SIMULATING PHYTOPLANKTON ASSEMBLAGES USING AN INDIVIDUAL-BASED MODEL INCLUDING STRUCTURE-, STORAGE-, AND ENERGY-DYNAMICS

Jochen Hurlebaus
Institute for Biotechnology, Forschungszentrum Jülich, Germany
mailing adress:
Kurt-Schumacher-Straße 18, 67663 Kaiserslautern, Germany
ph: 0049-631-15483
hurlebau@mathematik.uni-kl.de

Thomas G. Hallam
Department of Ecology and Evolutionary Biology
and
TIEM (The Institut of Environmental Modeling)
The University of Tennessee at Knoxville
Knoxville, TN, 37996, USA
ph: 001-423-974-4293
fax: 001-423-974-3067
hallam@tiem.utk.edu

key-words: phytoplankton assemblies, grazers, dynamics, physiology

Abstract

The effects of phytoplankton blooms are attracting world wide attention not only because of the ubiquity of eutrophication problems but because of a recent explosion of production of toxins by classes of dinoflagellates and diatoms. Nearly all primary production in oceans and lakes is performed by phytoplankton assemblages, incorporating huge amounts of CO_2 in the atmosphere and stimulating climate change. The toxins produced by phytoplankton can cause death of marine animals and impact ecosystem structure. Toxic effects have resulted in beach closure and limited human comsuption of marine mussels and fish.

Because of the complexity of aquatic systems, no simulation models are able to explain dynamics of unicellular algae assemblages. Composition of phytoplankton assemblages can vary in many aspects such as number and population size of different species, total density, and growth rate. Dynamic behavior of these phytoplankton assemblages is a result of many factors including changes in temperature, light

availability, and nutrient concentrations as well as the abundance of zooplankton. A realistic model has to include at least the most sensitive variables and parameters of the ecosystem. Further complications occur because many internal processes of the cells are not sufficiently researched.

We developed a mathematical model for phytoplankton assemblages based upon detailed physiology of the individual cell that focuses on nutrient and energy flows in the system. Flows of nutrients, production of storage, and growth are modeled separately which allows uncoupled dynamics of storage and structure pools in the cell. A system of 10 coupled, nonlinear, ordinary differential equations describes the dynamics of an individual. The species are coupled through the equations for external nutrient concentrations. Average photosynthesis was estimated using integration over depth of surface layer, considering irradiance at the surface, absorption of water, and self-shading effects of the phytoplankton. Grazing and sinking determine the losses of phytoplankton cells; a difference equation was used to model sinking and grazing.

Euler's and Runge-Kutta's Method for numerical solutions of systems of ordinary differential equations were implemented in a computer code written in C. The code was used to perform simulations of a population of the diatom *Skeletonema costatum* under various environmental conditions. Simulations were usually performed for 5-25 days in a homogeneous environment with equally distributed cells. Growth of cells was either limited through nutrient or energy shortage. The uncoupling of storage and structure production resulted in changes in cell composition and allowed detection of indirect effects of nutrient or energy limitations. Additional simulations included two species simulations to investigate species competition and dominance; here, the model showed effects of cell growth and composition that cannot be explained with less detailed models.

The model was applied to data from three batch culture experiments performed by Pan et al. These experiments lasted for 9 days with measurements taken once per day. Parameters of the simulation model were estimated from literature, from values given in the description of the experiments, and from the actual speed of growth in the experiments. The Naelder-Mead Simplex Algorithm was used to improve the fit of the model to the experimental data. A set of parameters was created that fits the model to all three batch-culture experiments. Different growth dynamics resulted from changes in the initial internal storage, nutrient, and energy pools demonstrating the importance of these compartments as part of a computer model simulating growth of unicellular algae.

The complexity of the model makes the use of analytical methods difficult. Many times in the field of ecological modeling, analytical results are obtained only by making extreme simplifications and assumptions. We used a minimal number of simplifications and assumptions and concentrated on simulation methods for solutions and analysis. This approach results in detailed numerical considerations, a large number of parameters that have to be estimated, and a rather complex computer code that requires high performance computers. Advantages of the apporach is that a wide range of dynamical behaviors are obtained, yielding new insights in dynamics of phytoplankton assemblages.

Extensions of this research presently underway include the addition of the algal assembly module to an ecosystem model and also the modeling of toxic effects.

Literature:

Hurlebaus, Jochen, An individual-based model for phytoplankton assemblages with application to *Skeletonema Costatum*, Master Thesis, The University of Tennessee at Knoxville, 1997. Available on author's homepage.
Youlian Pan et al, Changes in domoic acid production and cellular chemical composition of the toxigenic diatom *Pseuod-Nitzschia Multiseries* under phosphate limitation, *J. Phycol.* 32, 371-381(1996).