Chapter 12 Outline of an Arctic fjord Ecosystem Model for Kongsfjorden-Krossfjorden, Svalbard



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Abstract The main objective of this work is to present a detailed outline of an Arctic fjord ecosystem model using Kongsfjorden-Krossfjorden as a case study. Marine ecosystem models are compared, with emphasis on fjord models, towards defining best available modelling technologies. This comparison is based on an analysis of the differences in the variables and processes simulated by different models. We argue about the importance of: (i) coupling Arctic fjord models with land and glacier drainage models; (ii) including thermodynamic, hydrodynamic and ice dynamic sub-models; (iii) simulating biogeochemical processes in the water, ice and benthic environments for, at least, the macro-elements carbon, nitrogen and phosphorus. Furthermore, the energetic importance of higher trophic levels is discussed and used as an argument for their inclusion in fjord ecosystem models towards the development of end-to-end models. The complexity of all the processes mentioned above and respective interactions emphasizes the need for using different model tools and efficient couplers allowing the flow of data between them. A community-based approach with open source software seems to be the proper approach to handle the large complexity of the model strategy proposed herein.

Keywords Arctic fjords \cdot Ecosystem models \cdot Model coupling \cdot End-to-end models

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12.1 Introduction

Modeling in Arctic fjords has been limited to physical models for advected water masses, circulation and ocean-atmosphere interactions (e.g. Ingvaldsen et al. 2001; Nilsen et al. 2008). The biological components are rarely modelled.

Norwegian ecological ford models have been reviewed by Salvanes (2001) with emphasis on their relevance for fisheries management. The author classifies models as bottom-up and subdivides them into: (i) multispecies ecosystem models; (ii) hydrographical drift models for early life stages; (iii) life history models comprising age-structured Leslie matrix population models, and static and dynamic optimization models of behaviour. The "bottom-up" classification is based on oceanographic and meteorological drivers. The term "ecosystem model" is used to aggregate all models that simulate part of an ecosystem such as species interactions, physical transport processes or population dynamics of some species, according to the groups (i), (ii) and (iii) defined by Salvanes (2001). In this work, we choose to define "ecosystem model" as a mathematical representation of an ecosystem that includes interactions between different species and/or functional groups and interactions with the physical and chemical environment. Following this definition, population dynamic or behavioural models are not viewed as ecosystem models but may be part of them. However, models dealing with physical processes representing water circulation, biogeochemical cycles and their links with a different number of trophic levels are considered "ecosystem models" and these will be the focus of the present work, independently of the emphasis given to different processes.

The review presented by Salvanes (2001) suggests that models applied to Norwegian fjords are not all of the types defined here as "ecosystem model". However, the results obtained with those models provide some insight into the functioning of fjord ecosystems by focusing on specific parts of their complex physical, chemical and biological realms. Multispecies ecosystem models show that fish production in fjords is strongly dependent on production imported from the sea, decreasing from the open sea boundaries to the inner fjords. Hydrographical models show how wind direction might induce shifts in vertical circulation of fjords along the west coast of Norway, with alongshore northern and southern winds inducing upwelling and downwelling, respectively, as a result of Ekman pumping. Upwelling seems to reduce fish production by "diluting" zooplankton concentration as fjord deep water mixes with zooplankton-richer, advected seawater, whereas downwelling has the opposite effect since it facilitates the import of zooplankton from coastal areas. It is expectable that upwelling may enhance primary production in fjords, similarly to what happens in other coastal ecosystems (e.g. Figueiras et al. 2002) but, possibly, this effect does not enhance zooplankton abundance as much as the downwelling regime. Interestingly, in the Arctic-located Kongsfjorden, large surface mesozooplankton concentrations at its inner reaches, probably advected from the sea and displaced vertically by upwelled fresh water from the melting of calving glaciers, become prey to the surface feeding predators. This has been suggested to be the cause of large concentrations of birds and mammals in the area (Węsławski et al. 2000a; Lydersen et al. 2014).

A fjord ecosystem box model was developed by Ross et al. (1993) including a simplistic description of the physical processes. The fjord is divided vertically into surface, intermediate and bottom layer. A turbulent mixing parameterization is used to calculate fluxes between the different layers. Tidal exchanges are calculated between the sea boundary and the intermediate and surface layers – water enters the fjord through the intermediate layer, part of it is entrained in the surface layers and the exit to the sea occurs through these two layers. Freshwater runoff enters and leaves the fjord through the surface layer. Horizontal homogeneity of water properties is assumed for all layers. The biogeochemical component of the model comprises dissolved nitrogen, phytoplankton, zooplankton and carnivores, represented by the corresponding carbon and nitrogen stocks.

Ross et al. (1993) obtained a good semi-quantitative fit between predicted and observed data. However, this possibly could have resulted from the strong influence of external forcing on the internal system properties. In fact, tidal exchange corresponded to 80% of the surface layer volume per day. According to Ross et al. (1993), the simulated system (Loch Linnhe) behaves like a chemostat, being critically influenced by the balance between the inward and outward fluxes of nutrients and phytoplankton. In open fjord systems, such as Kongsfjorden-Krossfjorden where the width exceeds the baroclinic (internal) Rossby radius of deformation and circulation is strongly influenced by the Coriolis effect (Svendsen et al. 2002), the formation of eddies is expected to create more heterogeneity across the fjord axes and falsifying the assumption of lateral homogeneity, as used in box models.

A slightly more biologically complex version of the box model of Ross et al. (1993) was applied to other fjords of Scotland and Ireland, and the authors confirmed the physically dominated behaviour of the modelled fjords, with residence times <=1 day (Ross et al. 1994). They also report that phytoplankton is nitrogen limited only during the spring bloom, being limited by irradiance and grazing pressure for most of the year. Based on their results, they suggest that experimental sea loch studies should not focus only on nutrient dynamics and primary production but that equal efforts should be spent on studying secondary production and on accurate sampling of nutrients and phytoplankton along the sea boundaries.

