

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



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ARTICLE INFO

Article history:

Received 5 August 2013

Received in revised form 29 October 2013

Accepted 8 November 2013

Available online 1 December 2013

Keywords:

Lake model SALMO

Parameter optimization

Real-coded genetic algorithm

Algal bloom management

ABSTRACT

SALMO (Simulation by means of an Analytical Lake Model) describes the seasonal dynamics of PO₄-P, NO₃-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.

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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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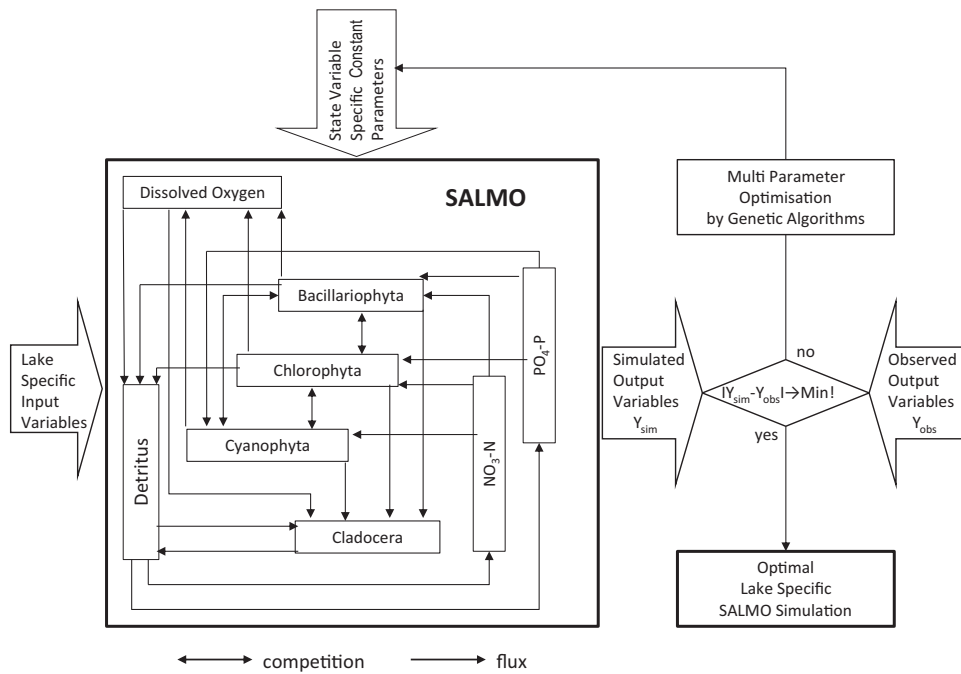


Fig. 1. Diagram of model structure and parameter optimization routine of SALMO.

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 $\text{PO}_4\text{-P}$, $\text{NO}_3\text{-N}$, 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.

$$\text{OAER} = \text{KRE} \cdot \frac{\text{SAT} - O}{\text{ZMIX}} \quad (1)$$

$$\begin{aligned} \text{DTRAN} = & \text{RATD} \cdot \left(\sum_{i=1}^3 (\text{RA}_i \cdot A_i) + \text{RZ} \cdot Z \right) \\ & + \text{RATMD} \cdot \text{ZMO} + \text{RATZD} \cdot (1 - \text{AZ}) \cdot \text{GRAZ} \cdot Z \end{aligned} \quad (2)$$

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

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