Numerical Modelling Course

@Marine Benthic Ecology 2019

Modulation of global change impact by biotic interactions, bioinvasion and parasitism

Anja Eggert

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Introduction

Ecosystems are complex and due to this complexity it remains difficult to grasp how ecosystems' state and functioning are modified by climate change, like ocean warming. We have a good understanding of temperature effects on single process rates of e.g. growth (photosynthesis, oxygen consumption), grazing or mortality. E.g., thermal performance curves are a standard lab procedure to evaluate the physiological performance of species. However, temperature effects on communities remain difficult to quantify. This is because ecological communities are networks, where the species are the nodes connected by biotic interactions. Global warming may have a negative impact on one process, but could be beneficial for another process.

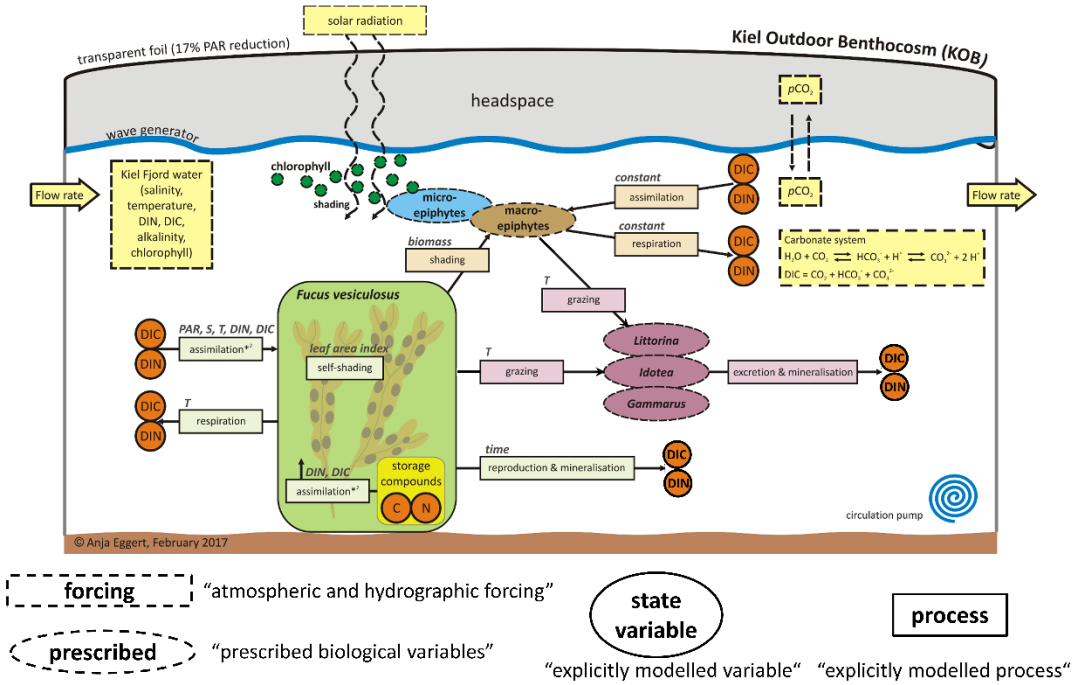
In this practical, you performed ecological experiments with key species of the benthic community in the Western Baltic Sea and you got to know the Kiel Indoor/Outdoor Benthocosms (KIBs and KOBs). Indeed, well-designed experiments in mesocosms are an excellent tool to study community effects of climate change. A model integrates the results in a very systematic way. It can improve our mechanistic understanding of the impacts of climate change.

In this two-days course on numerical modelling you will learn how to develop a so called boxmodel. Boxmodels are also called 0D-models as we only consider one grid cell, i.e. neither vertical nor horizontal transport. Nevertheless, we will consider temporal changes. In this exercise we will run simulations over two months.

