) The high-frequency dataset consists of 7161 measurements, while the long-term dataset contains 383 measurements.

Generation of high-frequency dataset

Scanning flow cytometry description

We used a scanning flow cytometer, the CytoSense (<http://www.cytobuoy.com>), to quantify the density of the total phytoplankton community as well as its cyanobacterial and eukaryotic algal fractions (estimated densities are strongly correlated with estimates from microscopy, Fig. S2). The CytoSense characterises the scattering and pigment fluorescence of individual phytoplankton cells. It measures cells and colonies across a large proportion of the phytoplankton length range, between approximately 2 μm and 1 mm in length. Particles that enter the system cross two coherent 15 mW solid-state lasers. The instrument's laser and sensor wavelengths are designed to target the fluorescence signals primarily from chlorophyll-a and phycocyanin, but also capture signals from phycoerythrin and carotenoids. We used two different instruments in 2014 and 2015, with small differences in configuration. Instrument settings and data processing steps may be found in the supplementary information.

SFCM field sampling procedure

All samples were collected from a floating platform (Aquaprobe, Pomati *et al.* 2011) near the middle of the lake (47.3663 °N, 8.665 °E). Every four hours, water was sampled automatically at each of the six depths (as described in Pomati *et al.* 2011). Water samples were pumped into a 150 mL sampling chamber at the surface through a tube with a 0.6-cm diameter opening. The sampling chamber was flushed with water from the sampling depth three to five times over 2 min before the CytoSense collected a subsample of up to 500 μL for measurement.

Environmental factors

The full list of environmental parameters is found in Table S1. We measured temperature, conductivity and irradiance at all depths. We also collected weekly depth-specific samples for dissolved nutrient (nitrate, phosphate, ammonium) concentration estimation, and integrated measurements of size-fractionated zooplankton (> 150 μm). We monitored meteorological factors including wind speed and rainfall, and made use of additional data on water inflow (including flow rate, temperature and nutrient concentrations) into the lake provided by the Office of Waste, Water, Energy and Air (AWEL) of Canton Zürich, Switzerland. Details of sampling procedures, instruments used and measurement methodology may be found in the supplementary information.