In the eighties and early nineties, the paradigm followed by Ross et al. (1993, 1994), with a simple parameterization of physical processes, neglecting tidal variability, not coupling biogeochemical with hydrodynamic models and the assumption of well-mixed large compartments, was adopted by several authors in various types of coastal ecosystem models (e.g. Baretta and Ruardij 1988; Bacher et al. 1998). The general approach was to calculate residual circulation from freshwater inputs and use mixing coefficients to guarantee the transport of properties against the residual flows. There were no attempts to realistically simulate 1, 2 or 3D circulation from hydrodynamic principles. Later, the usage of fully coupled hydrodynamic-biogeochemical models became more frequent (e.g. Luyten et al. 1999; Byun et al. 2005; Azevedo et al. 2014).

Apart from the trends of increasing physical complexity in coastal ecosystem models, some paradigm shifts appeared from the traditional Nitrogen-Phytoplankton-Zooplankton (NPZ) or the NPZ-Detritus (NPZD) approaches (e.g. Fasham et al. 1990; Franks 2002) to more complex models based on internal nutrient limitation and dynamic stoichiometry (e.g. Baretta-Bekker et al. 1997; Vichi et al. 2007). Most coupled hydrodynamic-biogeochemical models have focussed on lower trophic levels (LTL), but more recent efforts have involved end-to-end models for a complete description of the marine trophic web (Rose et al. 2010).

Physical models for the Arctic fjord Kongsfjorden-Krossfjorden have included upper layer circulation based on the SINMOD model (Slagstad 1987) with tides and wind patterns (Ingvaldsen et al. 2001), ocean-atmosphere interactions with a 1D ocean mixing model (Price et al. 1986) with wind, temperature and cloud cover as drivers (Cottier et al. 2007). Eddy overturning across the shelf edge front outside Kongsfjorden has been described by Tverberg and Nøst (2009) based on the MIT general circulation model (MITgcm), a finite volume incompressible Navier Stokes model (Marshall et al. 1997).

A study from Masfjorden in western Norway (Aksnes et al. 1989) suggests that transport of mesozooplankton may exceed local growth significantly and that advection may be an important factor underlying the carrying capacity for mesozooplankton predators. Most likely, similar conditions exist for Kongsfjorden, which is an open fjord system without a sill at the entrance and therefore well connected to the water masses in the West Spitsbergen Current (Basedow et al. 2004; Willis et al. 2006; Hegseth and Tverberg 2013).

The marine food web in Arctic fjords has mainly been described (rather than modelled), with estimates of production, ingestion rates and growth. Studies on ecosystem energy flows, carbon budgets, food webs (involving stable isotopes and fatty acids) and benthic metabolism have been conducted in Arctic fjords or embayments (Hobson and Welch 1992; Welch et al. 1992; Hobson et al. 1995, 2002; Hop et al. 2002, 2006; Rysgaard and Nielsen 2006; Renaud et al. 2011; Wold et al. 2011; McMeans et al. 2013; Sevilgen et al. 2014). Much of this type of information from marine food webs, with descriptions and estimates, is highly relevant for modelling work that may add quantitative projections of the conceptual models.

The main purpose of this work is to outline the structure of a state-of-the-art Arctic fjord ecosystem model using Kongsfjorden-Krossfjorden as a case study, considering much of what was described above with regard to development of marine ecosystem models and ongoing modeling work in this fjord system. Such a model may be used to answer several questions regarding, for example, possible shifts in ecosystem functions such as primary and secondary production, in a scenario of global warming with increasing effects of Atlantic Water (AW).

12.2 Conceptuals

Ecosystem models may include hydrodynamic, thermodynamic and biogeochemical sub-models and their feedbacks. In the next paragraphs, the structure of an Arctic fjord ecosystem model will be discussed in the light of available models. For the purpose of clarity, this will start with the general model structure in terms of domain, boundary and forcing conditions, with emphasis on the need to integrate various sub-models. Thereafter, separate sections will deal with forcing functions, physical and biogeochemical, lower trophic level (LTL) and higher trophic level (HTL) processes. Biogeochemical processes, such as biogeochemical cycles, are closely simulated with LTL interactions in available models. Therefore, the term "biogeochemical" is used to aggregate both biogeochemistry and LTL thereafter. The Kongsfjorden-Krossfjorden system will be used as a case study to illustrate the concepts discussed herein.

The general transport equation solved by a coupled physical-biogeochemical model takes the form (Eq. 12.1):

$$\frac{\partial S}{\partial t} + \nabla (v \cdot S) = \nabla (A \cdot \nabla S) + \text{Sources} - \text{Sinks}$$
(12.1)

Where, v is current velocity (in m s⁻¹); *S* is the concentration of any dissolved or particulate (living or non-living) property (in kg or other mass unit per m⁻³); *A* is the eddy diffusivity of the mentioned property (in m² s⁻¹); and ∇ , the nabla operator, inCartesian coordinates – it is a first order spatial derivation operator $\frac{\partial}{\partial x}, \frac{\partial}{\partial y}, \frac{\partial}{\partial z}$. Velocity is calculated by a hydrodynamic sub-model. The derivative on the left side of Eq. 12.1 represents advection, whereas that on the right side represents turbulent

mixing. The "*Sources*" and "*Sinks*" terms are null for conservative properties and must be calculated by proper rate equations for the thermodynamic and the biogeochemical variables by different sub-models. Typically, these rate equations are dependent on forcing functions or other variables. For example, photosynthetic rates depend on light intensity, which is an external forcing function of time and space, and it may also be dependent on nitrogen concentration, which is a model state variable. In the case of nekton or other highly mobile organisms, motion must be calculated based on habitat preferences or behavioural patterns, forced by food abundance or environmental conditions even though it may also be influenced by hydrodynamic processes.