We will develop an ecological boxmodel from scratch to simulate the temporal development of a benthic community in a mesocosm experiment (KOB). You will need to define the key species of the Western Baltic benthic community, which act like nodes in a network. Mathematical equations must be derived to describe the connecting processes and biotic interactions, which are the arrows in the network. You will use the Code Generation Tool (CGT), developed by Hagen Radtke @IOW (https://ergom.net). The CGT comes along with an editor (CGT-EDIT) for conveniently editing textfiles of the formal description and which does not require skills in programming.

The *Fucus* box model

Within the research project BIOACID (Biological Impacts of Ocean Acidification, https://www.oceanacidification.de/), we developed the first *Fucus* box model to simulate the seasonal growth of *Fucus vesiculosus* in its benthic community (Graiff et al., subm.). This work depends to a large extend on experiments performed in the KOBs to study impacts of ocean acidification and ocean warming.
The schematic of the model shows you the implemented state variables (nodes) and processes (arrows). We cannot achieve this complexity in a two-days course. However, you will learn how to develop a model like this.



Fucus vesiculosus biomass is a state variable of the model and is represented as 'carbon_in_Fucus' and 'nitrogen_in_Fucus'. Also dissolved nutrients (DIN, DIC) are modelled explicitly and the nutrient exchange in the flow-through system is considered. The implemented processes are shown in rectangles and their dependence on environmental variables is written above. *1 distinction between *Fucus* assimilation based on dissolved nutrients and growth based on storage compounds.

Model currency

The choice of the model currency is a first and major decision you have to make. As nitrogen is a key nutrient, it is the choice in most large-scale 3D-models. We will also use nitrogen as the model currency. This requires conversion of many measured parameters, like per-capita consumption rates into mol N m^{-3} d^{-1}.

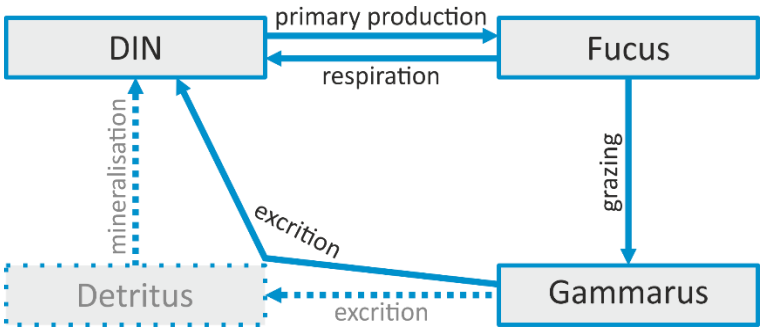
Defining your ecological model

The aim of this model exercise is to develop a numerical model based on the experiments of this practical:

State variable	Process	Factors
macroalga / *Fucus*	growth, primary production	native vs. invasive temperature
mesograzer / *Gammarus*	grazing rate (on *Fucus*), survival, feeding preference	native vs. invasive temperature

predator / *Asterias*	consumption rate (on mussel), growth, survival	salinity, temperature
filter feeder / *Mytilus*	respiration, filtration rate	Short-term temperature fluctuations

It is rather difficult to implement all state variables in a first simple numerical model. Together we start with including only DIN and *Fucus* as state variables and prescribing a number of *Gammarus* individuals.
We explicitly model DIN concentration in the water and *Fucus* growth as nitrogen increase (due to primary production). *Fucus* respires, i.e. releases ammonium. *Gammarus* is not explicitly modelled. But the given number of individuals grazes on *Fucus* and excretes faecal pellets. As we do neither include detritus nor mineralizing bacteria as state variables, the excreted pellets are directly transferred to DIN. All considered process rates will be temperature-dependent.



Possible extensions:

- Implementation of two *Gammarus* species (native and invasive) with different temperature preferences
- Two *Fucus* species (*F. vesiculosus* and *F. evanescens*) with different temperature-dependence and with different grazing preferences of *Gammarus*
- Run simulations with a global warming set-up.

