

低次海洋生態系モデル(3-D NSI-MEM)と遺伝的アルゴリズム( $\mu$ GA)を用いたデータ同化

Data assimilated state variables of a lower trophic level marine ecosystem model (3-D NSI-MEM) by a micro-genetic algorithm in North Pacific

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Lower trophic level marine ecosystem models have become increasingly important for understanding marine ecological systems, but there are two main difficulties for improving simulation results of marine ecosystem models. Firstly, lower trophic level ecosystem models have recently had many parameters with state variables increasing. The difficulty of estimating adequate parameters have also increased. Unbalanced parameter sets often lead to numerical divergence. Secondly, it is difficult for ecosystem models with one kind of ecological parameter set to reproduce realistic situations (*e.g.*, distribution patterns of phytoplankton, timing of spring phytoplankton bloom and so on), especially when coupled to physical three-dimensional models. Because the characteristics of local species are different with various provinces in the ocean. To estimate optimal parameter sets and approximate model results to a realistic situation, we used data assimilative approach by a genetic algorithm with a three-dimensional lower trophic level marine ecosystem model.

The marine ecosystem model 'NSI-MEM' based on NEMURO has been developed in Japanese communities. The ecosystem model has 14 compartments including two phytoplankton functional groups (non-diatom small phytoplankton (PS) and diatoms (PL)). The model was extended three-dimensionally and worked offline with the environmental physical field obtained from another realistic physical 3-D model (MRI.COM) experiment. One of the focuses of this study is to approximate the PS and PL concentrations to the values estimated from satellite data in the North Pacific region in 1998. We divided the region (15~65°N, 120~160°E) into three provinces based on dominant species and nutrients limitation, and set different ecosystem parameters for each province. The optimal parameters were estimated by the similar method to that in Shigemitsu et al. (2012) that used one-dimensional NSI-MEM with a micro genetic algorithm.

The correlation of phytoplankton concentration between the model result and satellite data is totally larger than that in the result without the estimated optimal parameters. For seasonal analysis in 1998, the correlation becomes relatively larger especially in winter (January to March) and smaller in spring (April to May), compared to that without the parameter estimation. This is because the timing of phytoplankton spring bloom in the model domain is shifted to the early period, due to the data assimilation process. As a result, roughly speaking, the satellite data-based assimilation by the genetic algorithm can help the model results to improve. For future works, we should investigate the values of the estimated ecosystem parameters (*i.e.*, the consistency between the ecosystem parameters and the real ecology of phytoplankton).

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