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Deliverable 3.10: Report on the ensemble model calibration and validation on the different sites

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Work package:**3**

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Estimated person months: **12**

Abstract

In response to the need to understand better the ecology of phytoplankton producers and predict the response of this key component of lacustrine food webs to changing environmental conditions, numerous computer models have been developed to simulate the seasonal development of lake phytoplankton. Most studies that have used such models to predict future impacts on lake phytoplankton have utilised a single model and while such studies have merit, applying multiple, independently developed models to a given lake system enable some of the inherent uncertainties in the model predictions to be quantified and reduced because the predictions of the individual models can be examined together. Hitherto, perhaps due to both the considerable resources required and the individual model expertise needed to apply a model to an aquatic ecosystem, no ensemble modelling studies have yet been carried out for prediction of lake phytoplankton dynamics. The initial aim of this deliverable was to explore variations in model performance for a range of aquatic ecosystem models used within the REFRESH project and the intention was originally simply to compare performance of different models that had already been applied to different systems. However, given the expertise available from the international network of modelling experts involved in REFRESH, we were able, for the first time, to apply three autonomously developed models to the same lake. In addition, we ran a series of potential future climate and nutrient load scenarios, and derived the predictions and uncertainties from the ensemble model run. Particular focus is given to changes in Cyanobacteria abundance. The lake modelled is Lake Engelsholm in Denmark, which, as is typical for lakes in many developed countries, is suffering from eutrophication as a result of decades of anthropogenic activities, with nutrient loading from both point sources and diffuse pollution. The results presented here will be written up for inclusion in a peer reviewed paper, to be submitted in July 2012.

REFRESH

Deliverable 3.10: Report on the ensemble model calibration and validation on the different sites

Work package: 3

Contributors: Dennis Trolle (AU) and Alex Elliott (NERC)

Abstract

The aim of this deliverable was to explore variations in model performance for a range of aquatic ecosystem models that are used within the REFRESH consortium. While the intention was originally simply to compare performance of different models that had already been applied to different systems (which has since been thoroughly described in Arhonditsis & Brett 2004, Mooij et al., 2010 and Trolle et al., 2012), we take a step further and apply three individual models to the same freshwater lake – an exercise that has never been done before. We further run a series of potential future climate scenarios, and derive the predictions and uncertainties from the ensemble model run. Particular focus is given to changes in Cyanobacteria abundance. The results presented in this report are planned for inclusion in a peer reviewed paper, to be submitted in July 2012.

Introduction

There has been growing evidence over many years that lakes, and their ecology, are particularly sensitive to environmental change. In particular, phytoplankton primary producers have proven to be particularly responsive to changes in factors such as nutrient load (e.g. Reynolds, 1984; Lampert & Sommer, 1997) and climate (e.g. Winder & Schindler, 2004; Huber et al., 2008; Jöhnk et al., 2008; Thackeray et al., 2008). Given their key role in many lake food webs, such sensitivity is of concern to lake managers around the world and, when coupled to the related health hazard of Cyanobacteria blooms (Chorus & Bartrum, 1999; Paerl & Huisman, 2008), makes understanding their ecology and predicting their growth of paramount importance.

The latter has proved to be challenging and has motivated the development of numerous computer models that have attempted to simulate the seasonal development of lake phytoplankton (Trolle et al., 2012). Nevertheless, with the additional pressure of a changing climate, the need for the predictive ability of such models has never been so important. However, most studies that have used such models to predict future impacts on lake phytoplankton have utilised only a single model (see Elliott, 2012). Whilst such studies have merit, the advantage of applying multiple, independently developed models to a given lake system is that some of the inherent uncertainties in the model predictions can be quantified and reduced because the predictions of the individual models can be examined together. Nevertheless, perhaps due to both the considerable resources and the individual model expertise needed to apply a model to an aquatic ecosystem, no ensemble modelling studies have yet been carried out for prediction of lake phytoplankton dynamics.

Therefore, in this study we take advantage of the expertise available within an international network of modelling experts, and apply to the same lake three autonomously developed models. We further test a range of climate change and nutrient load scenarios so that the different model predictions can be accessed. The lake tested is Lake Engelsholm in Denmark, which – as typical for lakes in many developed countries – is suffering from eutrophication, as a result of decades of anthropogenic activities, where nutrient loads are influenced by both point sources and diffuse pollution.

Methods

Study site

Lake Engelsholm is a small, shallow Danish lake. The lake has a maximum depth of 6.1 m, a mean depth of 2.4 m and a surface area of 0.44 km^2. Lake Engelsholm is currently in a eutrophic state, as a result of excess external nutrient loads from the surrounding catchment, resulting in an annual average Secchi depth of approx. 2 m, annual average chlorophyll *a* concentrations of approx. 25-30 mg m^{-3} Chl *a* (data from 1999-2001), and occasional occurrences of cyanobacteria blooms during summers. The catchment (15.2 km^2) consists mainly of cultivated areas (78%), forested hills (16%) and scattered dwellings (6%). As part of the EU Water Framework Directive, Lake Engelsholm will need to meet requirements to maximum phytoplankton biomass levels, and therefore actions must be taken to reduce external nutrient loads.