12.2.1 General Structure

One of the first steps in the implementation of any ecosystem model is the definition of its domain and boundaries. In defining these, it is important to place the boundaries far enough away from the area of interest to make it possible to assume that they are not influenced by the simulated system. This condition may be relaxed when model nesting is used, in which case feedbacks across the boundaries of nested grids are possible. A map of the Kongsfjorden-Krossfjorden system illustrates some of the forcing and interactions with/from the atmosphere, the land and the ocean boundaries, that may be provided by time series of relevant variables and/or outputs from other models (Fig. 12.1a).

The next step is to define a grid to represent the horizontal and vertical domains. Grids may differ in the way the vertical and the horizontal domains are represented. Three-dimensional (3D) grids are often used in ocean circulation modelling. Such a grid can be Cartesian in all three dimensions (Fig. 12.1b), or include a terrain following vertical coordinates (Fig. 12.1c). The former has a number of vertical layers of constant thickness across the horizontal, whereas the latter has layers of variable thickness and proportional to water depth, which allows for better vertical resolution in shallow than in deep areas. Horizontal grids applied to the Kongsfjorden-Krossfjorden system can be, for instance: a finite-difference Cartesian grid of variable spatial resolution (Fig. 12.1d) or a finite volume triangular unstructured grid (Fig. 12.1e). In both cases, resolution is increased in the more topographically complex areas for a better representation of the bathymetry and land boundaries. The type of grid used depends largely on the hydrodynamic model selected to simulate water circulation. For example, the Regional Ocean Model System (ROMS) (https://www.myroms.org/) uses finite-difference Cartesian horizontal grids and a vertical terrain following sigma coordinate system (Fig. 12.1c), EcoDynamo uses Cartesian grids with variable horizontal and vertical resolutions (Duarte et al. 2014; Fig. 12.1b, d) and the Finite-volume Community Ocean Model (FVCOM) uses horizontal unstructured triangular finite volume grids combined with a terrain following vertical grid (Huang et al. 2008; Fig. 12.1c, e). In Arctic fjords, it is also necessary to define a grid to simulate sea ice. This should also be a 3D grid if sea ice processes are to be resolved vertically as suggested by several authors (e.g. Arrigo et al. 1993; Mock and Gradinger 1999; Duarte et al. 2015). For example, the Los Alamos sea ice model (CICE) uses a 3D orthogonal grid (Hunke et al., 2013). If sediment biogeochemistry is included in the model, then a 3D sediment grid is also necessary to account for horizontal and vertical variability in simulated processes and organism distribution. The model of Chapelle (1995), developed for coastal lagoons, may be used to simulate sediment biogeochemistry in a two-layered system. Using grids for the ice and the sediments with the same horizontal resolution as for the water facilitates the calculation of exchanges between the different environments.



Fig. 12.1 (a) Kongsfjorden-Krossfjorden system illustrating some of the forcing and interactions with/from the atmosphere, the land and the ocean boundaries; (b) and (c) Examples of threedimensional grids with different vertical coordinate systems; (d) Finite difference Cartesian grid of variable spatial resolution, and (e) Volume finite triangular unstructured grid

Whatever grid is used, it is important to decide both on horizontal and vertical resolution ranges and it is difficult to agree on some general criteria for that. Regarding the vertical dimensions and considering the frequent presence of three distinct water layers in Arctic fjords (Cottier et al. 2010) – a fresh surface layer with a thickness of a few tens of metres, an intermediate layer with ~100 m thickness at the sill depth, and a deep layer below – it seems logical to have a higher vertical resolution at the surface layers, using thicknesses of ~ 10 m to properly resolve the mixed layer. This type of resolution may allow proper simulation of the vertical motions of phytoplankton and of the variability of production rates as a function of several potentially limiting factors such as irradiance, temperature and nutrient concentrations. This resolution may be decreased with depth, where less vertical variability is expected both in physical and in biogeochemical properties. However, for a better description of sediment water interactions, layer thickness should be reduced again at the bottom boundary layer. The horizontal resolution depends on the types of heterogeneity that are to be resolved by the model. Better resolution in the inner parts of the fjords is needed to properly represent and locate river and glacier outputs and respective plumes. The distribution and abundance of benthic organisms may also be important criteria. If their patchiness is not properly described by a coarse grid when biomass density is averaged over an area larger than the area of local patches, then local effects on the water and the sediments and their feedbacks on the benthic organisms will not be properly quantified. For instance, bivalve growth and production may be severely overestimated when local densities are not properly resolved (Duarte et al. 2003, 2005). The problem of soft-bottom fauna patchiness in Kongsfjorden was presented by Kendall et al. (2003), who showed that the size of a uniform patch of benthic fauna on flat deep sublittoral is about 800 m.

The most straightforward manner of coupling biogeochemical processes at LTL with physical processes is to use the same grids for the former as for the latter. Higher trophic levels may deserve a different treatment, as discussed below. The physical components are mostly based on well-established quantitative physical laws, such as the Newton laws of motion and the energy and mass conservation principles (Dike 2001). However, with the exception of this last principle that applies to all ecosystem variables, the biogeochemical counterpart is not based on well-established laws or generally accepted theories; it is much more "parameter dependent". This may lead to highly variable model results obtained with different models (Scholten and Van der Tol 1998). The degree of detail used to describe different processes may be determined by the importance assumed for each of them or by available knowledge (Pereira et al. 2006). The variables used to describe the physical realm, such as the velocity components, water density, temperature and salinity, are generally simple to select. However, when it comes to the biogeochemical components, there is a lot of ambiguity about which variables should be considered in each model.