Possible (other) models:

- Implementation of *Mytilus* and its predator *Asterias*, i.e. mussel filters water with phytoplankton. Consumption rate of the predator is salinity-dependent.

Technical description of the KOBs

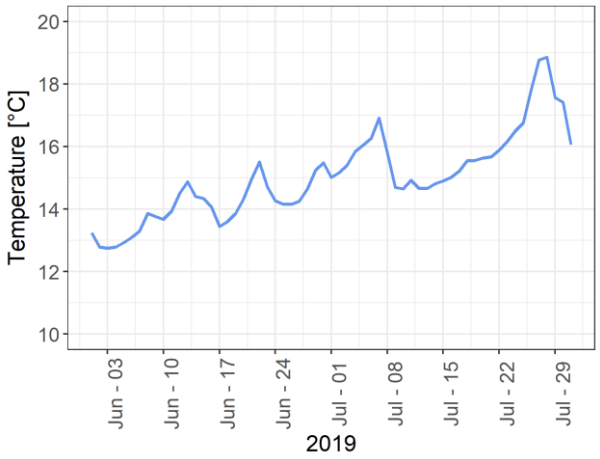
The KOB operates as a flow-through system and its inner dimension is 2 m x 2 m. The KOB runs in an open-circuit mode, i.e. flow-through of natural seawater pumped from Kiel Fjord at 1 m water depth.
In this exercise we set the water volume in the tanks to 1.5 m^3 and the flow rate of the pump to 1.8 $m^3\ d^{-1}$, i.e. the water exchange rate was 1.2 d^{-1}.

Forcing factors

All so called forcing factors are prescribed and not explicitly modelled! The time step of the forcing time series (also of the biogeochemical forcing, i.e. 'time-dependent constants') can be different. In the model, start time is defined and the respective value of the variable is used until a new date is reached = NO linear interpolation but step-wise changes between time steps

Physical forcing:

- Ambient temperature of the Kiel Fjord surface water pumped through the KOBs. Temperatures range between 13 and 19°C in June/July.

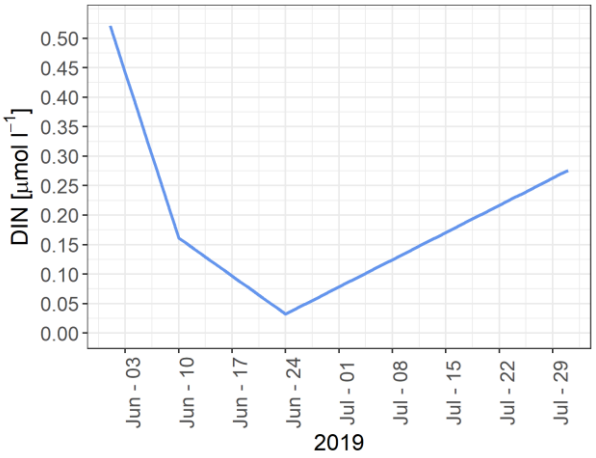


Measured temperature used to force the model.

- We only consider a very simple parametrization of *Fucus* growth, i.e. primary production. It growths during daylight (light=1), but does not in darkness (light=0).
- Effects of salinity are not considered in our model, otherwise we would need salinity data as well.

Biochemical forcing:

- DIN concentration of the Kiel Fjord water pumped through the KOBs. The maximal value is 0.52 µmol l^{-1}, which is far below the considered half-saturation constant of 7.3 µmol l^{-1}. I.e. in June/July, *Fucus* growth is always nitrogen-limited.



Measured DIN concentration in the Kiel Fjord surface water used to force the model.

Biological forcing:

- The mesograzer *Gammarus* grazes on *Fucus*, but number of individuals is pre-described. We consider 333 individuals in one KOB. If the water volume is 1.5 m³, *Gammarus* concentration is 222 ind. m^{-3}.