Model applications

The three models used are DYRESM-CAEDYM (Hamilton and Schladow, 1996), PROTECH (Elliott et al., 2010) and PCLake (Janse et al., 1992). DYRESM-CAEDYM (DYCD) is a one-dimensional water quality model developed by the Centre for Water Research (CWR) at The University of Western Australia. The model consists of two main components: a one-dimensional hydrodynamic model (DYRESM: Dynamic Reservoir Simulation Model), which resolves vertical mixing and the resulting distribution of temperature, salinity and density in a lake/reservoir, and an aquatic ecosystem model (CAEDYM: Computational Aquatic Ecosystem Dynamics Model), which simulates a range of biological and chemical variables, such as inorganic and organic forms of phosphorus and nitrogen, up to seven phytoplankton groups/species and up to five zooplankton groups/species. If a lake is characterized by a complex bathymetry, and higher spatial resolution is required due to the importance horizontal circulation and transport processes, CAEDYM can also be run in 3D, in a coupling to the Estuary and Lake COMputer model (ELCOM, a 3-D-structured grid hydrodynamics model). In either 1D or 3D studies, the model has been applied in around 70 peer reviewed studies (Trolle et al., 2012), and has typically been used to predict the effects of changed nutrient loads (Trolle et al., 2008) or climate (Trolle et al., 2011). The daily change in the phytoplankton biomass in a water column layer ($\Delta X/\Delta t$) attributable to each phytoplankton group is determined by:

$$\Delta X/\Delta t = (r' - R - S - G)\,X + RS + M - D \qquad (1)$$

where r' is the actual growth rate (d^{-1}), R is the accumulated loss due to respiration, mortality and excretion, S is the loss due to settling, G is the loss due to grazing (grazing preferences on each phytoplankton group can be specified for individual zooplankton groups), RS is a gain due to resuspension of phytoplankton biomass from the bottom sediments, M is the gain

or loss from active movement (optional) of phytoplankton from or to neighbouring water layers and D is the loss due to dilution (Hipsey et al., 2007). The actual growth rate (r', d^{-1}) is determined from:

$$r' = \mu_{max} \min\{ f(I), f(N), f(P), f(Si) \} f(T) \qquad (2)$$

where μ_{max} (d^{-1}) is the maximum growth rate at 20°C in the absence of significant limitation by light or nutrients, f(I), f(N) and f(P) represent limitation by light, nitrogen and phosphorus respectively and f(T) is a temperature function. The f(Si) function represents limitation by silica and applies only to diatoms. The nutrient limitation can be modelled either through a simple Michaelis-Menten expression or by inclusion of a dynamic intracellular nutrient store which is able to regulate growth.

PROTECH (Phytoplankton RespOnses To Environmental CHange) simulates the responses of up to 10 species of lake phytoplankton to annual seasonal changes. It has been applied in over 30 peer reviewed studies (Elliott et al., 2010). A detailed description of the model's equations and concepts has already been published (see Reynolds et al., 2001; Elliott et al., 2010) but the biological component of PROTECH can be summarised by the following simple equation. The daily change in the chlorophyll *a* concentration ($\Delta X/\Delta t$, mg m^{-3} d^{-1}) attributable to each phytoplankton taxon is determined by:

$$\Delta X/\Delta t = (r' - S - G - D)\, X + M \qquad (3)$$

where r' is the growth rate defined as a proportional increase over 24 hours, S is the loss due to settling out of the water column, G is the loss due to Daphnia grazing (phytoplankton > 50 µm are not grazed; Burns, 1969), D is the loss due to dilution and M is the gain from active

movement (optional) of phytoplankton from bottom water layers (optional). The growth rate (r', d^{-1}) is further defined by:

$$r' = \min\{r'_{(\theta,I)}, r'_P, r'_N, r'_{Si}\} \tag{4}$$

where $r'(\theta,I)$ is the growth rate due to temperature and daily photoperiod and $r'P$, $r'N$, $r'Si$ are the growth rates determined by phosphorus, nitrogen and silicon if respective concentrations of those nutrients are < 3, 80 and 500 mg m^{-3}, respectively (Reynolds, 2006). The r' values are phytoplankton-dependent (e.g. non-diatoms are not limited by silica concentrations below 500 mg m^{-3} and nitrogen-fixing Cyanobacteria are not limited by nitrogen), relating to the morphology of the alga (for $r'(\theta,I)$) and, because of the effects of temperature and light, vary with each time-step throughout the simulated water-column. Thus no one specific summary r' value exists for a given phytoplankton because they depend on temperature, available light and nutrients. Therefore, for each alga within the model, the starting value of X mg Chl a m^{-3} d^{-1} (Eq. 4) is modified on a daily time-step to predict the change in chlorophyll a concentration for each alga in each layer in the water column.