12.2.2 Model Forcing

Critical aspects of model forcing include: (i) meteorological data such as wind velocity and direction, air temperature, relative humidity, precipitation, heat and radiation exchanges with the atmosphere and solar radiation; (ii) hydrological data such as glacier and river discharges and associated nutrient and particulate matter loads; (iii) oceanographic data such as water, dissolved and particulate matter exchanges across the sea boundaries and tidal forcing; (iv) species migrations and utilization of the fjord system by species living in neighbouring areas.

In the case of Kongsfjorden-Krossfjorden, meteorological forcing data may be obtained from available databases or from models. Atmospheric fields, including wind stress and radiation forcing may be obtained from simulations of the higher-resolution Weather Research and Forecasting (WRF) model (Skamarock et al. 2008). Local meteorological data, including long-term time series from Ny-Ålesund, can be obtained from the Sverdrup Station (www.npolar.no), Alfred Wegener Institute (www.awi.de) and the Norwegian Meteorological Institute (www.yr.no), and in a recent review by Maturilli et al. (Chap. 2).

Tidal glaciers discharge fresh water directly into the fjords while terrestrial glaciers may feed a seasonal river network. The former discharge may hardly be measured directly, but it may be calculated using a distributed energy balance model (Reijmer and Hock 2008). Energy and mass balances have been determined for several glaciers in the Kongsfjorden area with models (Rasmussen and Kohler 2007; Nuth et al. 2012; Kramer et al. 2013). This discharge may have important implications on fjord hydrography and ecology (Beszczynska-Möller et al. 1997; Zajaczkowski and Legezynska 2001; Svendsen et al. 2002; Lydersen et al. 2014). In front of the terrestrial glaciers of Kongsfjorden-Krossfjorden, there is a seasonally active river network and some rivers have permanent valleys (Svendsen et al. 2002). The SWAT (Soil Water Assessment Tool) model may be used to calculate river flows to force the fjord model. SWAT is a model developed by the USDA Agricultural Research Service to predict the impact of land management practices on water, sediment and agricultural chemical yields in large complex watersheds with varying soils, land use and management conditions over long time periods (Neitsch et al. 2002). It is a continuous time model, not designed to simulate detailed, single-event flood routing. Both the glacier and the river network models may be forced by the meteorological data mentioned above.

Migrations are a sort of model forcing since they constitute inputs/outputs from/ to the model domain. However, the abundance and/or biomass of migrating species may be treated as "normal" state variables in the model for the time periods of their permanence within the fjord model boundaries. Species migrations and utilization of the fjord system concern intermediate-to-higher trophic level taxa (Hop et al. 2002; Weslawski et al. 2006; Lydersen et al. 2014). This may include fish, bird and mammal migrations, and removal of food and deposition of excreta by birds (Stempniewicz et al. 2007).

12.2.3 Physical Processes

Different physical models can be used to simulate fjord circulation, e.g., the Princeton Ocean Model (POM) [Blumberg and Mellor 1987], FVCOM [Huang et al. 2008] or ROMS [https://www.myroms.org/]). In the specific case of Kongsfjorden-Krossfjorden there are two issues that may have very important influence on fjord circulation, ice build-up and biogeochemical processes: inputs of AW and freshwater discharges from calving glaciers. Svendsen et al. (2002) present results for Kongsfjorden-Krossfjorden obtained with the POM model to describe upper circulation and analyse the interactive effects of freshwater and local winds. They show up-fjord and down-fjord flows along the southern and northern margins, respectively. This pattern is intensified under down-fjord wind but it is also observable under up-fjord wind, which piles up water at the fjord's head and produces a down-fjord pressure gradient. The Bergen Ocean Model (Berntsen 2000) was used by Cottier et al. (2005) to model shelf-fjord dynamics, concluding that northern winds enhance frontal instabilities near the shelf break leading to pockets of AW being advected onto the shelf. These authors use the model to explain the restrictions to the intrusion of AW in winter by the density gradients at the fjord mouth. In summer, the relaxation of these gradients allows AW to enter into the fjord. In recent years, advection of AW into Kongsfjorden has also happened during winter, as shown by mooring data for the winter of 2005/06 (Cottier et al. 2007). EcoDynamo has been used to implement a 3D model for Kongsfjorden-Krossfjorden. Details on the numerics of EcoDynamo can be found in Duarte et al. (2014). Model runs were carried out to test the effects of tides and glacier discharges on fjord circulation as part of an effort to implement a coupled physical-biogeochemical model. Model resolution was increased in the inner parts of Kongsfjorden with the aim of obtaining a more detailed description of the effects of fresh water flow on hydrodynamics at the fjord's head. The current velocity field for a sub-surface layer (roughly between 10 and 20 m depth) indicates that most of the water flows along the southern margins of both fjords during flood tide (Fig. 12.2a), whilst during the ebb most of the water flows along the northern margins (Fig. 12.2c). An eddy pattern becomes visible at the mouth of Kongsfjorden during slack of both flood and ebb tide (Fig. 12.2b, d). Rotational effects tend to be more important in Arctic fjords due to the higher latitude and corresponding Coriolis parameter. During the ebb, the flow pattern is similar to what was described by Svendsen et al. (2002), with most of the water flowing out along the northern margins. These patterns are mostly apparent at surface layers and become simpler with depth (not shown), with the fluxes exhibiting a more linear behaviour following the direction of the tide with less eddies and cross-fjord velocity gradients as likely results of the increased drag (not shown).