Conversion factors (wet biomass, dry biomass, N-content)

As the model currency is "mol nitrogen", we need conversion factors to dry and fresh biomass for all state variables.

- molar mass of N = 14 g mol^{-1}
- mean N-content of *Fucus* = 1.8 g N 100 g^{-1} dm
- thus, mean N-content of *Fucus* = 0.129 mol N 100 g^{-1} dm

- **thus, 1 mol N *Fucus* ≈ 775 g dm *Fucus***

- typical *Fucus* water content = 80.5%
- thus, 100 g fm of *Fucus* = 19.5 g dm of *Fucus*
- thus, 1 g dm *Fucus* = 5.1 g fm *Fucus*

- **thus, 1 mol N *Fucus* ≈ 4000 g fm *Fucus***

Initial values

The model needs initial conditions of its state variables, in our case for *Fucus* biomass and DIN. The initial value of DIN is simply set to the DIN concentration in the flow-through water on day 1 of the experiment (0.0005 mol m^{-3}).

To derive the initial value for *Fucus*, we need to calculate:

- 20 *Fucus* in one KOB
- The individual plants have a fresh biomass of 60 g
- Applying the conversion factor, this is 0.015 mol nitrogen per *Fucus*
- With a water volume of 1.5 m³, the mean "concentration" of one *Fucus* is 0.010 mol N m^{-3}
- In total, the initial value for *Fucus* is 20*0.010 mol N m-3

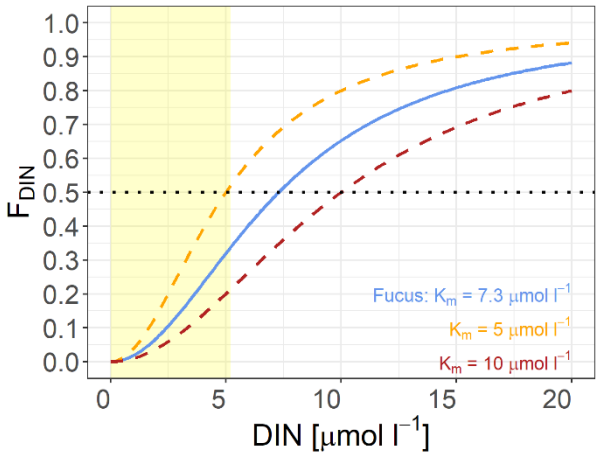
DIN assimilation of Fucus

Nutrient uptake, i.e. DIN uptake, is described with a modified Michaelis-Menten formula with squared arguments (Fennel & Neumann, 1996) which results in a sigmoid functional response:

$$F_{DIN} = \frac{DIN^2}{K_m{}^2 + DIN^2},$$

with K_m being the half-saturation constants of DIN uptake. And F_{DIN} ranges between 0 and 1.

Based on Wallentinus (1984), we choose K_m = 7.3 µmol l^{-1} = 7.3·10^{-3} mol m^{-3}.



The effect of parameter choices of K_m on the factor F_{DIN}. The yellow box marks the DIN concentrations during the experiment, i.e. *Fucus* growth is DIN-limited and F_{DIN} < 0.35.

