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Adaptation and multiple parameter optimization of the simulation model SALMO as prerequisite for scenario analysis on a shallow eutrophic Lake

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ABSTRACT

SALMO (Simulation by means of an Analytical Lake Model) describes the seasonal dynamics of PO_4-P, NO_3-N, detritus, chlorophyta, bacillariophyta, cyanophyta and cladocerans of the epilimnion and hypolimnion of stratified lakes by complex ordinary differential equations. This study adapted the model for shallow polymictic lakes and developed a real-coded genetic algorithm to optimize key parameters identified by sensitivity analysis. Meiliang Bay of Taihu Lake is taken as a study case, and 5 years data were collected for model calibration and validation. Given the good performance of the adapted and optimized SALMO, the model was applied to analyze four management scenarios for the Meiliang Bay, including 50% reduction of external nutrient loads, 50% reduction of internal nutrient loads, 50% reduction of zooplankton mortality and 1 °C increase of water temperature. The study showed: the adapted SALMO model is applicable to shallow polymictic and hypertrophic lakes; the real-coded genetic algorithm significantly improved the model efficiency and accuracy; reduction of nutrients from sediment release appears to be a key measure for controlling cyanobacteria blooms in Lake Taihu; biomanipulation is very delicate and can only be implemented with sufficient investigation and great caution; the increase of algae biomass due to water temperature rise indicates extra potential threat from climate change to lake ecosystems.

1. Introduction

Models that combine limnological theory and experimental research results can be powerful tools for studying lake ecosystem dynamics, and determining management measures for eutrophication control (Han et al., 2003; Chen et al., 2009). Over the past 30 years, numerous process-based models have been developed and applied to study eutrophication and algal blooms, such as EFDC (Hamrick, 1992), WASP (Ambrose et al., 1993), CE-QUAL-W2 (Cole and Buchak, 1995), DYRESM-CAEDYM (Gal et al., 2009) and Delft3D-Eco (Los et al., 2008). For shallow lakes such as Taihu, several three-dimensional hydro-environmental models have been developed (Zhu and Cai, 1998; Hu et al., 1998; Mao et al., 2008) to simulate the hydrodynamics and nutrient cycling as well as algae dynamics. Alternatively, powerful rule-based models are being developed utilizing the information content of ecological data and heuristics by means of artificial neural networks (Recknagel et al., 1997), fuzzy logic (e.g. Chen and Mynett, 2003), and evolutionary computation (Recknagel et al., 2013). These models show superior performance in short-term forecasting of phyto- and zooplankton population dynamics, and allow simultaneous simulation of phyto- and zooplankton dynamics in lakes by model ensembles (Recknagel et al., 2013).

The lake model SALMO (Benndorf and Recknagel, 1982; Recknagel and Benndorf, 1982) aggregates the algae into three functional groups (diatoms, green algae and blue-green algae), and allows simulation of the seasonal dynamics of the phytoplankton phyla diatoms, green algae and blue-green algae and the herbivorous zooplankton cladocera, as well as concentrations of phosphate, nitrate, detritus and oxygen, by process-based first-order kinetics represented by ordinary differential equations (Recknagel et al., 2008). Previous applications of SALMO (Recknagel et al., 1995, 2008; Walter et al., 2001) have demonstrated the applicability of the model to a variety of stratified lakes and climate conditions.

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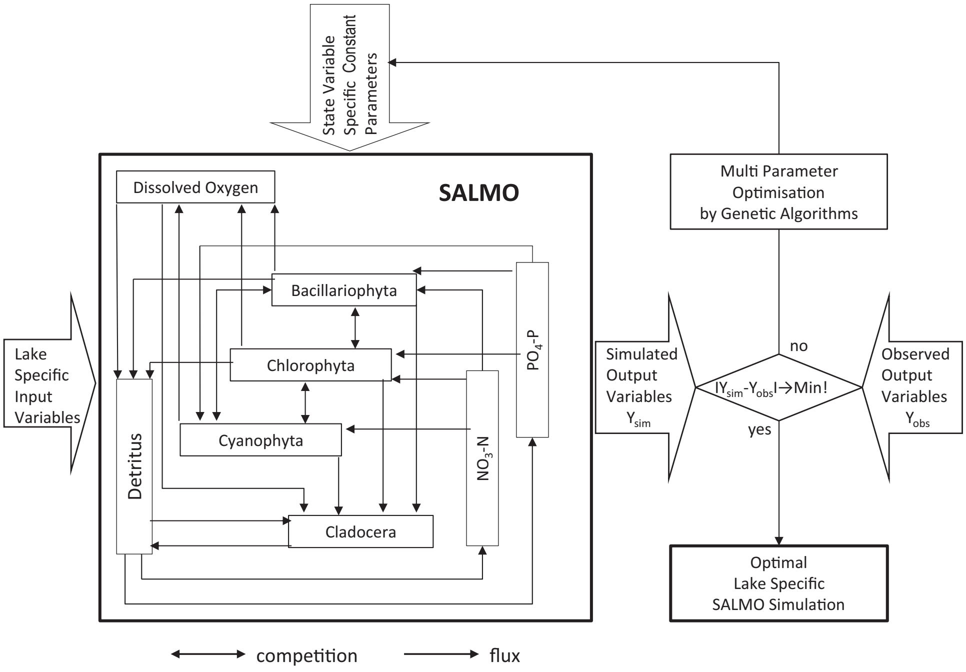

Fig. 1. Diagram of model structure and parameter optimization routine of SALMO.