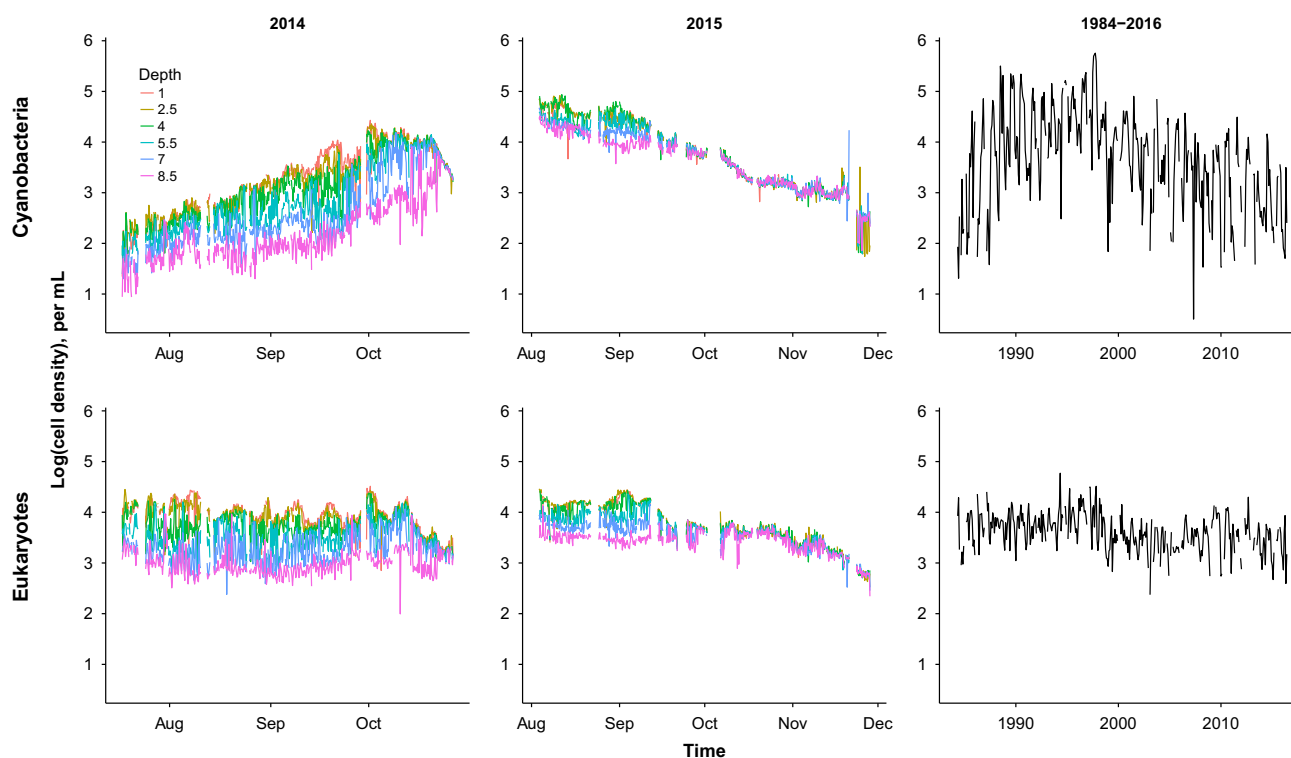


Figure 2 Dynamics of cell density of the cyanobacteria and eukaryotic phytoplankton, in both the high-frequency and long-term datasets from Greifensee. High-frequency measurements were made every 4 h in summer–fall 2014 and 2015, at six depths. Long-term measurements were made monthly from 1984 to 2016 and were integrated over the top 20 m. Note that X-axes are on different scales in each column.

Generation of long-term dataset

Field sampling procedure

Approximately every month, water samples were collected for physical, chemical and biological measurements near the centre of the lake (47.3525°N, 8.6748°E), about 1.5 km from the floating platform used for the high-frequency measurements. For microscopic counts of the phytoplankton community, an integrated water sample was collected over the upper 20 m of the water column with a Schröder sampler (Bürgi *et al.* 2003).

Environmental factors

The full list of parameters is found in Table S2. To measure chemical and physical parameters, water samples were collected every 2.5 m over the whole water column. These were taken at the same location and on the same dates, and were analysed using standard limnological methods (Rice *et al.* 2012). Integrated zooplankton samples were collected over the upper 20 m of the water column. More details about sampling procedures, instruments used and measurement methodology may be found in Bürgi *et al.* (2003). We also made use of a publicly available surface irradiance dataset (Schulz *et al.* 2008; Müller *et al.* 2015) to estimate the monthly averaged irradiance at the water surface based on estimates at a location approximately 2 km from our sampling location (47.35°N 8.65°E).

Data processing

For every time point, we calculated the maximum and minimum value of every depth-specific parameter (such as

phosphate concentration) across the entire water column, and used these for subsequent analyses. Additionally, samples were not collected on the same day every month and, in rare cases, more than one sample was collected in a month. We therefore aggregated measurements by rounding to the nearest month and then averaged duplicate values.

We found that the smallest phytoplankton species in the lake (*Synechococcus* sp.) could not be detected by the flow cytometer, so we excluded this species from the microscopy dataset to enable a better comparison of the two datasets.

Machine learning analyses

Random forests overview

Random forests (RFs) are a robust ML tool comprising ensembles of regression trees (or classification trees) (Breiman 1999). In each regression ‘tree’ within the random ‘forest’, a randomly selected subset of the data is recursively partitioned based on the most strongly associated predictor. At each node, a random subset of the total number of predictors is considered for partitioning. The final tree prediction for new data is given by the average value of the data within each branch of the tree. By aggregating predications across trees, RFs are able to reproduce arbitrarily complex shapes without *a priori* functional form specification.

We took advantage of three features that make RFs a flexible and useful tool for examining ecological systems: (1) *permutation importance*, (2) easy quantification of *partial effects* of individual predictors, and (3) *out-of-bag prediction*.

(1) The importance of each predictor in a RF is assessed by permuting the predictor across all trees in the forest and quantifying the resulting change in the forest's error rate. More important predictors lead to a greater increase in error when permuted.

(2) The partial effect of any single predictor on the dependent variable can also be quantified, allowing us to examine the functional form of the relationship (which may be arbitrarily nonlinear, though non-bifurcating).