A high-resolution (160 m in the horizontal) hydrodynamic numerical model has been established recently for Kongsfjorden (Sundfjord et al. 2017). This model was nested into a larger scale model with a 4-km grid covering the Nordic and Barents seas and the Arctic Ocean, and an 800-m grid regional model covering the shelf and fjords in Svalbard. This model system is an extension of the NorKyst800 implemen-



Fig. 12.2 EcoDynamo results regarding current velocity field for a sub-surface layer (roughly between 10 and 20 m depth), based on the grid shown in Fig. 12.1b, d (refer text). Maximum velocities are \sim 7 cm s⁻¹

tation of the ROMS ocean model (Haidvogel et al. 2008; Albretsen et al. 2011). This nesting solves some of the problems related to the definition of boundary conditions (see Sect. 12.2.1). One of the reasons why high-resolution simulations may be necessary in Kongsfjorden-Krossfjorden is the need to properly represent the plumes of freshwater released from calving glaciers that may have an important impact on zooplankton, through osmotic shock, and on the associated food web (Węsławski and Legezynska 1998; Węsławski et al. 2000a; Zajaczkowski and Legezynska 2001).

Whatever physical model is implemented to simulate water circulation, it is desirable to couple it with a sea ice model. When considering which sea ice model to use, it is important to take into account the need to simulate sea ice biogeochemistry and to resolve corresponding processes vertically within the ice (Duarte et al. 2015). Thus, the community Los Alamos Sea Ice Model (CICE V5) seems to be one of the best available options (Jeffery et al. 2011; Hunke et al. 2013). The CICE model resolves physical processes vertically in a variable number of ice layers and it has been used in pan-Arctic simulations coupled with ocean circulation and biogeochemical models (Jin et al. 2012). The Louvain-la-Neuve Sea Ice Model (LIM) also resolves vertically the ice and has been used in pan-arctic simulations (http://www.elic.ucl.ac.be/repomodx/lim/).

12.2.4 Biogeochemical, LTL and HTL Processes

Arctic fjord models are rather scarce, but biogeochemical (Jin et al. 2008) and coupled hydrodynamic-biogeochemical models have been implemented and used at a pan-Arctic scale (e.g. Popova et al. 2010; Slagstad et al. 2011; Jin et al. 2012). An analysis of these models reveals some important differences with regard to how hydrodynamic and biogeochemical processes were simulated. Regarding the former, less variability is observed since such models are all based on the same physical laws of momentum conservation and continuity. Therefore, differences among models are mostly related to the type of grids used, their spatial resolution and the turbulence closure schemes employed. However, differences between the biogeochemical counterparts are often substantial, as discussed below.

The biological sub-models of Jin et al. (2008), Popova et al. (2010) (the MEDUSA model [Yool et al. 2010]) and Slagstad et al. (2011) (Figs. 12.3, 12.4 and 12.5) have several conceptual similarities, with a strong emphasis on the nitrogen cycle, even though silicate limitation (regarding diatoms) and iron limitation, in the case of the MEDUSA model, are also considered. Nutrient limitation of phytoplankton and ice algae growth is based on a Michaelis-Menten dependence of nitrate and ammonium or silica present in the environment (in the case of the Jin's model, this may be sea ice or water). There are some small differences in the detritus, phytoplankton and zooplankton compartments, but these are still relatively consistent among the three models. The model of Slagstad et al. (2011, Fig. 12.5) is more detailed since it includes dissolved organic carbon (DOC), part of the microbiological food web,



Fig. 12.3 Ice-ocean ecosystem model for 1-D and 3-D applications in the Bering and Chukchi seas. (Jin et al. 2008)



Fig. 12.4 Model for Ecosystem Dynamics, Carbon Utilisation, Sequestration and Acidification (MEDUSA) (Yool et al. 2010)

with the explicit inclusion of bacteria, and marine copepods characteristic of Arctic mesozooplankton (*Calanus finmarchicus* of Atlantic origin and *C. glacialis*, an indicator of Arctic waters). It is important to emphasize the relevance of including DOC, since some fraction of new production is not exported, but it is accumulated in the surface ocean as DOC and particulate organic matter (POM; Sanders et al. 2005).

The model of Moore et al. (2002; Fig. 12.6) has been coupled to CICE to investigate the relationship between Arctic sea ice extent and primary production (Jin et al. 2012). Moore's biogeochemical model is based on a different paradigm than that of all previous models. The Moore model considers several nutrients simultaneously, including phosphate and iron as well, possibly stimulated by the discovery of the High Nitrate – Low Chlorophyll regions of the Southern Ocean and the iron limitation Martin's hypothesis (see Smetacek et al. 2012) and keeps track of their values in the various compartments. This allows the calculation of phytoplankton cell quotas and constrains them to biologically realistic values. This approach



Fig. 12.5 Biogeochemical component of the SINMOD model. (Slagstad et al. 2011)



Fig. 12.6 Marine ecosystem model of intermediate complexity for the global domain. (Moore et al. 2002)

implies the acceptance of limitation by other nutrients than nitrogen and silica. Furthermore, it permits calculating nutrient limitation based on phytoplankton cellquotas instead of the usual environmental concentrations. Therefore, limitation becomes dependent on the capacity of cells to absorb and accumulate nutrients and the models must use more proxies (e.g. carbon, nitrogen, phosphorus,...) to represent organism abundance/concentration for book keeping calculations. This is more realistic from a biological perspective, since it is known that microalgae have some capacity for luxury consumption of nutrients. The approach of decoupling carbon assimilation through photosynthesis from nutrient uptake has been suggested by other authors (e.g. Baretta-Bekker et al. [1997] in the ERSEM model). Another important point in favour of this model is the possibility of "following" the atomic ratios of particulate matter. In fact, some studies have shown that when Redfield