Although SALMO has been successfully used in different lakes across the world, application to distinctively shallow polymictic and hypertrophic lakes is little reported. Adapting the model structure as well as calibrating the model parameters for lakes with such extreme conditions is of interest.

In addition, SALMO contains a large number of parameters, making traditional model calibration methods such as trial and error, fast gradient, HSY (Hornberger-Spear-Young) (Beck, 1987) and GLUE (Generalized Likelihood Uncertainty Estimation) (Beven and Binley, 1992; Li et al., 2013) unsuitable. The trial and error method requires manual adjustment of model parameters, which makes it difficult to adjust several parameters at the same time (Liu et al., 2007). The HSY and GLUE algorithms are based on random sampling, which leads to their calculation time growing exponentially when the number of parameters is increased (Wang et al., 2005). Fast gradient is a complex algorithm depending on initial parameter values, and usually gets stuck at local optima (Li et al., 2013). In order to have a high efficient and unbiased model, an auto-calibration process is needed for SALMO.

This study modified the SALMO structure for shallow polymictic lakes and developed a real-coded genetic algorithm (RCGA) to optimize the key parameters of the adapted model, and then applied the calibrated model for management scenario analyses.

2. Materials and methods

2.1. SALMO model and adaptation

The model SALMO was developed to study the eutrophication processes in stratified lakes and reservoirs (Benndorf and Recknagel, 1982) by allowing simulation of the population dynamics of diatoms, green algae, blue-green algae and cladocerans as well as concentrations of PO_4-P, NO_3-N, DO and detritus in lakes. Fig. 1 shows the model structure of SALMO, along with the embedded subroutine for parameter optimization.

SALMO is a two-layer model to simulate the epilimnion and hypolimnion of stratified lakes. For shallow lakes without stable seasonal stratification but having temporary diurnal stratification, some modifications were made to SALMO before applying it. These improvements included adding a reaeration equation (Arhonditsis and Brett, 2005), transferring plankton residues to the detritus (Law et al., 2009), and removing the equation for vertical flux between the epilimnion and hypolimnion. The equations added are as follows.

$$OAER = KRE \cdot \frac{SAT - O}{ZMIX} \tag{1}$$

$$DTRAN = RATD \cdot \left(\sum_{i=1}^{3} (RA_i \cdot A_i) + RZ \cdot Z \right) + RATMD \cdot ZMO + RATZD \cdot (1 - AZ) \cdot GRAZ \cdot Z \tag{2}$$

$OAER$ is the rate of re-aeration ($\mathrm{g\,m^{-3}\,d^{-1}}$), KRE is the reaeration coefficient ($\mathrm{m\,d^{-1}}$), O is the dissolved oxygen concentration ($\mathrm{g\,m^{-3}}$), $ZMIX$ is the mean mixing depth (m); $DTRAN$ is the rate of transformation from the plankton residues to the detritus ($\mathrm{g\,m^{-3}\,d^{-1}}$), $RATD$ is the transformation coefficient of the plankton endogenous metabolism, RA_i is the respiration rate of algae ($\mathrm{d^{-1}}$), A_i is the biomass of three algae ($\mathrm{g\,m^{-3}}$, $i = 1$: diatoms; $i = 2$: green algae; $i = 3$: blue-green algae), RZ is the respiration rate of zooplankton ($\mathrm{d^{-1}}$), Z is the biomass of zooplankton ($\mathrm{g\,m^{-3}}$), $RATMD$ is the transformation coefficient of dead zooplankton, ZMO is the rate of zooplankton mortality ($\mathrm{g\,m^{-3}\,d^{-1}}$), $RATZD$ is the transformation coefficient of zooplankton excretion, AZ is the assimilation coefficient, $GRAZ$ is the grazing rate of zooplankton ($\mathrm{d^{-1}}$).