(3) Out-of-bag (OOB) prediction allows us to make accurate estimates of error rate and goodness of fit (model R^2) via a process akin to cross-validation (Breiman 1999). Each data point is present in the training data of only a subset of all trees that comprise the forest. Therefore, the value of every point may be predicted using the trees that have not been trained with it. The 'OOB prediction error', or mean difference between the OOB predictions and the true value of all points in the dataset (see Fig. S3, S4 for examples using our data) can be used to quantify the RF's predictive ability through a pseudo- R^2 :

$$R^2 = 1 - \frac{MSE}{var(y)}$$

where MSE is the mean squared error of the OOB predictions when compared with the true values, and $var(y)$ is the variance in the dependent variable. As in the case of a standard R^2 , a pseudo- R^2 has an upper bound of 1, indicating perfect model performance. However, note that unlike a standard R^2 , there is no lower bound. It is possible for the pseudo- R^2 to be negative, if $MSE > var(y)$. This may be interpreted as saying that the model prediction is worse than the mean value of the dependent variable in the entire dataset. In our analyses, we saw low, negative values of pseudo- R^2 in a few cases; we rounded these values to zero to avoid confusion, while noting this in the figure captions.

Data pre-processing

In our analyses, we omitted: (1) all entries where the dependent variable was missing, and (2) the predictors *sampling depth* and *sampling time*. We omitted the latter in order to accurately estimate the effects of predictors that covary with depth and time. In other words, we believe that gradients in light, temperature and nutrients should characterise most of the relevant information contained within depth and time.

Quantifying predictability

We quantified the *predictability* of log cell density of the total phytoplankton community, and the cyanobacterial and eukaryotic fractions, using the pseudo- R^2 calculated based on the OOB predictions of the fitted model (see details above). We estimated predictability at time lags ranging from 4 h to 1 month in the high-frequency dataset, and from 1 month to 10 years in the long-term dataset. For every time lag, we fit two models. They predicted log cell density using: (1) only log cell density at the specified time lag, and (2) both log cell density and environmental parameters at the specified time lag. For example, our simplest model considering a time lag of four hours predicted log cell density at all time points using

only log cell density from the measurements four hours prior to them.

Predictor importance

We assessed the importance of predictors at all time lags using the change in model error rate when the predictor values were permuted.

Partial effects of environment on growth

We characterised the model-inferred effects of environmental factors on cyanobacteria and eukaryotes. Instead of examining the effects of these predictors on cell density, we quantified how they influence the population growth rate (i.e. specific growth rate, the rate of change in density between time points). We did this to facilitate comparison between the partial effects in our field dataset and extensive prior laboratory findings for the same predictors. However, the functional forms remained highly similar to the model explaining cell density.

We focussed on two factors that are known to strongly influence phytoplankton growth (Litchman & Klausmeier 2008) and were identified as important in our analyses: light and temperature.

Because laboratory studies typically measure the effects of environmental factors on population growth rate *per day*, we multiplied the estimates of growth rate over 4 h by a factor of 6 to express them in the same units. We then fitted RFs to these population growth rates using environmental parameters at a 4-hour lag and estimated the partial effects of light and temperature. Note that we omitted log density as a predictor, but model structure was otherwise identical to those previously described.

Although we were also interested in the effects of dissolved nitrate, phosphate and N:P ratio, we had data of lower temporal resolution for these predictors, which limited the power of analyses of these factors.

Model fitting and settings

Analyses were done in the *R* statistical environment v3.3.3 (R Core Team 2017) using the package *randomforestSRC* (Ishwaran & Kogalur 2007; Ishwaran 2017). We used 2000 trees for every forest, and set the number of predictors to be considered at each node to one-third of the total number of predictors. Missing data among the predictors were imputed for model fitting, but not for predictor importance assessment (Ishwaran & Kogalur 2007; Ishwaran 2017).

RESULTS

Phytoplankton cell density was highly predictable on time-scales of hours to months. In our high-frequency dataset, pseudo- R^2 of the RF models trained with cell density and environmental data decreased from 0.89 at a 4 hour lag to 0.74 at a lag of 1 month (Fig. 3). The model using only cell density as a predictor had a lower R^2 at all time lags. As time lag increased, including environmental data led to larger improvements in predictability: the difference in R^2 between the two models was 0.03 at a 4 h lag, and 10

times higher (0.30) at a 1 month lag (Fig. 3). In the long-term dataset, R^2 of the model trained with cell density and environmental data decreased from 0.46 at a 1 month time lag to 0.35 at 6 months, after which it remained relatively stable (Fig. 3). R^2 in the density-only model was lower at all time lags.