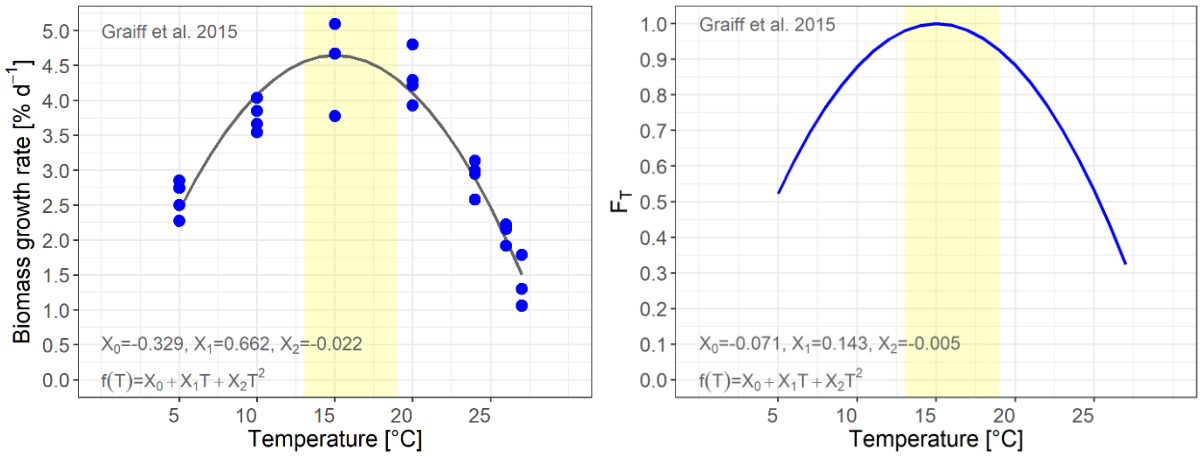
While typical winter DIN are 5 to 10 µmol/l, late spring / early summer DIN concentrations are always low. Thus, in the experimental period, *Fucus* is DIN-limited.

Temperature dependence of Fucus growth

We fit a quadratic regression model to the growth-temperature-response biomass data obtained in laboratory experiments (Graiff et al. 2015).

$$F_T = X_0 + X_1 T + X_2 T^2$$

To obtain F_T ranging between 0 and 1, we normalise the function to a maximum of 1.



Temperature dependence of growth rate of *Fucus* collected in the Kiel Fjord (left) and derived limiting function [0, 1] (right). The yellow box marks the temperature range during the experiment, i.e. *Fucus* growth is not temperature limited (F_T>0.9).

Fucus growth

We consider a very simple light-dependent growth of *Fucus*. It only depends on day/night cycle and the external temperature and DIN concentration.

$$\mu_{fuc}=\mu_0 \cdot \text{light} \cdot F_T \cdot F_{DIN}$$

with μ_0 = maximal growth rate for Fucus [d^{-1}] and μ_0 = 0.047 (Graiff et al. 2015). Light can be 0 (darkness) or 1 (daylight). F_T and F_{DIN} are limiting functions [0, 1] and their parametrization depends on experimental data.

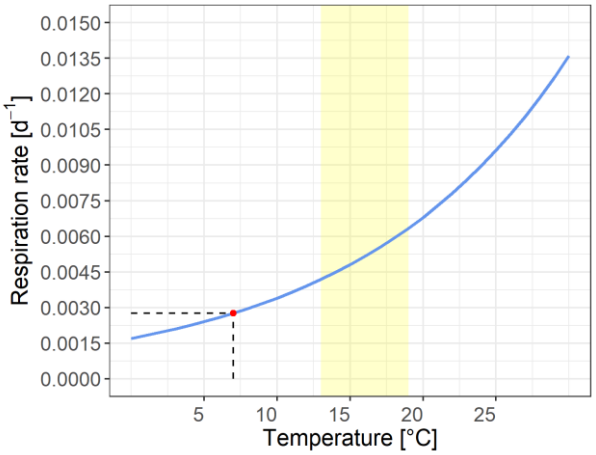
Fucus respiration

Markager & Sand-Jensen (1992) measured at 7°C dark respiration rates of *Fucus serratus* from Denmark of 0.0027 mol C mol^{-1} C cell d^{-1}. We adopt this value for nitrogen.
We apply the the van't Hoff's rule to describe the temperature-dependent respiration rate of *Fucus*. We set Q_{10} = 2, i.e. rate increases by factor 2 when temperature increases by 10°C. Accordingly, respiration rate is defined as:

$$resp_{fuc}=r_0 \cdot \exp^{(q_{10} \cdot temp)}$$

with q_{10} = ln(2)/10 = 0.0693 and r_0 is the respiration rate at 0°C.