ratios are applied in models that use nitrogen as their "currency" to calculate carbon sinking, this may be underestimated due to the higher C:N ratios of sinking matter in the Arctic than those predicted by the traditional Redfield ratio (Daly et al. 1999; Tamelander et al. 2013). Results obtained by Thingstad et al. (2008), using mesocosm experiments with Arctic plankton, emphasize the importance of stoichiometric coupling between carbon and limiting nutrients not only in the autotrophic but also in the heterotrophic food web compartments, with emphasis on the nutrient-competing role of bacteria. These results point to the need for incorporating the microbial loop in models that aspire to capture the details of pelagic interactions in Arctic food webs. Several studies of microbial processes have been carried out in Kongsfjorden (Piquet et al. 2010; de Corte et al. 2011; Rokkan Iversen and Seuthe 2011; Seuthe et al. 2011). The work of Hessen et al. (2008) demonstrated the coupling between the intensity of photosynthetically active radiation (PAR) and the stoichiometric ratios in Arctic photoautotrophs and suggested that increased PAR leads to increased C:N and C:P ratios. In a study conducted in the Sylt-Rømø Bight ecosystem of the German Wadden Sea, Baird et al. (2011) report that nitrogen and, especially, phosphorus are recycled much faster than carbon. All these lines of evidence emphasize the importance of simulating separately the main macronutrients instead of forcing their stoichiometry by using Redfield ratios.

None of the previous models includes dissolved organic pools, except for dissolved carbon in the case of the Slagstad model. Thus, it is not possible to close completely the biogeochemical cycles represented in the various models. The importance of these pools is related to nutrient recycling in the water column and regenerated production. Guildford and Hecky (2000) stress the importance of total nitrogen and phosphorus, i.e., dissolved inorganic plus organic forms and not only the former, as it is usually the case in studies conducted in the marine realm, for a more realistic assessment of nitrogen and phosphorus availability in their various forms.

In sea-ice biogeochemical modelling, most of the models are based on the traditional approaches inherited from NPZ models as, for example, the models of Arrigo et al. (1993), Lavoie et al. (2005) and Jin et al. (2008; Fig. 12.3). However, there are also models based on the more recent paradigms discussed above of internal nutrient limitation and dynamic stoichiometry (e.g. Tedesco et al. 2010). Sea ice biogeochemical models published over approximately the last 20 years have been reviewed by Tedesco and Vichi (2014). These may be roughly classified into three groups, according to the vertical distribution of ice algae and associated biogeochemical processes: a) one-layer models of prescribed thickness; b) onelayer models of variable thickness, and c) multi-layer models (Fig. 12.7). The first type simulates biogeochemical processes only at the ice bottom (e.g. Jin et al. 2008). The second type simulates the same processes only in the bottom permeable layer that has a variable thickness - the Biological Active Layer (BAL) -(Tedesco et al. 2010, 2012; Tedesco and Vichi 2014). The third type resolves vertically the concentration of ice algae and associated biogeochemistry within the ice for a given number of layers (e.g. Arrigo et al. 1993; Vancoppenolle et al. 2010; Pogson et al. 2011; Saenz and Arrigo 2012; Duarte et al. 2015). Therefore, when considering sea-ice algal and biogeochemical modelling, the diversity of



Fig. 12.7 Schematic representations of different sea ice biogeochemical models. Bottom layer models consider biogeochemical processes only at the bottom layer (e.g. Jin et al. 2008). Biologically active layer models assume that biogeochemical processes may occur not only at the ice bottom, defining the thickness of the biological active layer (BAL) as a function of brine channel density but not resolving the biological processes within the BAL, as a function of environmental variability (e.g. Tedesco et al. 2010). Vertically resolved models resolve vertically the sea–ice biogeochemical processes (e.g. Arrigo et al. 1993). (Adapted from Duarte et al. 2015)

approaches results not only from the way the same processes are simulated by different models, but also from the model's vertical extent and corresponding resolution. The rationale to justify using only one ice layer in several models applied to the Arctic Ocean is because ice algae are usually found in highest concentrations near the bottom of sea ice (Tedesco and Vichi 2014). Mock and Gradinger (1999), using a method of measuring ice algal primary production that resolved its vertical variability, concluded that traditional methods restricted to the study of bottom communities may have severely underestimated Arctic as well as Antarctic primary production. Also, empirical and model results presented by Tedesco et al. (2010) provide further evidence that ice algal biomass and production can be vertically highly variable within sea ice. Most recent CICE versions include a new halo-thermodynamic scheme that enables 3D computations of the sea ice microstructure and a vertical bio-grid, which can be used to resolve the vertical transport equations of biogeochemical tracers (Jeffery et al. 2011; Hunke et al. 2013).

It is important to emphasize that increasing model complexity brings the need to use more parameters that may not be easily obtained and, especially, to properly constrain within biologically realistic values due to the lack of knowledge about some of them. Furthermore, several authors suggest that there is a parabolic relationship between model efficiency and model complexity, whereby, efficiency is maximized at intermediate complexity. As science evolves, the parabolic curve shifts towards higher complexity (Hannah et al. 2010 and references therein).

All the previously discussed models focus on biogeochemistry and LTLs. However, there is growing interest in end-to-end models of marine ecosystems, i.e., models combining physicochemical oceanographic descriptors and organisms ranging from microbes to HTL, including humans, in a single modeling framework (Fulton 2010; Rose et al. 2010). According to the last authors, ecosystem-based management requires quantitative tools dealing with bottom-up and top-down controls of the food webs, allowing to test the effects of global climate change, among other possible environmental changes. Another argument in favour of this type of model is the need to properly close the biogeochemical processes in a more realistic manner, embedding the functional role of HTL organisms in the biogeochemical cycles. This argument will be developed below using the Kongsfjorden-Krossfjorden system as a case study.

The integration of processes in end-to-end models poses several challenges such as dealing with different spatial and temporal scales, acclimation and adaptation, behavioural movement, software and technology and model coupling (Rose et al. 2010). Most of these challenges may be dealt with by using available tools and technology (e.g. the Atlantis model; Fulton 2010). One of the crucial aspects here is the way different sub-models are coupled in different modelling environments.