Apart from cell density, which was the strongest predictor at all time lags in our high-frequency dataset, the most important predictors were light, temperature and thermocline depth, the last of which is itself an indirect effect of temperature (Fig. 4). Light and temperature were also most important in our long-term dataset on time-scales of months (Fig. 4). At time-scales of years, dissolved phosphorus and zooplankton density become more important.

Cyanobacteria were more predictable than eukaryotes at all time-scales, in both high-frequency and long-term datasets (Fig. 3). Model R^2 for cyanobacteria was consistently higher than that for eukaryotes by approximately 5–20 percentage

points (Fig. 3), in both types of models (cell density only and cell density with environmental data).

To motivate the development of process-based models of phytoplankton competition, we also examined the partial effects of environmental factors on the growth rate of cyanobacteria and eukaryotic algae (Fig. 5). Temperature and light, the strongest predictors in our dataset, showed biologically realistic nonlinear patterns. Additionally, in both cases, each group dominated a region of parameter space, suggesting the presence of trade-offs in performance.

DISCUSSION

Assessing the predictability of natural communities is crucial if we are to develop forecasts of how ecosystems will be altered by environmental change (Mouquet *et al.* 2015; Petchey *et al.* 2015; Houlihan *et al.* 2017). However, our ability to predict community dynamics has been limited by our