2.2. Real-coded genetic algorithm for multiple parameters optimization

The genetic algorithm (GA) is a biologically inspired optimization technique based on natural selection, reproduction and mutation (Holland, 1975). Because a GA applies probabilistic rules rather than deterministic transition rules, it can obtain and guide optimizing space automatically. Compared with conventional methods, a genetic algorithm (GA) is more efficient for global optimum searches and has a faster convergence speed. GA has been increasingly used for parameter optimization in hydro-environmental models (Pelletier et al., 2006; Goktas and Aksoy, 2007; Wang et al., 2010; Bau and Lee, 2011). Due to their strong capability in multiple parameter optimizations, this study applied a genetic algorithm to calibrate SALMO.

Results of a sensitivity analysis by Recknagel (1984) were used to select 30 key parameters (Table 1) that are strongly related to algae growth for optimization (Guo et al., 2012a,b). Their value ranges within the optimization were obtained from relevant literature (Bowie et al., 1985; Pei and Ma, 2002; Arhonditsis and Brett, 2005; Cao et al., 2008; Qin et al., 2011).

These 30 selected parameters of SALMO were calibrated and optimized by GA through the following main procedures.

2.3. Encoding the parameter optimization

The parameters for optimization should be first encoded into a chromosome-like structure called a ‘string’. Although binary encoding is the most common method to represent the optimized parameters, it occupies too much computer memory, and introduces discretization errors when it encodes a real number. In addition, encoding and decoding operations take more computation time, which leads to low efficiency (Pan et al., 2006). As an alternative, real encoding uses the real number as the gene of chromosomes and works directly on the real number, so it is more suitable for dealing with continuous search spaces with large dimensions. Real encoding reduces the computational complexity and improves the calculation efficiency. Therefore, this paper developed a real-coded GA to calibrate the sensitive parameters of SALMO. The real encoding method is shown as follows:

$$x_j = r \cdot (x_{j\,\max} - x_{j\,\min}) + x_{j\,\min} \quad (j = 0, 1, \ldots, n) \tag{3}$$

In this equation, x_j stands for the first j gene of the individual in population, which is the first j parameter to be optimized. r is a random number between (0,1), $x_{j\max}$ and $x_{j\min}$ are the maximum and minimum values of the first j gene respectively, n is the number of parameters to be optimized.

2.4. Fitness function

The GA searches for the best individual that has the largest fitness under the guidance of the fitness of the entire population. The SALMO model has eight state variables, the concentrations of PO_4-P, NO_3-N, dissolved oxygen, diatoms, green algae, blue-green algae, zooplankton and detritus. However, in this study the focus and consequently the selected parameters for calibration were mainly related to the three types of algae, zooplankton and dissolved oxygen (DO). Therefore, the fitness function is defined as:

$$f = \left[\frac{\sum_{i=1}^{n} (|P_i' - P_i/P_i' + |A_{1i}' - A_{1i}/A_{1i}' + |A_{2i}' - A_{2i}/A_{2i}' + |A_{3i}' - A_{3i}/A_{3i}' + |Z_i' - Z_i/Z_i')}{m} \right]^{-1} \tag{4}$$

where m is the total number of observations; $P_i', A_{1i}', A_{2i}', A_{3i}', Z_i'$ and $P_i, A_{1i}, A_{2i}, A_{3i}, Z_i$ respectively stand for the measured and simulated values of DO concentration, algae (diatoms, green algae, blue-green algae) biomass and zooplankton biomass in the ith day. The larger the function value, the better fitness the individual has.

2.5. Selection operator

The genetic algorithm generates new individuals by operations of crossover and mutation, and the roulette wheel selection method was used in this study to select individuals for operations. The probability of each individual being selected is proportional to its fitness. To prevent damage to the good individuals in the population by these operations, an elite-preserving operator was adopted. If the fitness of the best individual in the next generation is lower than the current generation, after crossover and mutation, the worst individual in the next generation should be replaced by the best individual in the current generation.

2.6. Crossover operator

The arithmetic crossover operator, which is often used in real encoding, combines the two new individuals linearly. Arithmetic crossover can be divided into uniform and non-uniform methods. In this study, non-uniform arithmetic crossover was adopted. It produces two new offspring according to the following equations.

$$\begin{cases} \begin{cases} X_1^{T+1} = r_1 \cdot X_1^T + (1 - r_2) \cdot X_2^T \\ X_2^{T+1} = (1 - r_1) \cdot X_1^T + r_2 \cdot X_2^T \end{cases} & \text{if} \quad \text{random}(0, 1) = 1 \\ \begin{cases} X_1^{T+1} = (1 + r_1) \cdot X_1^T - r_2 \cdot X_2^T \\ X_2^{T+1} = r_1 \cdot X_1^T + (1 - r_2) \cdot X_2^T \end{cases} & \text{if} \quad \text{random}(0, 1) = 1 \end{cases} \tag{5}$$

X_1^T and X_2^T are the selected individuals for crossover; X_1^{T+1} and X_2^{T+1} are the new individuals after crossover; r_1 and r_2 are random numbers in [0, 1].