Whereas variables related to biogeochemistry and LTLs are generally simulated over the entire model domain, except in the case of benthic organisms that are substrate dependent, the spatial complexity in the distribution of HTLs may be handled by using individual-based models (IBM) with organism distribution being influenced by environmental drivers and biological factors (Fulton 2010) provided by the physical and the LTL models. HTL models may be based on mechanistic principles to simulate physiology and population dynamics. For example, physiology may be based on the Dynamic Energy Budget (DEB) theory (Kooijman 2000). Molnár et al. (2010a, b) attempted to predict survival, reproduction, abundance and litter size of polar bears under climate warming scenarios using a DEB model combined with a population dynamics model. The DEB model was used to predict starvation (Molnár et al. 2010a) and litter size (Molnár et al. 2010b). These physiological variables may be integrated in a population dynamics model to predict changes in the abundance of different age or size/weight classes by using, for example, a stagestructured matrix population model. HTL models may be influenced by environmental conditions predicted by physical and biogeochemical models and may also include feedbacks through consumption, excretion and mortality. The end-to-end model by Serpa et al. (2013) integrates all these complex feedbacks. Furthermore, population dynamic models of different species may feedback onto each other by using, for example, predation, as a closure term for part of the mortality losses of prey organisms.

Links between physiologic, population dynamic, consumption, migratory and transport processes for a species or functional group are represented in Eq. 12.2 and may be replicated for any number of age, size or weight classes:

$$\frac{\partial Ni}{\partial t} = G_i - M_i + R_i - E_i + I_i \pm Tr_i$$
(12.2)

Where,

i is class number (for the sake of simplicity only the class index is indicated but indices are also needed to identify the geographical position of the organisms in the grid); G_i – growth; M_i – mortality; R_i – recruitment; E_i – emigration; I_i – immigration; Tr_i – transport.

It is noteworthy that this is just another form of representing the dynamics of a biological variable analogous to Eq. 12.1, but emphasizing here the biological processes integrated in Eq. 12.1 in the *Sources* and *Sinks* terms. These are discriminated here in G_i , M_i , R_i , E_i and I_i . The last three terms represent transport processes but, whereas E_i and I_i are active transport resulting from the motility capacity of the organisms, Tr_i is passive transport and it is calculated from the advection and turbulent mixing of Eq. 12.1. Even HTL organisms may be under some influence of physical transport. For example, fish velocity results from swimming speed and background currents. A *DEB* sub-model can be used to calculate G_i and M_i . These values may be used in a population dynamics model solving the above equation for each class, which may be represented by a homogeneous number of individuals or, if an *IBM* is used, by individuals or groups of homogeneous individuals.

Studies in Kongsfjorden suggest a trophic web with up to six trophic levels (TLs). Pelagic and benthic food webs have been adapted from Hop et al. (2002), respectively (Figs. 12.8 and 12.9), including the TLs and their net production (*NP*) estimates, in the case of the pelagic food web. Phytoplankton Net Primary Production (*NPP*) estimates (4 – 180 g C m⁻² y⁻¹) reported by Eilertsen et al. (1989), Hop et al. (2002) and Piwosz et al. (2009) have been used to calculate the *NP* of consecutive TLs, assuming a 10% energy transfer efficiency (*ETE*) (Pauly and Christensen, 1995; Eq. 12.3):

$$NP = NPP \cdot ETE^{TL-1} \tag{12.3}$$

Each value of the secondary production ranges (Fig. 12.8) was based on the minimum and maximum values of *NPP*, and when a TL range is presented (for example, in the case of 2nd-3rd TLs) instead of a unique value, the median value of the range was used to replace TL in Eq. 12.3. The decreasing magnitude of *NP* along the food web may lead to the wrong impression of a relatively low importance of higher TLs for ecosystem total throughput. However, bearing in mind that TL consumption is larger than *NP*, due to losses associated with the efficiency with which prey are utilized by predators, it is more meaningful to look at consumption values. Using values reported in Hop et al. (2002), after converting mass of food to carbon, assuming carbon contents to be roughly 40% of dry weight, food consumption should be



Fig. 12.8 Kongsfjorden pelagic food web. (Adapted from Hop et al. 2002). Trophic levels and corresponding net productions are also shown (refer text)

around 0.2 and 0.3 g C m⁻² y⁻¹ for the birds and the mammals, respectively. These values imply that birds and mammals alone may consume an amount of food that may be up to 13% of *NPP*. Some other estimates of historical food web (Weslawski et al. 2000b) and present day HTL energy demand in Svalbard fjords show similar proportions of energy division (Weslawski et al. 2006). Considering the potential importance of consumption by fish, it is most likely that HTLs have an important impact on ecosystem functioning including nutrient recycling. Therefore, model efforts should be towards an end-to-end model for a realistic representation of the fjord ecosystem. There are obviously other non-quantitative arguments in favour of including HTLs in an ecosystem model, when species have a special economic, conservation or aesthetic value.

Regarding the benthic food web, primary production values are not available, except for the microphytobenthos (Woelfel et al. 2010). These authors report values in the range 2-14 g C m⁻² year⁻¹. Considering that the microphytobenthos values alone may be of the same order of magnitude as those of phytoplankton (Glud and Rysgaard 2007; Woelfel et al. 2010; Hodal et al. 2011), it seems important to include the benthos in a fjord ecosystem model. To get a full picture of benthic primary production, it is necessary to account for the macroalgal contribution as well. The distribution of kelp in Kongsfjorden is generally limited to a band from 2 to 15 m



Fig. 12.9 Kongsfjorden benthic food web. (Adapted from Hop et al. 2002). Trophic levels are shown on the left (refer text)

depth on hard substrata, except for the inner bay where there are few macroalgae below 5 m depth (Hop et al. 2012; Kruss et al. 2012; Fredriksen et al., Chap. 9). Since macroalgae are mostly associated with hard substrata, the distribution within the fjord is probably limited to about 20–30% in outer-middle fjord and <10% in inner fjord. The macroalgal belt is wide (100–200 m) at the outer locations of Kongsfjorden, such as Kapp Mitra and Kapp Guissez, but less (<50 m) at Hansneset and Juttaholmen (Hop et al. 2016). The annual production in the shallow coastal waters may be 2–3 kg C m⁻² y⁻², as determined for fjords in Greenland (Borum et al. 2002; Krause-Jensen et al. 2007, 2012).