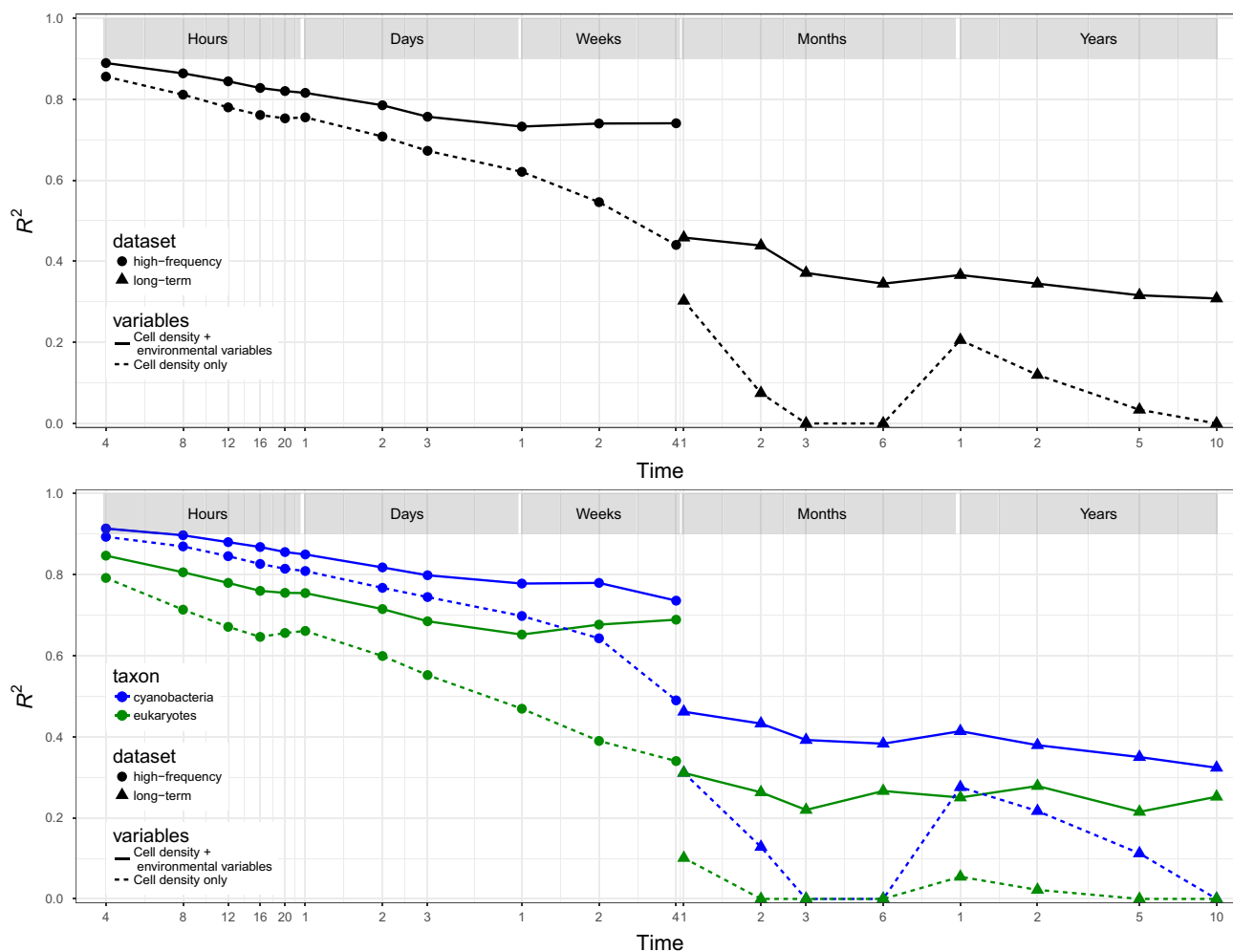


Figure 3 Decline in predictability of the phytoplankton community (whole community in black, cyanobacteria in blue, eukaryotes in green) with time, characterised by the random forest pseudo- R^2 . The predictive contribution of environmental information increased with increasing time lag (i.e. distance between solid and dashed lines increases). Cyanobacteria were consistently more predictable than eukaryotes. Despite overlap between high-frequency and long-term datasets at a time lag of 1 month, there is a sharp decline in predictability. This is likely driven by the lack of depth resolution in plankton and environmental data in the long-term dataset. The spike in R^2 of the ‘cell density only’ models at 1 year reflects strong annual cycles in density. Note that pseudo- R^2 values can go negative (see Methods), and we rounded a few slightly negative values up to zero. We present the same results in terms of change in Mean Absolute Error with increasing time lag in Fig. S5.

