

Inherent Scales of Variability of Ecosystem Models

Ecosystems can vary on multiple time and space scales. Some, or even much, of this variability may be correlated with physical forcing (see, e.g., Fig 1). Nonetheless, ecosystem dynamics is itself inherently nonlinear, and hence capable of producing space/time variability, even in the absence of variations in physical forcing. The purpose of this project is to study the internal dynamics of existing ecological models, and to characterize their ability to produce temporal and spatial variability similar to that observed in nature. While there are many possible models that could be considered for such analysis, we will limit our study to mass balance models, those with very limited representation of life history structure.

Although existing biological models are greatly simplified from reality they are still too complex to permit analytical analysis of the inherent dynamics or time-scales. The ecological models are spatially explicit including varying degrees of both biological sophistication and coupling with the physical environment. Only a numerical approach has the potential to disentangle the convoluted influences that drive the ecosystem models. However the complexity of the fully coupled bio-physical models in space and time is enormous. It will therefore be necessary to apply some degree of idealization in the physical forcing and/or dimensionality of the problem to make progress.

A hierarchy of idealized problems will be developed through further discussion among those participating in this project. As an example of what might be undertaken, we could explore the issue of inherent time-scales by running existing biological models with physical forcing in which interannual variability had been excluded. This could be accomplished by repeated runs of the target biological model with forcing by a single climatological year, run cyclically. Any interannual variability observed to develop could then be diagnosed for its dependence on internal processes.

For maximum simplicity, and to allow some degree of referencing to observations, these runs could first be performed in a one-dimensional form at selected locations in the North Pacific and North Atlantic. Such a 1-D approach permits more efficient exploration of dependence on model structure and/or parameter space making both the numerical analysis and interpretation more straightforward. As an example, dependences may be expected on the parameterization of temperature-dependent growth and metabolism or degree of predatory-prey coupling which may depend on the local seasonal cycle structure. The results of the 1-D explorations could be used to guide further model sensitivity simulations run in full 3-D mode. While the most interesting results might in the end be obtained with some life history representation, initial investigations would utilize mass balance models of varying complexity.

Georges Bank NAO - Salinity - Plankton - Cod

