

Interactive comment on “Incorporating genomic information and predicting gene expression patterns in a simplified biogeochemical model” by P. Wang et al.

Anonymous Referee #1

Received and published: 20 February 2013

The authors propose an approach based on chemostat model analysis to explain phytoplanktonic biodiversity and species successions through different scenario representing various seasons and latitudes. The model combines genomic information to the uptake and growth rate of 3 N and 3 P substrates. Changing environmental conditions are then simulated, in order to simulate phytoplankton community structure.

This work can be seen as an attempt to give more mechanistic explanations to the work of Follows et al., but I don't think it achieves this goal.

The three principal limit of the paper are 1/ the frightening assemblage of hypotheses, most of them being difficult / impossible to verify, 2/the use of chemostat framework to

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extrapolate results in the ocean 3/ the lack of systematic simulation exploration of the possible parameter values:

1- The set of hypotheses which are assumed in order to derive the model strongly limit the breadth of the model. The list of fragile and unverified hypotheses gives the feeling of an abstract exercise. Equations (5) (6) and (8) would require more experimental support. Maximum and minimum cell quota are derived from allometric hypotheses, but the publications which are mentioned do not refer to a nitrogen or phosphorus quota, but to the chl_a quota, this is rather different. Moreover, the parameter choice is not very convincing and seems very arbitrary. This is particularly true for the parameters of Table 3. The authors should give a better justifications of this choice, and more important, they should assess the influence of a given parameter set on the model results (sensitivity analysis). The way the parameters are chosen is unclear, especially for the parameters which play a key role, such as the critical extracellular concentration.

2- This is not clear how many simulations have been run to get the results, and if there is a preliminary simulation to reach periodic values, and how many seasons are tested. The results should be stable despite various initialisation and parameter choice. ¶ Despite not having light controls, the patterns of phytoplankton community diversity in the model scenarios share some similarities with observed biodiversity patterns. ¶ This assertion seems rather weak and too vague. It should be supported by statistical analysis of large simulations sets initiated from arbitrary choices of parameters and initial conditions. This property could be claimed only if it turns out to be stable, for randomly chosen initial conditions, parameters and dilution rate (in a given range).

3- The reduction of the model to a CSTR is of course a tremendous assumption which strongly shorten the work scope. Moreover, the choice of the dilution is arbitrary, it is well known however that it can be determinant for the competition outcome.

4- Other comments: Because of the crucial role of the nitrogen fixing cyanobacteria which is highlighted by the model, a more accurate representation of the underlying

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mechanism should be included. It should include the (high) energetic cost to activate the nitrogenase.

Two crucial parameters (light and temperature) are not represented, and they may have a large impact stronger than the nitrogen and phosphorus limitations.

The genomic side in the model is very rough and simply consists in assuming some cell capability, and it links the number of these pathways to a maximal growth rate value. At the end, there is no real contribution of any genomic knowledge, and I have the feeling that the results obtained by this approach are less clear than for Follows approach, despite more fragile underlying hypotheses. Finally, the gain of the approach is not clear.

The authors should work hard to address these points and propose a more convincing revision.

Minor comment:

Equation (2) should involve μ , instead of u , this seems to be simply a typo

The meaning of the parameters is unclear and inconsistent. What the authors denote μ_{max} is not the maximum growth rate. The maximum growth rate depends on the ratio Q_{min}/Q_{max} . Change μ'_{max} into $\bar{\mu}$ to avoid any confusion. But then, several relationships along the paper should be revisited.

Interactive comment on Biogeosciences Discuss., 10, 815, 2013.