PCLake is an integrated ecological model developed for shallow non-stratifying lakes, which describe phytoplankton, macrophytes and a simplified food web, within the framework of a closed nutrient cycle (Janse et al., 1992, Mooij et al., 2010). Additional model developments have been based on the PCLake core (Mooij et al., 2010) and the model has been used in approx. 15-20 peer reviewed studies (Trolle et al., 2012). PCLake is designed to provide a representation of organic and inorganic forms of nitrogen and phosphorus, and the interactions between up to three phytoplankton groups, one zooplankton group, planktivorous fish (sub-divided into adults and juvenile), piscivorous fish and submerged macrophytes – all within a fully mixed water column. The model is able to analyse the probability of transition

between a macrophyte-dominated clear-water state and a phytoplankton-dominated turbid state. The daily change in phytoplankton biomass ($\Delta X/\Delta t$) attributable to each phytoplankton group is determined by:

$$\Delta X/\Delta t = (r' - R - S - G) X + RS - D \qquad (5)$$

where r' is the actual growth rate (d^{-1}), R is the accumulated loss due to respiration, mortality and excretion, S is the loss due to settling out of the water column, G is the loss due to zooplankton grazing (preference factors can be specified for individual phytoplankton groups), RS is a gain due to resuspension of phytoplankton biomass from the bottom sediments, and D is the loss due to dilution (or gain if phytoplankton biomass is supplied from inflow boundary). The actual growth rate (r', d^{-1}) is defined by:

$$r' = \mu_{max} \min\{ f(I), f(N), f(P), f(Si) \} f(T) \qquad (6)$$

where μ_{max} (day^{-1}) is the maximum growth rate at 20°C in the absence of significant limitation by light or nutrients, f(I), f(N) and f(P) represent limitation by light, nitrogen and phosphorus respectively, f(T) is a temperature function. The f(Si) function represents limitation by silica and applies only to diatoms. The nutrient limitation is modelled by inclusion of a dynamic intracellular nutrient store, described through the Droop equation (Riegman & Mur, 1984).

Calibration and validation of phytoplankton dynamics

As DYRESM-CAEDYM is the only model of the three that includes thermodynamics, DYRESM-CAEDYM was initially set up to derive water column temperatures for input to PROTECH and PCLake. To calculate the vertical distribution of temperature, DYRESM-CAEDYM requires daily average input data for six meteorological variables, including air

temperature (°C), short-wave radiation (W m^{-2}), cloud cover (fraction of whole sky) or long-wave radiation (W m^{-2}), vapour pressure (hPa), wind speed (m s^{-1}) and rainfall (m). These data were acquired from 10-20km national grids derived meteorological stations across Denmark. Daily inflow and outflow data are also required as boundary conditions to produce an accurate water and nutrient balance in the models. Where continuous flow data were not available, linear interpolation between monthly samples for flow and nutrient concentrations was used to derive daily values within the period 1990-2001. Residual inflow and/or outflow were derived from a water balance applied with daily time steps. A warm-up run of DYRESM-CAEDYM was run for the period 1990-1998, after which the model was calibrated for years 1999 and 2000. Model validation was subsequently performed on a dataset from 2001.The two year calibration and one year validation was performed for all three models. The coefficient of determination (r^2) and the mean relative absolute error (RE, %) were derived and used as means to quantify and compare goodness of fit for the three models to observed data for phytoplankton biomass, represented by total Chlorophyll a. Chlorophyll a measurements were available at monthly to biweekly intervals throughout the calibration and validation periods.

Calibration of phytoplankton dynamics in DYRESM-CAEDYM was mainly done by modifications to release rates of nutrients from the bottom sediments, intracellular nutrient parameters, maximum growth rates and zooplankton grazing rates. For PROTECH, the only modification during calibration was to allow for the release of sediment derived SRP (Soluble Reactive Phosphorus). PROTECH does not model this process directly, but can be forced through the addition of SRP to the water column during certain periods of the year. Therefore, 2.4 mg m^{-3} SRP was added to the water column each day between 1 June to 31 August. No parameters in the model were altered for the calibration. PCLake includes a

dynamic sediment nutrient pool, which will equilibrate with water column dynamics. Therefore, a warm-up period of 1990-1998 was also used for this model before calibration of years 1999-2000. For PCLake, calibration of phytoplankton dynamics was mainly done by modifications to internal nutrient parameters, maximum growth rates and zooplankton grazing parameters.

Future scenarios

Based on the EU ENSEMBLES project (van der Linden & Mitchell, 2009), where 19 regional climate models were used to generate an ensemble simulation of the IPCC A1B scenario for the location of seven major cities in Denmark (Boberg, 2010), three individual climate scenarios were derived (Table 1). In addition, two future nutrient load scenarios were generated and combined with climate scenarios, based on previous studies on the potential effects of future climate on total nitrogen (Jeppesen et al., 2011) and total phosphorus (Jeppesen et al., 2009) losses from land to waterways.