2.7. Mutation operator

The mutation operator is analogous to natural genetic mutation, which ensures the individual diversity and prevents the premature termination of GA at local optimal. Non-uniform mutation was adopted in this study. If the gene x_k in individual $X = \{x_1, x_2, \ldots, x_k, \ldots, x_n\}$ is selected to mutate and the value range of gene x_k is $[x_{k\min}, x_{k\max}]$, then the value of the new gene can be calculated by the following equation:

$$x_k' = \begin{cases} x_k + \Delta(t, x_{k\,\max} - x_k) & r' < 0.5 \\ x_k + \Delta(t, x_{k\,\min} - x_k) & r' > 0.5 \end{cases} \tag{6}$$

$$\Delta(t, y) = y \cdot (1 - r^{(1-t/T)^2}) \tag{7}$$

where t is the generation number; T is the maximum number of generations; and r' is a random number between [0, 1].

2.8. Configuration of genetic algorithm

The efficiency of the GA was influenced by the population size, crossover probability and mutation probability. In this research, these parameters were determined after many trials, and the final configuration was: population size 200; maximum number of generations 400; crossover probability 0.8; mutation probability 0.05. Calculation terminated when the total iterations reached the maximum number of generations or the fitness f of the best individual was over 10.

2.9. Model performance evaluation

To quantitatively evaluate the model performance, the index of agreement (Willmott, 1981) was calculated. The index of agreement (d) measures the standardized agreement degree between model outputs and observations. It is given by:

$$d = 1 - \frac{\sum_{i=1}^{m} (x_i - x_i')^2}{\sum_{i=1}^{m} (|x_i' - \bar{x}| + |x_i - \bar{x}|)^2} \tag{8}$$

Table 1
Key parameters to be optimized for the adapted SALMO model.

Parameter	Meaning	Value range
GI	Inhibition factor of the ingestion rate due to light (dimensionless)	0.6–1.0
GMAX	Maximum grazing rate by zooplankton (d^{-1})	1.0–1.9
GMIN	Minimum grazing rate by zooplankton (d^{-1})	0.1–0.4
RZMIN	Respiration rate of zooplankton at optimal temperature for feeding but without food supply (d^{-1})	0.06–0.16
RZTMIN	Respiration rate of zooplankton near 0 °C and optimal food supply (d^{-1})	0.02–0.06
RXMF	Portion of the gross photosynthesis rate which is consumed by respiration additionally to the basis respiration (dimensionless)	0.24–0.36
KP_1	Half-saturation constant of the relationship between phosphorus and rate of photosynthesis of the diatoms at minimum diatoms biomass ($mg\,m^{-3}$)	1.0–9.0
KP_2	Half-saturation constant of the relationship between phosphorus and rate of photosynthesis of the green algae at minimum green algae biomass ($mg\,m^{-3}$)	5.0–24.0
KP_3	Half-saturation constant of the relationship between phosphorus and rate of photosynthesis of the blue-green algae at minimum blue-green algae biomass ($mg\,m^{-3}$)	1.0–15.0
PFA_1	Grazing preference factor for diatoms (dimensionless)	0.55–1.0
PFA_2	Grazing preference factor for green algae (dimensionless)	0.5–1.0
PFA_3	Grazing preference factor for blue-green algae (dimensionless)	0.18–0.5
$PHOMAX_1$	Maximum photosynthesis of diatoms under optimal conditions (d^{-1})	1.0–3.0
$PHOMAX_2$	Maximum photosynthesis of green algae under optimal conditions (d^{-1})	2.0–4.0
$PHOMAX_3$	Maximum photosynthesis of blue-green algae under optimal conditions (d^{-1})	1.0–5.0
$PHOMIN_1$	Minimum photosynthesis of diatoms under low temperature (d^{-1})	0.0–0.55
$PHOMIN_2$	Minimum photosynthesis of green algae under low temperature (d^{-1})	0.0–0.7
$PHOMIN_3$	Minimum photosynthesis of blue-green algae under low temperature (d^{-1})	0.0–0.41
$RXTOPT_1$	Optimum respiration rate of diatoms (d^{-1})	0.05–0.25
$RXTOPT_2$	Optimum respiration rate of green algae (d^{-1})	0.05–0.25
$RXTOPT_3$	Optimum respiration rate of blue-green algae (d^{-1})	0.05–0.25
$TOPTA_1$	Optimum temperature for growth of diatoms (°C)	14–22
$TOPTA_2$	Optimum temperature for growth of green algae (°C)	20–25
$TOPTA_3$	Optimum temperature for growth of blue-green algae (°C)	25–32
VA_1	Sinking velocity of diatoms ($m\,d^{-1}$)	0.017–0.35
VA_2	Sinking velocity of green algae ($m\,d^{-1}$)	0.016–0.25
VA_3	Sinking velocity of blue-green algae ($m\,d^{-1}$)	0.020–0.15
YPA_1	Phosphorus yield coefficient of diatoms ($g\,mg^{-1}\,d^{-1}$)	0.5–1.0
YPA_2	Phosphorus yield coefficient of green algae ($g\,mg^{-1}\,d^{-1}$)	0.3–0.6
YPA_3	Phosphorus yield coefficient of blue-green algae ($g\,mg^{-1}\,d^{-1}$)	0.8–1.2