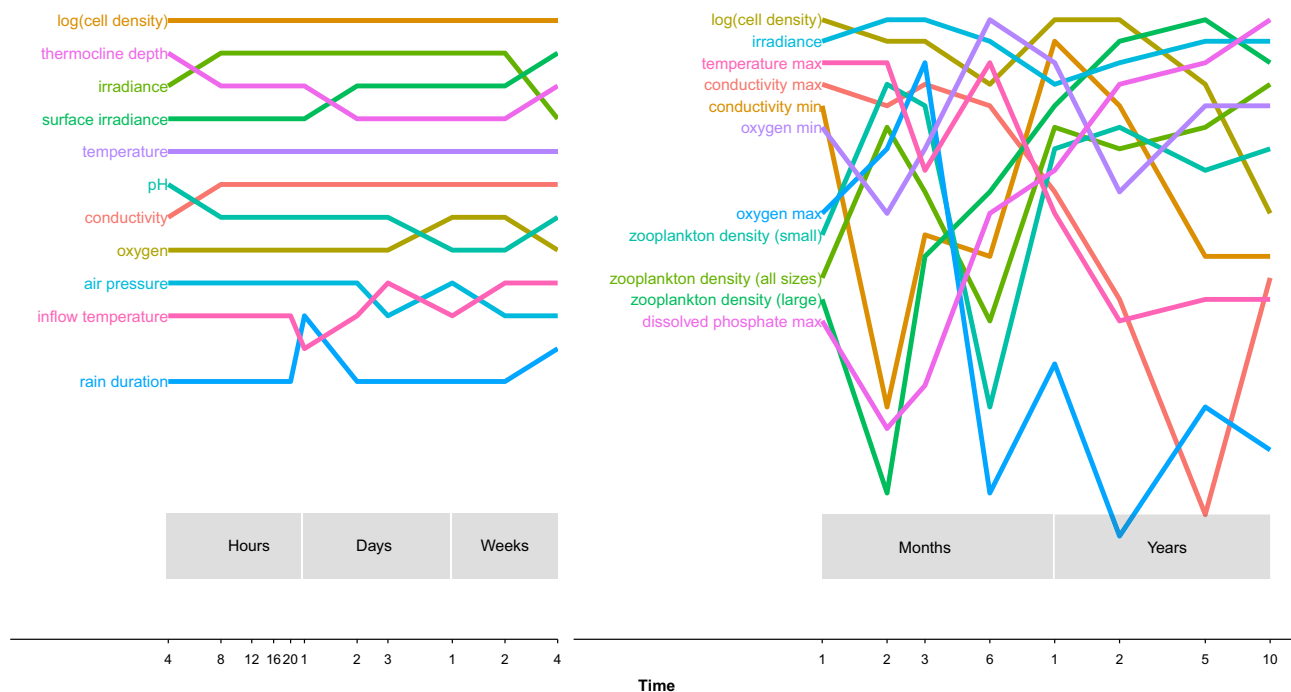


Figure 4 The most important predictors of phytoplankton cell density at different time lags, ordered by descending rank. Light and temperature (directly, or indirectly through thermocline depth) were important predictors at most time-scales. In the long-term dataset, phosphorus and zooplankton density become highly important predictors at time-scales of > 1 year. Only the most important predictors are shown here, for legibility (the top five predictors contribute > 80% of the predictive power in most cases). In the high-frequency dataset, only predictors that are in the top 10 most important for at least one time lag are shown, while in the long-term dataset, we show only predictors that appear in the top five most important at least once. See Tables S4 and S5 for the importance score of all predictors tested.

understanding of environmental dependencies and biotic interactions (McGill *et al.* 2006). Our results suggest that lake phytoplankton communities are highly predictable over timescales of hours to months (approximately 10^{-1} to 10^2 generations), and possibly longer (Figs 3, S5). Our approach quantifies the decline in predictability with increasing time lag, identifies the predictors that contribute to predictive power and points towards realistic trade-offs and parameterisations through the examination of partial effects. Together, these can inform the development of process-based models, set targets for their forecasts and help identify a forecast horizon for adaptive management strategies. This is especially true in the case of cyanobacteria, many of which are a threat to human health and aquatic ecosystem services because of toxin production. This group is also believed to be hard to forecast (Chorus & Bartram 1999; Paerl & Huisman 2009; Paerl *et al.* 2011). In contrast, we find cyanobacterial densities to be consistently more predictable than those of eukaryotes (Fig. 3).

As our understanding of ecological processes improves, the limits to predictability of ecological systems will be determined by more fundamental constraints such as stochasticity and sensitive dependence on initial conditions. Despite these, we find strong, ecologically important environmental forcing in a natural system across a range of time-scales (Figs 3–5). Consequently, we believe that process-based models are very likely to provide us with useful predictions over the medium-to-long term. In other words, we believe that despite the

complexity of phytoplankton communities, the ecological forecast horizon (Petchey *et al.* 2015) is sufficiently distant for ecologists to provide useful input into adaptive management strategies. Note that we do not quantify a specific horizon here because this requires the specification of a (arbitrary) forecast threshold; readers may choose these thresholds for themselves and identify the resulting forecast horizon using Fig. 3 and Fig. S5.

Light and temperature were strongly predictive of phytoplankton dynamics across time-scales (Fig. 4), consistent with existing ecological understanding (Litchman & Klausmeier 2008). We also found that zooplankton density and dissolved phosphorus concentrations become highly predictive on time-scales longer than a year, consistent with an ongoing, multi-decadal decrease in phosphorus and biomass in Greifensee (Bürgi *et al.* 2003). This identification of variables that are known to play a major role in phytoplankton ecology strengthens our confidence in the relationships underlying our metric of predictability. However, we note that predictor importance – while a useful tool – is sensitive to missing data patterns. Our estimates therefore understate the importance of two major groups of predictors in our high-frequency data: nutrients and zooplankton density. Unlike most other predictors that were measured every four hours, these were measured weekly in 2014 and twice a week in 2015 (Table S1). To partially correct for this difference, we also assessed the relative importance of all predictors when these were interpolated