Table 1. Potential future climate scenarios, derived from the ENSEMBLES project (van der Linden & Mitchell 2009, Boberg, 2010).

	Daily temperature change relative to base (°C)	Increase in total nitrogen and phosphorus loads relative to base (%)
Base	-	-
Scenario 1	1.5	0
Scenario 2	3	0
Scenario 3	5	0
Scenario 4	5	+5
Scenario 5	5	+15

The future climate scenarios were implemented by a simple delta-change method, relative to daily air temperatures of the base scenario, where scenario 1 represents the time period around year 2050, scenario 2 represents the time period around 2100, and scenario 3 represents a very warm 2100 period. All scenarios have previously been identified as plausible in the ENSEMBLES project (van der Linden & Mitchell, 2009), where Boberg (2010) derived these future scenarios from probability density plots of predictions by 19 individual regional climate models. Boberg (2010) suggests, albeit to a small degree, that precipitation by 2050 and 2010 will change, generally with increases during winter and decreases during summer periods (in orders of magnitude of $0.1 - 0.5$ mm day^{-1}). Assuming that no interventions are done in terms of land-use management, this may to some extent result in increased nutrient loads to lakes. Hence, Jeppesen et al. (2009, 2011) also suggest that total phosphorus and nitrogen loads to temperate Danish waterways may increase by roughly 5-15% by the year 2100. To reflect this potential, we adapted an additional two scenarios, where phosphorus and nitrogen loads were increased by 5 and 15%, respectively, while at the same time climate change has caused air temperature to increase by 5ºC as simulated in Scenario 3 (Table 1).

Results

Calibration and validation

The models generally performed to the level achieved in other peer reviewed studies (e.g., review by Arhonditsis & Brett, 2004). The variation explained by the models increased considerably when looking at monthly means (Table 2), and even further when excluding the single, extremely high chlorophyll *a* concentration recorded in September 2001. While PCLake and PROTECH generally exhibited considerably higher r^2 values, relative to

DYRESM-CAEDYM, for the calibration and validation periods, the three models showed more similar performance when looking at the relative errors. In general, it was found that the ensemble mean of all three models was superior to any of the individual models (Fig. 1), in describing phytoplankton dynamics for the whole 1999-2001 period (Table 2).
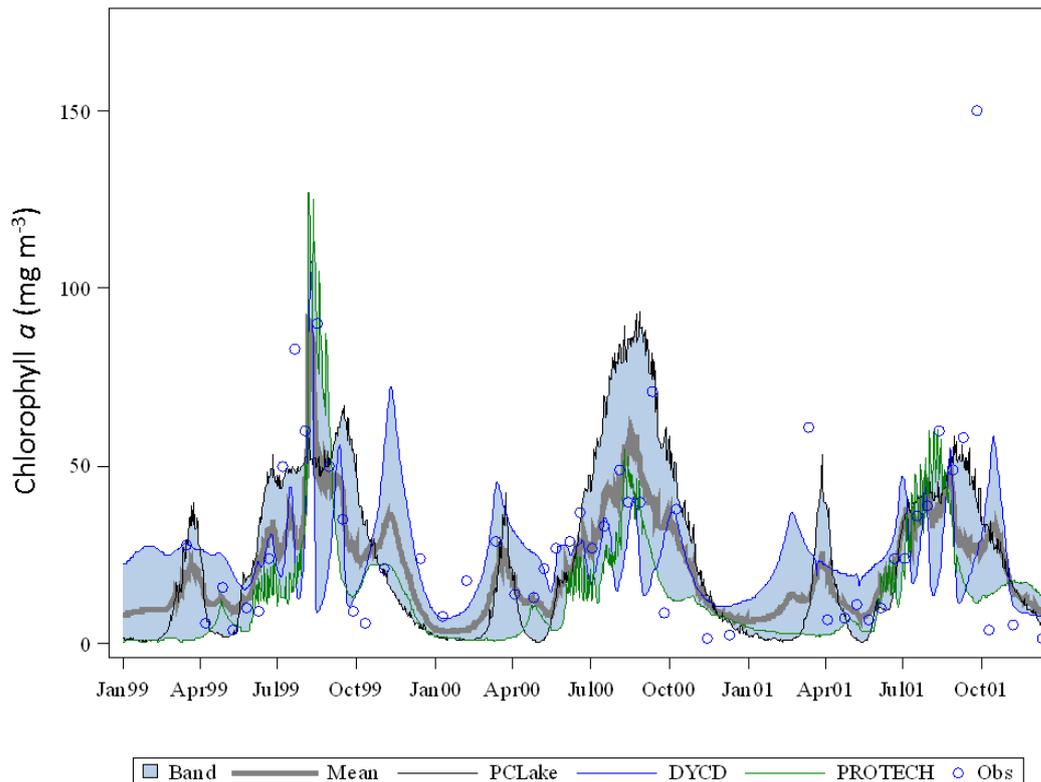

Figure 1. Calibration (1999-2000) and validation (2001) of the three ecological models (line plots) to observed phytoplankton dynamics (blue circles in scatter plot). The blue shaded "Band" represents the total range (maximum/minimum) of the three models and the thick grey "Mean" line represents the ensemble mean of all three models. PCLake is represented by black line, DYRESM-CAEDYM (DYCD) by blue line and PROTECH by green line.