where m is the number of observations; x_i is the ith observation; x_i' is the corresponding model output; $\bar{x}$ is the mean of the observations. The value of d has a range between 0 and 1, where 1 indicates a perfect match, and 0 indicates no agreement at all.

2.10. Study area and data collection

Lake Taihu, which is characterized by its large surface area and shallowness, is the third largest lake in China. It has a total volume of $4.43 \times 10^9\ m^3$, with a surface area of $2338\ km^2$ and a mean depth of 1.9 m (Mao et al., 2008). It is located in the Yangtze delta, which is a highly industrialized area that largely depends on the water supply from the lake. However, rapid economic development and population increase over the past 20 years is coinciding with pollution and deteriorating lake water quality (Qin et al., 2007), making eutrophication and cyanobacteria blooms critically important issues for the Taihu basin (Hu et al., 2006; Yang et al., 2008). Although great efforts are being undertaken for the ecological restoration of Lake Taihu, there is a need to improve the understanding of lake behaviour in response to control measures, and to inform decisions on lake management.

Meiliang Bay is one of the four major embayments of Lake Taihu, and is situated in the north of the Lake. It is the major water source and scenic area of Wuxi city. The bay is 8 km wide from east to west, and 14 km long from north to south, with an average depth of 1.95 m (Zhu and Cai, 1998; Zhang et al., 2008). There are several tributaries flowing into Meiliang Bay, while this study only considered three main rivers (Fig. 2). The water exchange between Meiliang Bay and the centre of the Taihu Lake was also considered. There are five sampling sites for water quality in Meiliang bay (Fig. 1). As the Tuoshan site is located at the interface between central Taihu Lake and Meiliang bay, the data is used to represent the quality of water exchanged between the central lake and the bay. Water quality data for the years 2005, 2006, 2009, 2010 and 2011 were collected during the study at a monthly interval including water temperature, dissolved oxygen, chemical oxygen demand, ammonia, nitrate, nitrite, total nitrogen, phosphate, total phosphorus, green algae biomass, diatom biomass, blue-green algae biomass, chlorophyll-a and zooplankton biomass. The data in 2005 and 2010 were used to calibrate the model, and the data in 2006, 2009 and 2011 were used for model validation.

3. Results

3.1. Validation of SALMO

The calibration results in year 2005 and 2010 are presented in Fig. 3, and the values of parameters before and after optimization

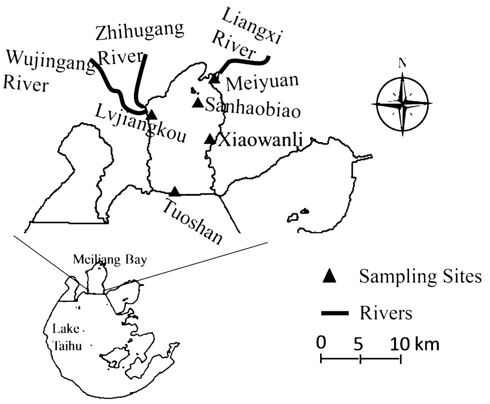

Fig. 2. Rivers connected with Meiliang Bay and the distribution of sampling stations.