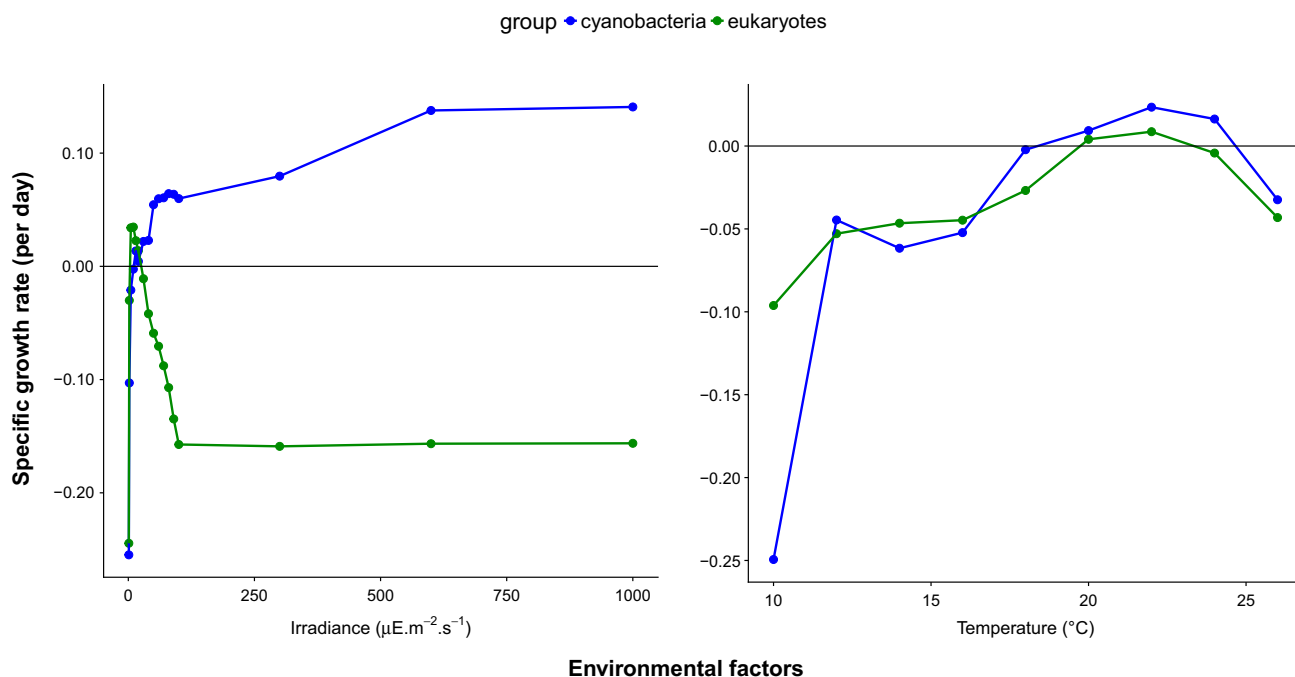


Figure 5 Partial effects of important environmental factors on the population growth rates of cyanobacteria and eukaryotes, based on an RF model with a 4-hour time lag. The patterns reveal environmental dependencies consistent with laboratory experiments and suggest trade-offs with important ecological implications. Cyanobacteria appear to benefit from high light and high temperature. The predominantly negative partial effects reflect the fact that in 2015, the community was decreasing through the majority of the monitoring campaign leading to imprecise estimates of the drivers of mortality (such as predation). Therefore, differences in shape and magnitude are highly informative, but the absolute estimates are only indicative. Better estimates of the drivers of mortality would likely change the intercept on these curves, moving the entire curves up or down the Y-axis. Additionally, interactions between factors are captured by the complete forest prediction, but are not visible in single-dimension partial effects plots. Note that Y-axes are on different scales.

using generalised additive models (GAMs) (Fig. S6). Models with interpolated nutrients and zooplankton predictors had marginally higher R^2 values and these predictors rose considerably in importance, especially dissolved nitrogen (Fig. S6). We believe that these results are noteworthy and highlight the potential value of high-frequency monitoring of these variables. However, we choose not to focus on them here because we are unable to validate the interpolated estimates.

Importantly, the predictive power of environmental factors in our models arises from nonlinear dependencies that are consistent with causal relationships established through laboratory studies (Fig. 5; Litchman & Klausmeier 2008). Light, one of the most important predictors, has a partial effect on growth that is a saturating function for cyanobacteria and a right-skewed unimodal function for eukaryotes (Fig. 5); these are the only shapes consistent with laboratory measurements of light-dependent growth (Eilers and Peeters 1988, Edwards *et al.* 2015). The partial effect of temperature is an increasing function and possibly a left-skewed unimodal curve, consistent with prior eco-physiological findings, including in phytoplankton (Kingsolver 2009, Thomas *et al.* 2012, 2016). This concordance between controlled laboratory studies and ML-derived field patterns increases our confidence in this ML approach, and suggests that the relationships we have uncovered will be useful in guiding process-based model creation. Furthermore, it suggests that ML approaches may be used to discover novel ecological patterns. This is particularly important in the case of interactions between factors, which presently require labour-intensive and

expensive multifactorial experiments to understand. However, we note that at present, these partial effects contain uncertainty in the intercept because of our lower frequency measurements of predator-driven mortality (Fig. 5). In other words, a constant value may need to be added to each curve to achieve quantitative accuracy; this would have the effect of moving curves a small amount up or down the Y-axis. But importantly, this would not influence estimates of important parameters from these curves, such as the optimal temperature and optimal irradiance for growth, and alpha (the slope of the growth-irradiance curve at low irradiance). These parameters are crucial to understanding and modelling competitive dynamics.