Table 2. Summary of calibration (1999-2000) and validation (2001) statistics for individual models and by using the ensemble mean of all models.

		R^2				RE			
		1999-2000	2001	2001*	1999-2001	1999-2000	2001	2001*	1999-2001
Day-by-day match	PCLake	0.34	0.24	0.33	0.24	121	120	123	121
	DYCD	0.01	0.01	0.02	0.01	102	162	167	121
	PROTECH	0.49	0.05	0.31	0.24	72	102	103	82
	Ensemble mean	0.47	0.13	0.32	0.27	83	113	115	92
Monthly means	PCLake	0.48	0.68	0.62	0.44	65	74	77	67
	DYCD	0.13	0.04	0.27	0.08	59	103	106	73
	PROTECH	0.55	0.11	0.31	0.31	53	101	103	68
	Ensemble mean	0.61	0.36	0.53	0.45	39	79	80	52

* Excluding the September 2001 observation of 150 mg Chl$a$ m^{-3}

Future scenario simulations

Throughout the three climate scenarios, where temperatures are steadily increasing (SC1 through SC3), the ensemble mean simulation suggested that total phytoplankton biomass will increase, in particular during summer months (Table 3), albeit there are considerable variation between the individual model predictions (Fig. 2). Concurrently, the contribution of cyanobacteria to the total phytoplankton biomass increased and consequently the number of days where their biomass increased beyond WHO limits for recreational use increased from 150 to 181 and 8 to 42 days per year for the 10 and 50 mg m^{-3} WHO limit, respectively.

Table 3. Summary of ensemble mean results from the scenario simulations based on annual and summer (June-August) averages.

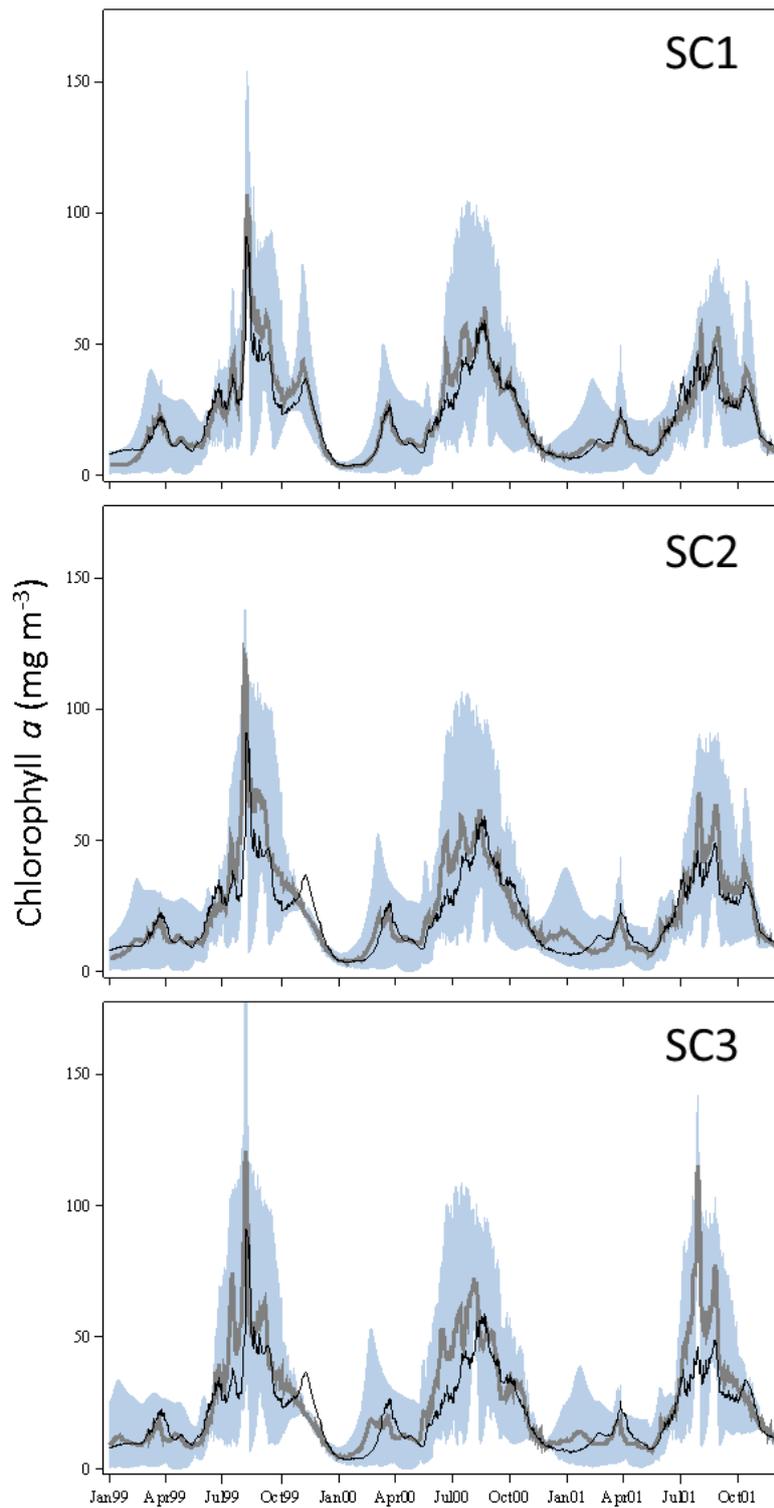|	Total Chlorophyll a (mg Chla m^{-3})		% cyanobacteria biomass of total chlorophyll a		Days per year exceeding WHO limits (cyanobacteria chlorophyll a)	
	Annual	Summer	Annual	Summer	10 mg m^{-3}	50 mg m^{-3}
Base	21.1	28.9	59.2	51.7	150	8
SC1	22.2	30.2	65.3	66.0	157	23
SC2	23.1	34.1	71.7	77.7	172	27
SC3	24.8	42.8	76.1	85.9	181	42
SC4	25.0	41.8	75.6	84.9	180	37
SC5	24.5	40.0	72.2	84.3	175	27

