

Report from NORACIA workshop on Biophysical modelling and Arctic warming 2007 at Solstrand Hotel & Bad 6-7 December 2007

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Seminar

The focus this year was on linking trophic levels in biophysical ecosystem levels. This is a challenging topic, particularly when including the higher trophic levels. It is also very relevant in terms of climate related issues where there is a growing demand for predictions about how ecosystems will respond to the anticipated global warming. In order to improve our abilities in this respect it is important to focus on trophic coupling and how to model these in the best way. The seminar started with four introductory talks on biophysical ecosystem models, emphasizing the linking of trophic levels. The introductions were followed by a discussion of critical processes and knowledge gaps in coupling of trophic levels in biophysical ocean modelling with particular focus on Arctic ecosystems. The following presentations were given (summaries of talks are provided below):

Corinna Schrum: A method to utilize zooplankton bulk biomass for larvae-IBMs.

Dag Slagstad: Effect of climatic change on the production and distribution of *Calanus finmarchicus* in the Norwegian and Barents Seas.

Morten Skogen: Coupling a Eularian phytoplankton model with a Calanus IBM.

Geir Huse: Modelling encounter rate and distribution of mobile predators and prey.

Critical processes and knowledge gaps in coupling of trophic levels in biophysical ocean modelling

The discussion was focused on recognising critical processes and knowledge gaps and below is a list of the points considered to be the most important for modelling of Arctic ecosystems in non-prioritised order.

Optimal level of aggregation in models

What is the optimal level of aggregation in models? This is a topic that modellers need to address all the time and is particularly important for subdividing the ecosystem components in ecosystem models. The optimal level of aggregation is likely to depend on what the model is being used for. For bulk biomass prediction

there is likely to exist an optimal number of functional groups. However, other purposes such as predicting the distribution of a particular trophic level or species might benefit more from a totally different level of model aggregation. It is therefore important to consider the different usages for models when deciding on the level of aggregation of ecosystem models. Important distinctions in aggregating ecosystem components into functional groups are: assimilation mode (e.g. heterotrophs or autotrophs), size, taxonomy, traits (e.g. diapause, which is particularly important to Arctic species, annual or biannual life cycles, environment adaptation), habitat preferences and others.

Technical challenges in modelling interactive feeding

There is a general time step problem in biophysical models particularly related to quantification of feeding processes. The problem is associated with time integration of predation and it is not a problem when modelling predator feeding and prey depletion in real time. Threshold concentrations of prey below which there is assumed to be no predator feeding in a patch (or square) is an appropriate parameterisation for lower trophic levels, for example interactions between zooplankton and phytoplankton. There remains a thorough assessment of how to set the threshold concentrations. Estimating prey-predator ratios from field studies is a possible way to get around this. However, such a parameter is likely to vary as a function of light level and temperature and can be a parameter with great impact on model performance.

When several different groupings utilise the same resource it becomes a problem the problem of over utilising the prey population becomes a concern. This is also seen for individual based models that use super individuals that together can deplete the prey in a square. For these cases with multiple predators capable of depleting the prey in a square, feeding can be calculated in two steps. First, an initial estimate of the consumption of each predator super-individual is calculated by letting each super-individual feed sequentially according to the prey density in the square, taking into account the reduction in prey biomass caused by predator feeding. Then the biomass of prey eaten by the predator super-individuals in each square is summed. Next the total prey consumption in the square is divided by the predator biomass in the square to yield an estimate of prey biomass consumed per predator biomass, which is then used to calculate the total consumption by each predator super-individual. In cases where you have actively searching piscivorous fish that feed on schooling fish it may actually be fairly realistic that the predators eat the last prey in square. This depends on the specific nature of the predator prey interaction.

How to model 3D overlap of interactions?

Mortality of zooplankton can be sensitive to their vertical distribution. Assumptions of relations between zooplankton and phytoplankton vertical distribution will have consequences for light dependent zooplankton mortality. In many cases the predator can be assumed to be flexible enough to search up prey wherever they are in the water column. Thus a certain proportion of the predators can be assumed to overlap with the prey. In this way a 2D distribution of predators can be used to calculate mortality rates for the prey without modelling the predator vertical distribution explicitly.

Behavioural flexibility can be important to implement for the higher trophic levels. Fish and marine mammals have important flexibility in all three dimensions. This

is highly relevant for interactions both between the higher trophic levels, but also for the interaction between fish and zooplankton.

Sub grid patchiness

The importance of sub grid patchiness depends on the degree of non-linearity of relevant processes such as nutrient fluxes, functional responses, etc. Simulations with fine scale models can be useful to reveal sub grid patchiness (mesoscale).

Microbial loop

Microbial loop: more research is needed to investigate consequences of inclusion and exclusion of the microbial loop in ecosystem models, particularly with regards to how it affects nutrient regeneration.

Light

There is need for better representation of light in ecosystem models: community specific light absorption and scattering, water mass specific attenuation. Light is particularly important in the Arctic due to high degree of light limitation (as opposed to nutrient limitation) in this area. This is in contrast to equatorial waters that are abundant in light but generally poor in minerals and nutrients. Light is also important for interactions between prey and visual predators. This has a strong effect on predation rates along the vertical axis, but also between water masses with different optical properties, such as coastal and Atlantic water masses.