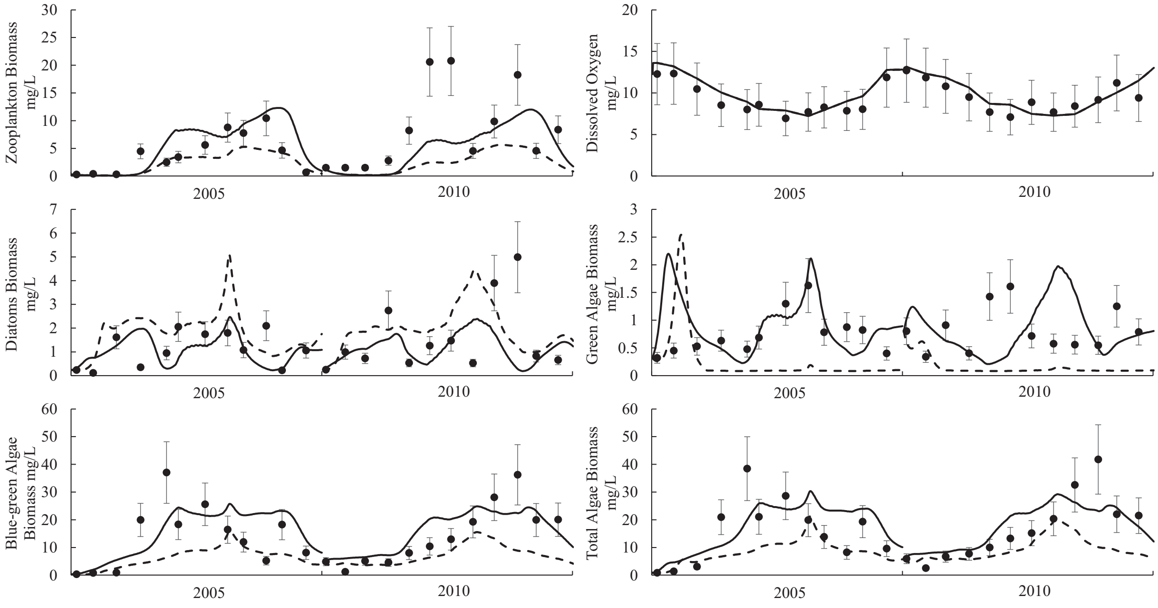

Fig. 3. Comparison between simulation results before and after optimization for the model calibration data (the solid line is the results after optimization; the broken line is the results before optimization; the dots are the measured values).

Table 2
The optimized values of the 30 key parameters.

Parameters	GI	GMAX	GMIN	RZMIN	RZMAX	RXMF	KP1	KP2	KP3	PFA1
Before optimization	0.8	1.3	0.26	0.08	0.05	0.3	1.7	9.5	1.7	1.0
After optimization	0.76	1.9	0.13	0.1	0.02	0.3	2.0	6.0	3.0	0.6

Parameters	PFA_2	PFA_3	$PHOMAX_1$	$PHOMAX_2$	$PHOMAX_3$	$PHOMIN_1$	$PHOMIN_2$	$PHOMIN_3$	$RXTOPT_1$
Before optimization	1.0	0.3	2.37	3.3	2.37	0.17	0.35	0.0	0.06
After optimization	0.5	0.18	2.2	2.8	4.0	0.30	0.50	0.0	0.20

Parameters	$RXTOPT_2$	$RXTOPT_3$	$TOPTA_1$	$TOPTA_2$	$TOPTA_3$	VA_1	VA_2	VA_3	YPA_1	YPA_2	YPA_3
Before optimization	0.06	0.06	21	23	30	0.1	0.1	0.05	0.8	0.41	1.0
After optimization	0.20	0.17	16	21.5	30	0.1	0.064	0.03	0.98	0.3	1.2

are listed in Table 2. In general, the optimized values are within the ranges from the literature (Table 1). From the value of $TOPTA_i$, it is seen that the diatoms prefer low temperature, while blue-green algae prefer high temperatures. With the consideration of $PHOMAX_i$ and $PHOMIN_i$, it is found that temperature has the lowest effect on the photosynthetic rate of blue-green algae.

Fig. 4 illustrates the simulation results of Meiliang bay in 2006, 2009 and 2011 for the validation data, using the optimized values of the parameters.

Both Figs. 3 and 4 indicate that the parameter optimization improved the simulation accuracy of DO, zooplankton, green algae and blue-green algae biomass. The assessment of the model performance by the index of agreement *d* is shown in Table 3. For the calibration data, the *d* values are 0.52, 0.49, 0.80 and 0.80 for diatoms, green algae, blue-green algae and total algae respectively. They are mostly higher than 0.5 except for green algae; in particular, the model captured blue-green algae dynamics well. For the validation data, the *d* values are 0.40, 0.52, 0.69 and 0.69 for diatoms, green algae, blue-green algae and total algae respectively. They are mostly higher than 0.5 except for diatoms. This indicates that the model performance is in general acceptable. However, Fig. 3 shows that the model failed to capture some high peaks of blue-green algae biomass.

Table 3
Quantitative evaluations on the performance of the calibrated model.

	Dissolved oxygen	Zooplankton	Diatoms
Calibration	0.92	0.65	0.52
Validation	0.88	0.48	0.40

	Green algae	Blue-green algae	Total algae
Calibration	0.49	0.80	0.80
Validation	0.52	0.69	0.69

The measured concentrations of diatoms displayed fast changes in late spring and summer, which was not matched by the model simulation. However, there was a good correspondence between measured and simulated values in the other periods. For the green algae, both the simulation results before and after optimization differed from the measured values in summer, but the optimized results improved during spring and autumn.