Figure 2. The ensemble mean simulation of total phytoplankton biomass (chlorophyll *a*) for scenarios (SC) 1-3 (grey lines) relative to the uncertainty range of the three models (blue shaded band), and the ensemble mean from the base simulation (black line).

When the very warm climate scenario (SC3) was combined with increased nutrient loads

(SC4 and 5), there was only a small effect observed in the ensemble mean simulations (Table

3, Fig. 3). Furthermore, when nutrient loads were increased the most (Fig. 3, SC5), there was

even a tendency for the overall phytoplankton biomass decrease slightly, relative to the

scenario where only temperatures are increased (Fig. 2, SC3). However, the modelled

uncertainty for scenarios 4 and 5 was somewhat greater, which was illustrated by a widening

in the ensemble uncertainty range (Fig. 3 relative to Fig. 2), suggesting that the three

individual models were most divergent in their predictions for these particular scenarios.
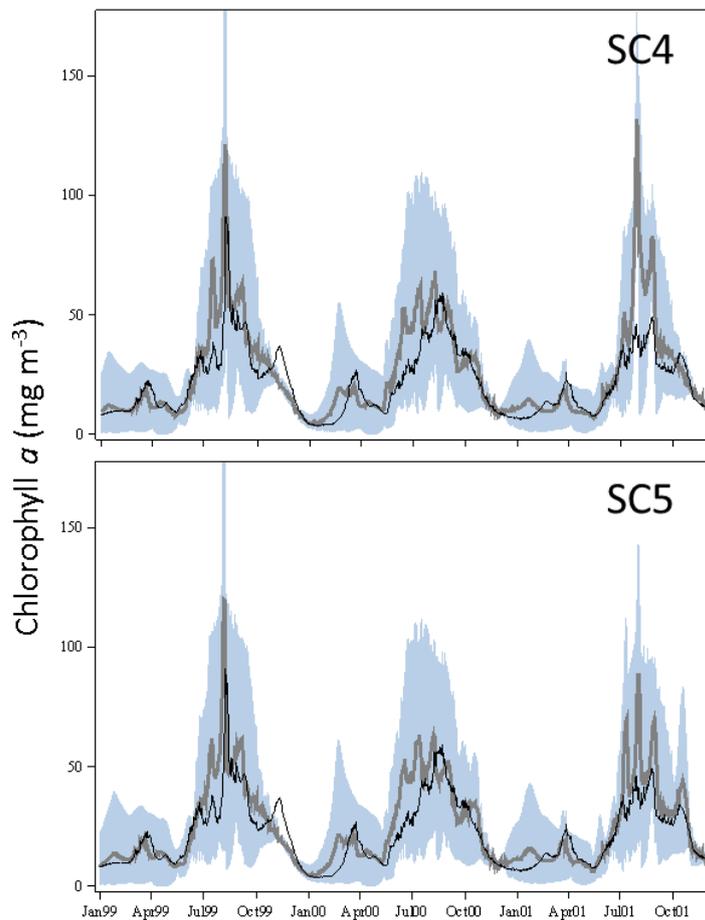

Figure 3. The ensemble mean simulation of total phytoplankton biomass (chlorophyll *a*) for

scenarios 4-5 (grey lines) relative to the uncertainty range of the three models (blue shaded

band), and the ensemble mean from the base simulation (black line).