The partial effects we show here (Fig. 5) point towards trade-offs that could enable the co-existence of cyanobacteria and eukaryotes. Cyanobacteria appear to benefit from high light intensity and high temperature, while eukaryotes have a growth advantage in the converse conditions. Therefore, temporal heterogeneity in one or both of these dimensions could allow for the maintenance of both these groups (Chesson 2000). Cyanobacteria do possess higher optimal temperatures for growth than eukaryotic phytoplankton at temperate latitudes (Thomas *et al.* 2016), consistent with the temperature-dependence we see (Fig. 5). The apparent trade-off between growth at high and low light intensities was not seen in a synthesis of laboratory-measured light traits (Schwaderer *et al.* 2011), but at present, lab measurements are available only from a few species and may be influenced by interactions with other factors. Laboratory data on a broader range of species

and under a greater range of conditions will help resolve this discrepancy. If true, the ML-derived field pattern we identify here also suggests an explanation for the formation of surface scums by cyanobacteria through buoyancy regulation (Paerl *et al.* 2011; Carey *et al.* 2012). Scum formation – important due to the negative impact on lake ecosystem services – is consistent with a cyanobacterial benefit from higher irradiance. In contrast, eukaryotes appear to have a lower optimal irradiance and might experience photo-degradation from surface growth. These observations offer an example of the insights that may be gained through a combination of high-frequency monitoring and machine learning.

Our models may understate the long-term predictability of the phytoplankton community. The difference in predictability between high-frequency and long-term datasets at a time lag of 1 month suggests that if a similar methodology was followed in the long-term dataset, reasonably high R^2 values may have been obtained over time-scales of years. This difference is driven by several factors: (1) our high-frequency dataset includes measurements of both phytoplankton and environmental factors at specific depths, as opposed to integrated values across the water column as in the long-term dataset, (2) the high-frequency dataset has more than an order of magnitude more data points (7161 vs. 383) with which to train the ML algorithm, and (3) the long-term dataset explores a greater range of parameter space in temperature, nutrient concentration, zooplankton density and unmeasured factors. Of the three, we believe depth-specific sampling may be the most important determinant, as the difference in model R^2 at a lag of one month is < 15% in the case of the cell density-only models, and 30% in the models with both cell density and environmental factors (Fig. 3). However, we also note that in more complex systems where migration is important – such as coastal and open-ocean communities – predictability may be lower unless physical circulation patterns are highly predictable as well.

It is important to note that although pseudo- R^2 provides estimates of predictability that are robust (Breiman 1999), we have not assessed a true *forecast*, in which error is allowed to compound through time. Our approach can in principle be used to make a forecast, but we chose not to do so because of the long winter-to-spring break in our high-frequency dataset, and the large changes in environmental conditions towards the end of the two monitoring seasons. Attempting to forecast would require us to predict in conditions well outside those that the model was trained on, where it will inevitably perform poorly. Despite this limitation, we believe that out-of-bag error is a useful proxy for forecast error: the realistic environmental dependencies (Fig. 5) highlight that we are uncovering the mechanisms underpinning ecological dynamics. In the future, a broader sampling of parameter space and a longer time series (through year-round monitoring) should allow us to make forecasts and test true forecast skill.

We have shown that high-frequency environmental monitoring and machine learning approaches can be employed to identify patterns in complex ecological communities, to assess their predictability, and to uncover dependencies that can be incorporated into process-based models of communities and ecosystems. This can help us address fundamental questions in ecology: What are the drivers of ecological processes and how

does this change through time? How large of an effect does environmental and demographic stochasticity have on communities? What are the dominant trade-offs that maintain diversity in natural systems and how do they operate in dynamic environments? But perhaps more importantly, it can help us to improve our forecasts of ecological systems, fulfilling a fundamental obligation that ecology owes to society.

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DATA ACCESSIBILITY STATEMENT

Data available from the Dryad Digital Repository: <https://doi.org/10.5061/dryad.r4454>

AUTHORSHIP

MKT and FP conceived the study. MKT, SF, MR and FP collected the data. MKT analysed the data. MKT wrote the manuscript with substantial input from FP, SF, MK and MR.

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