3.2. Scenario analysis

SALMO can quantitatively evaluate different restoration options for eutrophication by scenario analysis (Benndorf and Recknagel, 1982), so the optimized SALMO model was used to analyze four scenarios that are of theoretical nature or management relevance. Scenario 1 simulates the effects of reducing the external loads of PO_4-P and NO_3-N by 50%; Scenario 2 simulates the effects of reducing the internal loads of PO_4-P and NO_3-N by 50%; scenario 3 simulates a biomanipulation of reducing the zooplankton

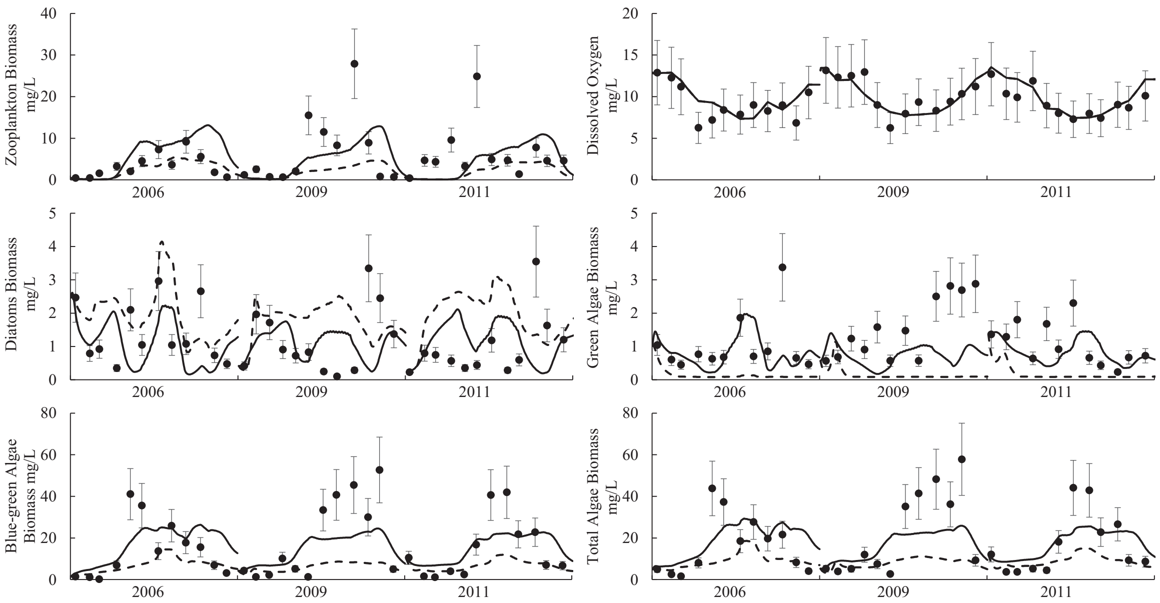

Fig. 4. Comparison between simulation results before and after optimization for the model validation data (the solid line is the results after optimization; the broken line is the results before optimization; the dots are the measured values).

Table 4
Changes of maximum and mean biomass under different management scenarios.

		S1	S2	S3	S4
Total algae change (%)	Max	−0.35	−21.19	2.88	22.73
	Mean	−1.62	−33.45	−0.83	7.96
Blue-green algae change (%)	Max	−1.15	−22.45	2.89	17.23
	Mean	−1.52	−32.68	0.29	7.49
Green algae change (%)	Max	−1.33	−36.91	−0.30	50.08
	Mean	−3.76	−61.00	−1.96	14.29
Diatoms change (%)	Max	−0.24	−1.74	−0.09	19.50
	Mean	−1.45	−23.83	−15.92	9.97

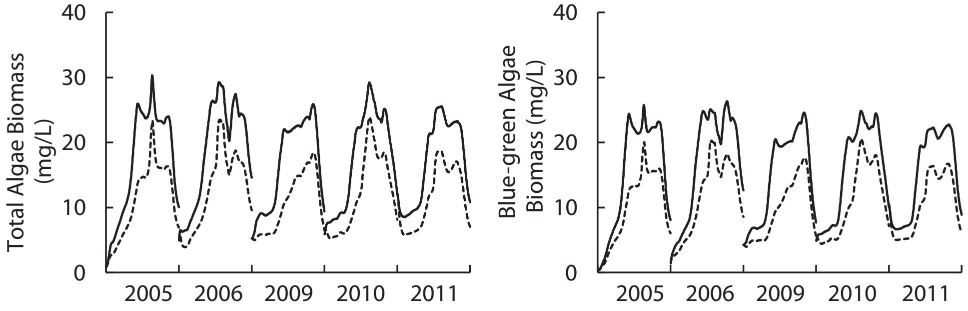

Fig. 5. Biomass concentrations of total algae and blue-green algae before and after management measures (the solid line is the original concentrations; the broken line is the concentration under 50% reduction of sediment release).

mortality by 50%; scenario 4 simulates the effects of an increase in water temperature by 1 °C by future climate change. The scenario analyses have been simulated for all 5 years of Meiliang Bay, and the changes in maximum and mean concentrations of algal biomass are summarized in Table 4. Both scenario 1 and scenario 2 could reduce the biomass of the three functional groups of algae. The changes of total algae biomass and blue-green algae biomass resulting from the internal load reduction of scenario 2, which is the most effective measure, are presented in Fig. 5. The increase of zooplankton in scenario 3 slightly reduced the mean algae biomass, but it increased the maximum value. In addition, it decreased diatom and green algae but increased blue-green algae. The increase of water temperature by 1 °C in scenario 4 would cause an obvious increase of all the three types of algae, in particular green algae.