If respiration rate at 7°C is 0.0027 d^{-1}, we can derive r_0 = 0.0017 d^{-1} at 0°C.



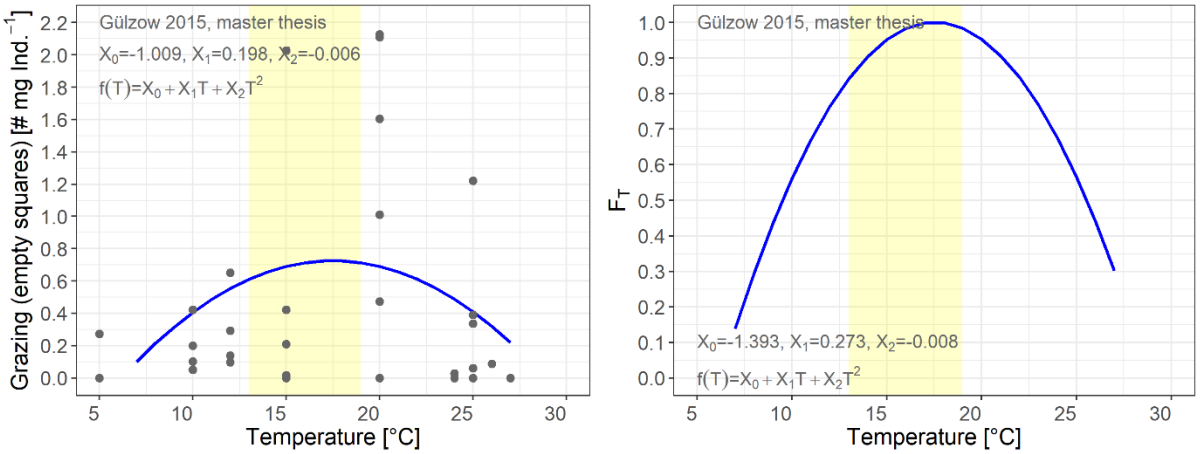
Temperature dependence of respiration rate of *Fucus*. The red dot marks the rate 0f 0.0027 d^{-1} measured at 7°C. The yellow box marks the temperature range during the experiment.

Temperature effect on grazing

We fit a quadratic regression model to the grazing-temperature-response data obtained in laboratory experiments of the master thesis of Elisa Gülzow (2015).

$$F_T = X_0 + X_1 T + X_2 T^2$$

To obtain F_T ranging between 0 and 1, we normalise the function to a maximum of 1.



Temperature dependence of consumption rate of *Gammarus* on *Fucus* (left) and derived limiting function [0, 1] (right). The yellow box marks the temperature range during the experiment, i.e. *Gammarus* consumption is not temperature limited (F_T>0.8).

Grazing rate of *Gammarus*

Göcker & Kall (2003) studied grazing rates of *Gammarus* [mg FM Ind^{-1} d^{-1}]. They determined a mean consumption rate of 0.7 10^{-3} g FM Ind^{-1} d^{-1}. Using the conversion factors of *Fucus*, this is equivalent to 0.137 10^{-3} g DM Ind^{-1} d^{-1} and 0.175 10^{-6} mol N Ind^{-1} d^{-1}.

$$graz_{gam} = \#Indiv \cdot graz_0 \cdot F_T$$

with #Indiv = number of Gammarus individuals m-3, $graz_0$ = maximal grazing rate of 0.175 10^{-6} mol Ind^{-1} d^{-1} and F_T the limiting functions [0, 1].

As we consider *Gammarus* as a prescribed grazer, i.e. we do not model *Gammarus* growth explicitly, the ingested *Fucus* does not cause increase in *Gammarus* biomass. Furthermore, no detritus state variable is considered, i.e. no mineralisation of detritus takes place. The ingested *Fucus* is directly transferred to dissolved nitrogen.

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