The effects of warming in SC1-SC3 were most pronounced for cyanobacterial biomass, with a considerable simulated increase during summer (Fig. 4). Hence, whilst annual and summer total chlorophyll *a* biomass in SC3 relative to the Base scenario increased on average by 18 and 48 %, respectively, cyanobacterial biomass increased by 29 and 66%, respectively. The combined effects of warming and increased nutrient loads showed little effect on cyanobacteria relative to warming alone. As was observed for total phytoplankton biomass, the ensemble mean simulation also suggested that cyanobacterial biomass could be slightly reduced in scenarios 4 and 5 relative to scenario 3, albeit, as noted before, the model uncertainty is also greater for scenarios 4 and 5 (Fig. 5 relative to Fig. 4).
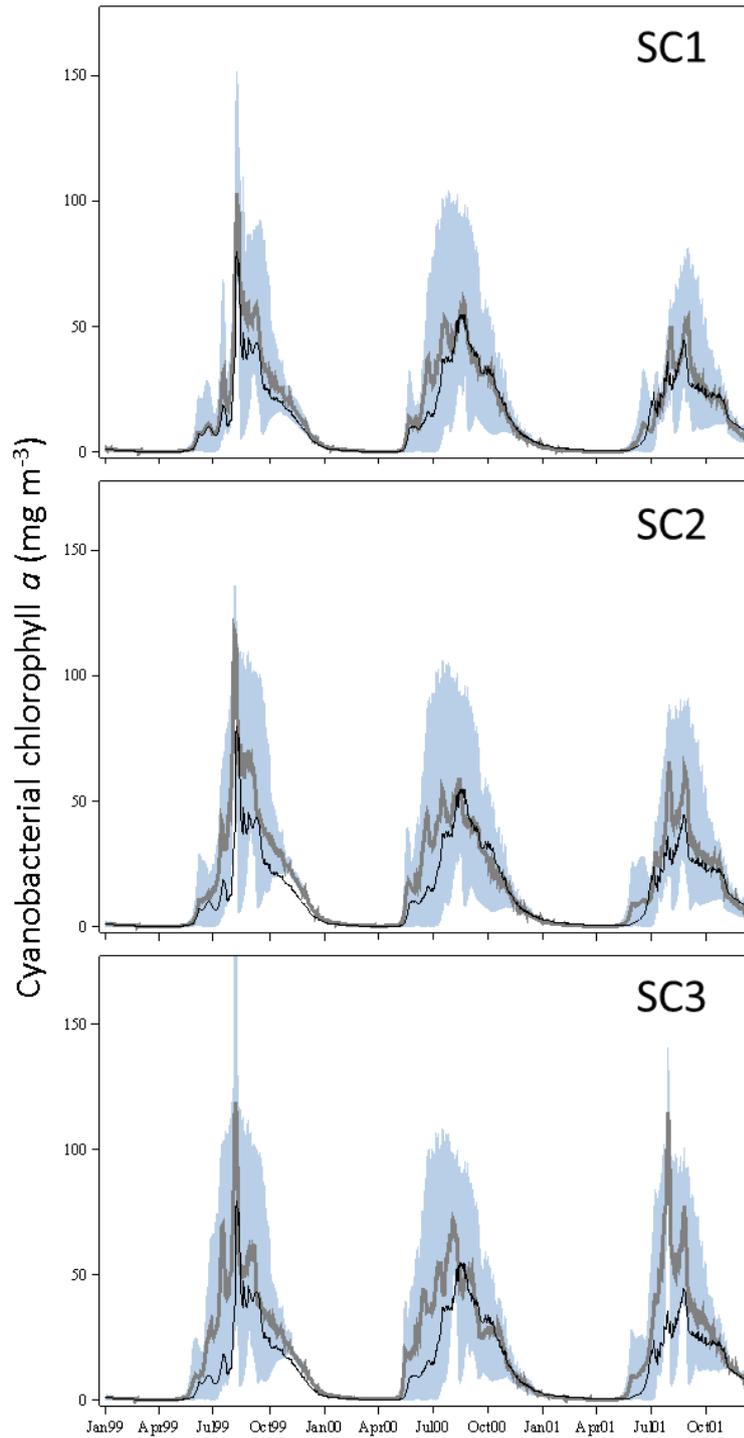
Figure 4. The ensemble mean simulation of cyanobacteria biomass (chlorophyll *a*) for scenarios 1-3 (grey lines) relative to the uncertainty range of the three models (blue shaded band), and the ensemble mean from the base simulation (black line).
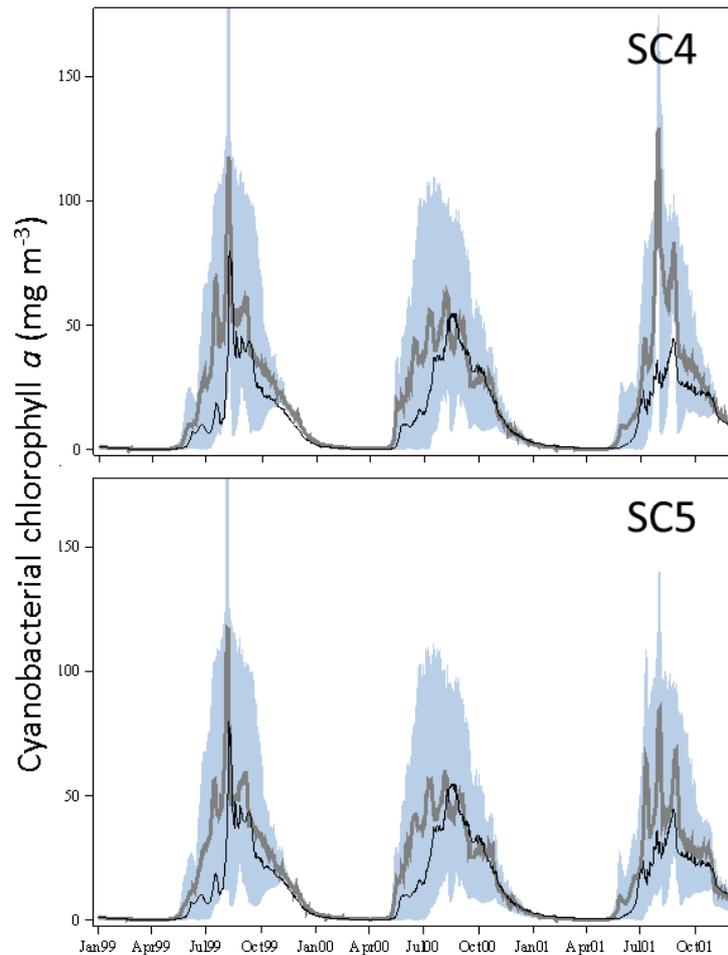
Figure 5. The ensemble mean simulation of cyanobacteria biomass (chlorophyll *a*) for scenarios 4-5 (grey lines) relative to the uncertainty range of the three models (band), and the ensemble mean from the base simulation (black line).