4. Discussion

4.1. Multiple parameter optimization of SALMO

The optimized results for the blue-green algae agreed well with the observations except that the peak value was slightly lower than the observation. The possible reason is that SALMO does not consider the recruitment of blue-green algae from the sediment in spring, which plays an important role in algal bloom in Taihu Lake.

According to the theory of "four phases of cyanobacteria bloom development" (Kong et al., 2009), blue-green algae sink to the sediment of the lake overwinter and recruit from the sediment into the water body in spring when temperature increases and irradiance reaches a threshold. Verspagen et al. (2005) studied the contribution of the recruitment of blue-green algae from sediment to the algae bloom, and their results indicated that the absence of benthic recruitment would reduce the algal bloom up to 50%. In addition, floating buoyant blue-green algae can be occasionally driven by the prevailing south wind, and drift from central Lake Taihu to Meiliang bay. As a result algae blooms may intensify in summer and therefore algae biomass increases. However, SALMO is a zero dimensional water quality model which assumes a well-mixed water body, so it cannot simulate the algae migration induced by water flow and wind drift, leading to the slightly lower peak values of blue-green algae.

In general, the results after optimization were clearly better than before optimization (Guo et al., 2012a,b), and the model accuracy was remarkably improved as well. This research suggests the real-coded GA can efficiently optimize the parameters of the SALMO model, and the model can capture the dynamics of water quality reasonably well after optimization.

4.2. Algal bloom management in Lake Taihu

It can be seen from Table 4 that the total algae biomass in all the scenarios except scenario 4 decreases. Scenario 2 has the largest effect, which indicates that reducing the sediment release of nutrients is an effective way to control algal blooms. Although the increase of zooplankton by biomanipulation slightly reduced the total algae biomass, it imposes more predation pressure on diatom and green algae, which in consequence is of benefit to the notorious blue-green algae, as shown in scenario 3. This indicates that biomanipulation is a very delicate measure, and can only be implemented with sufficient investigation and caution. During the analyses, it was observed that PO_4-P is a more sensitive factor than NO_3-N in the growth of algae in Meiliang bay, which is different from the results of previous studies (Chen, 2001; Mao et al., 2008). A possible reason is that SALMO does not simulate ammonia nitrogen, an important form of nitrogen for algae growth. Comparing scenario 1 and scenario 2, it is found that the concentrations of PO_4-P and NO_3-N are mainly affected by the sediment release, which implies that internal load is the main source of nutrients in the water of Meiliang Bay. The results show clearly that reduction of sediment release is the most effective way to control the algae blooms in Meiliang Bay. The increase of algae biomass due to temperature rise indicates extra potential threat from climate change to lake ecosystems.

5. Conclusions

The model SALMO was adapted and applied to simulate the dynamics of water quality in Meiliang Bay of Lake Taihu. Since SALMO has a large number of parameters, this study developed a real-coded genetic algorithm to optimize the major 30 parameters that are important to algae growth. The results have demonstrated that the real-coded genetic algorithm is effective and efficient in optimizing multiple model parameters. The simulation accuracy was improved greatly after optimization, and the index of agreement of diatoms, green algae, blue-green algae, total algae and zooplankton biomass on the validation data reached 0.40, 0.52, 0.69, 0.69 and 0.48, respectively. However, there is still considerable room for further improvement, and more data should be obtained to increase the model accuracy.

The peak value of blue-green algae simulated by SALMO was slightly lower than the measured value, and this may be because SALMO does not consider the recruitment of blue-green algae from the sediment in spring, which plays an important role in algal blooms. Besides, SALMO is a zero-dimensional model, which does not simulate the algae migration induced by water flow and wind drift, causing the relatively low peak value of blue-green algae.

Given that the performance of the optimized SALMO is acceptable, the model was applied to analyze 4 management scenarios for the Meiliang Bay. The results indicated that the essential option to control algae blooms is to reduce nutrients, especially nutrient release from sediment. Biomanupulation can only be used with sufficient investigation, and future climate change may bring extra stress to lake ecosystems.

It is always important to analyze the uncertainty of model results, in particular when the results are used for management. The uncertainty of the adapted SALMO model had been studied and was presented in a separate paper (Li et al., 2013).

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