Conclusions

This list of topics is not exhaustive, but reflects points that the group found particularly important with regards to linking species in biophysical models. There are several ongoing initiatives for developing biophysical models that incorporate most parts of the ecosystem. There are also complete ecosystem models such as the Australian ATLANTIS packages that do this, albeit with a reduced spatial and temporal resolution compared to many current biophysical models. The theme for the seminar is therefore quite timely, and the group found the seminar valuable and productive and suggests that a follow up seminar is arranged in September 2008. This seminar will focus on end to end modelling of ecosystem dynamics with regards to Arctic warming. This theme follows naturally from the previous two workshops that have focussed on biophysical models for predicting the impact of global warming on ecosystem structure and functioning and linking trophic levels in biophysical models respectively. The intention is to increase the number of participants for this last workshop and invite foreign experts to provide lectures and take part in discussion on the end to end modelling of ecosystems.

Summary of presentations

Corinna Schrum: A method to utilize zooplankton bulk biomass for larvae-IBMs

Larval fish IBMs are used to resolve the effects of climate variability on the recruitment of key marine species. This requires knowledge about climate-induced changes in the spatial-temporal dynamics of prey, in addition to resolving environmental conditions such as temperature, salinity, light, large scale transport pattern and turbulence. So far, 2 main strategies have been applied to utilize such information, i.e. (i) using data from observations (Hinrichsen *et al.*, 2002) and (ii) derive prey field information from structured population models (Neumann and

Fennel, 2006). The disadvantage of a modelling strategy only based on direct prey field observations is obvious, under-sampling and limited predictive potential define the limitations of such a strategy. Severe limitations are found as well for a modelling strategy utilizing the stage based models for larvae fish IBMs. The huge number of variables and key rates required to resolve natural variability of prey fields as well as the necessary requirement for accurate initial conditions for all stages and considered species make a stage-based zooplankton modelling strategy inappropriate for addressing climate induced variability and future climate impacts in complex regional systems. For developing a sustainable modelling strategy it is necessary to focus on the processes we are able to observe and parameterize, instead of increasing the number of uncertain parameters. Here an alternative approach to gain prey field information directly from a NPZD model was presented. Size-structured prey fields were generated based upon estimates of zooplankton bulk biomass from a 3-d ecosystem model "ECOSMO". Results of a detailed validation of this NPZD model utilizing CPR data were presented, which show a high predictive potential for the model not only for estimating average and seasonal structures and variability, but as well with respect to interannual variability. The approach has been tested for larvae fish IBMs for Sprat and Cod. These models were forced by a homogenous spawning distribution (egg release homogeneously in the whole North Sea). It was shown that potential survival areas estimated from the model compare well with observed spawning grounds, a fact that provides strong evidence for the presented approach.

Hinrichsen, H.-H., Möllmann, C., Voss, R. and Kornilovs, G. (2002) Bio-physical modelling of larval Baltic cod (*Gadus morhua*) growth and survival. *Can. J. Fish. Aquat. Sci.*, **59**, 1858–1873.

Neumann, T. and Fennel, W. (2006) A method to represent seasonal vertical migration of zooplankton in 3D-Eularian models. *Ocean Model.*, **12**, 188–204.

Dag Slagstad: Effect of climatic change on the production and distribution of *Calanus finmarchicus* in the Norwegian and Barents Seas

Morten Skogen: Coupling a Eularian phytoplankton model with a *Calanus* IBM

The talk will focus on an ongoing work on the coupling of the biophysical model NOREWECOM to an IBM *Calanus finmarchicus* in the Norwegian and Barents Seas. The coupling started out with a simple one-way coupling where the IBM got its inputs from NOREWECOM (temperature, currents, phytoplankton), and has been through a phase where the biophysical model used the resulting time dependent zooplankton field of grazers on the phytoplankton. The simple one-way coupling has improved the outputs of both models. At present there is work to implement an online 2-way coupling of the models. This is the first time an IBM is coupled to a full 3D biophysical model over a larger area. Status of the work will be presented and a few of the problems faced will be discussed.

Geir Huse: Modelling encounter rate and distribution of mobile predators and prey

Predators tend to aggregate in areas where prey are abundant or easily caught, whereas prey on the other hand tend to avoid predators. These two responses can

be referred to as predator and prey responses respectively. When prey is relatively immobile the predator response should dominate, yielding aggregated predator distributions. On the other hand when the prey is relatively mobile and has spatial refuges, the prey response should dominate. If both predators and prey are mobile and there are no refuges, no general predictions can be made. This talk will focus on addressing interactions between mobile predators and –prey using individual-based modelling. The modelling framework captures both the population dynamics of the predator and prey as well as their behavioural interactions. This is achieved through a spatially explicit model system capturing: movement driven by rules and physics, and growth and mortality resulting from local encounters between predators and prey. The usage of super-individuals allows the model to simulate real population sizes within an individual-based modelling framework. Here the general modelling framework will be presented along with some case studies including cod-capelin and herring-Calanus interactions.