Discussion

The ensemble modelling approach

While we are the first to apply several individual lake models to the same aquatic ecosystem, the ensemble modelling approach has been used for a number of years for weather forecasts and global circulation models (GCM), and is common practise when, for example, the IPCC reports on the potential effects of anthropogenic activities on future climate. It was found that

the ensemble mean of the three models applied in this study generally was superior to any individual model in describing the observed seasonal phytoplankton dynamics, which corresponds well with the experiences found in climate modelling studies (Palmer et al., 2005). From a climate modelling perspective, Tebaldi & Knutti (2007) elaborates that "for a single given diagnostic or variable, the multi-model performance might not be significantly better than the single best model, but studies indicate that the improvements are more dramatic if an aggregated performance measure over many diagnostics is considered", and Hagedorn et al. (2005) argue that the largest benefit is seen in "the consistently better performance of the multi-model when considering all aspects of the predictions". While our study supports their findings, it is difficult to see how the ensemble modelling approach will become common practise in aquatic sciences within the near future, because there are currently no – on the contrary to weather forecasting and global circulation models – operational systems for data sharing, data assimilation and automatic calibration, that would readily allow scientists to embark in such studies. Nevertheless, given the results in our study, this is something that should clearly be strived for.

Deriving uncertainty from the ensemble simulation

The uncertainty of the model predictions, represented by the blue-shaded range delineated in figures (e.g. Fig. 1), suggest that the uncertainty is greatest around the time where biomass levels peak during spring and summer months. Hence, the models generally tend to agree on the timing of the clear-water phase between the spring and summer blooms, as the uncertainty band clearly narrows around the ensemble mean (e.g. Fig. 1). For the scenario simulations, the uncertainty around the ensemble mean was largest for scenarios where climate warming and increased external nutrient loads were combined, relative to the scenarios with warming alone. This is likely the result of the different models conceptual

handling of nutrient cycling (see Mooij et al., 2010 for comparison), and how this cycle interacts with phytoplankton dynamics. Mooij et al. (2010) suggest that improving the ability to describe interactions between nutrients in bottom sediments and the overlying water column is a key element for further enhancing model performance of aquatic ecosystem models. Such improvement would therefore also likely reduce the uncertainty of the models predictions.

Future predictions by the ensemble simulation

Long-term effects of climate change (e.g. by the year 2100) have been studied using models before (e.g. Mooij et al., 2007; Trolle et al., 2011) with conclusions similar to ours, that overall phytoplankton biomass is likely to increase, and cyanobacteria will become a more dominant feature of the phytoplankton species composition. In our study, given even the relatively modest increases in air temperature of the near-future scenario (SC1, representing 2050), the ensemble simulation suggests, rather alarmingly, that the number of days where the cyanobacteria biomass exceeds the highest WHO limit will increase dramatically from 8 to 23 days per year. As Lake Engelsholm is a very typical Danish lake, in terms of size, trophic status and species composition, is it very likely that many other lakes in Denmark as well as worldwide could suffer a similar fate. The need for reliable model predictions are therefore likely to accelerate further, as water quality degrades, and land and water management authorities are on the lookout for ways to quantify the necessary actions required to maintain or even improve water quality.

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