12.3 Synthesis

A schematic setup of an end-to-end fjord ecosystem model for Kongsfjorden includes exchanges and inputs, biogeochemical cycles, food web components for pelagic and benthic food webs and trophic interactions, as shown in Fig. 12.10. In the upper right corner, a diagram shows the sub-models necessary for the end-to-end coupled model as well as their feedbacks. Sub-models simulate ice physics,

water circulation, biogeochemistry and LTLs, and single species dynamics for HTLs (possibly including *IBM* models). All sub-models interact with each other. Biogeochemistry and LTLs are simulated in water, ice and benthic compartments using different grids (cf. – General structure) that are shared with the physical counterparts. For simplicity, only the grid used to represent water circulation is shown in Fig. 12.10.

The number of HTL sub-models may increase with time as knowledge is accumulated about more species. The physical and biogeochemical sub-models provide the environmental context for the HTL models. Ideally, biogeochemical models should combine the approaches of the SINMOD model (Fig. 12.5) and those described by Moore et al. (2002, Fig. 12.6), including micro- and mesozooplankton, the microbial loop and variable stoichiometry. Part of the LTL organisms may later be replaced by detailed population dynamics models, depending on accumulated knowledge, questions of interest and available computer power. According to Rose et al. (2010), the extent to which multistage (composed of several weight, size or age classes) LTL models will be required to describe the development of some species groups, for example, the copepods, is yet unknown.

Biogeochemical cycles in the water and benthic compartments and their interactions are also in Fig. 12.10. These include sedimentation, re-suspension, adsorption, desorption and diffusion fluxes across the bottom-water interfaces. Ideally, soft bottom areas should be represented by, at least, two layers to account for aerobic (surface layer) and anaerobic processes. Sediment biogeochemistry should include the same dissolved variables in the pore water that are simulated in the water column for proper closure of pelagic-benthic coupling. Furthermore, macroelements associated with some of those variables, such as nitrogen and phosphorus, should be simulated in the sediment solid phase as well (e.g. Duarte et al. 2007; Serpa et al. 2013).

In parallel with the biogeochemical cycles, the pelagic and benthic schematic trophic webs and their interactions are presented in Fig. 12.10 as closed structures, not to mean that trophic chains are closed to exchanges across the system boundaries but to emphasize the importance of closing the loss terms of some species or functional groups as input terms for other species or other trophic groups. Also, there is a tight link between trophic interactions and the biogeochemical cycles since the former feeds back on the latter through processes such as photosynthesis, respiration, excretion, and faecal production. Dots in the grid represent the hypothetical distribution of a high trophic level species. In this case, it is suggested that the same grid used for hydrodynamics and water biogeochemistry may be used to represent the spatial distribution of a HTL species. However, this may not be appropriate for all species and it may be desirable to overlay different spatial grids applicable to different species, integrating different spatial and temporal scales.

The forcing functions and boundary conditions shown earlier (cf. – Fig. 12.1) are also represented in Fig. 12.10: (i) inputs from glaciers and rivers (water, nutrients, suspended matter, etc.); (ii) exchanges with the atmosphere (in the form of precipitation, evaporation, radiation, wind momentum transfer, carbon dioxide, oxygen, etc.); (iii) exchanges with the open ocean (water, momentum transfer, nutrients, suspended matter, dissolved gases, plankton, nekton). Contaminants may also be added if relevant for the study area. Ice inputs influence directly the ice model,



Fig. 12.10 Schematic setup of an end-to-end fjord ecosystem model. In the upper right corner, a simple diagram shows the sub-models necessary for the end-to-end coupled model as well as their feedbacks. More "high trophic level" (HTL) species may be added as long as relevant physiologic and population dynamics data are gathered and made available for model development. Biogeochemical processes in the water, the ice and the sediments (mineralization, nitrification,

whereas water inputs influence directly the hydrodynamic model because of density differences with the fjord water and because of momentum transfer. Ice and water properties (including plankton) are advected by the current velocity field of the hydrodynamic model and changed locally by thermodynamic and biogeochemical processes.

The complexity of a model such as the one represented in Fig. 12.10 poses several technical challenges. Frequently, biogeochemical models, such as those available in ROMS, include all biogeochemistry in one subroutine (https://www.myroms. org/). This makes it very difficult to combine different approaches to simulate the various components of the biogeochemical system. Also, the number of HTL species in the pelagic and benthic webs (Figs. 12.8 and 12.9) potentially implies a large number of sub-models. Therefore, it is important to have a coupling method that makes it easy to link more models as these become available and they should be as modular as possible. Object-oriented programming is one sound approach towards this modularity following Ferreira (1995). Whatever the approach followed, the recommendations of Rose et al. (2010) about adopting a community-based approach with open source software seems to be the right way to handle the large complexity of end-to-end models.

Ecosystem model complexity is a matter of great debate (see for example: Allen and Fulton (2010); Hannah et al. (2010) and references therein). According to Hannah et al. (2010), the optimal model complexity shifts to higher values as knowledge accumulates. Therefore, increasing model complexity is a sort of "natural" process whether it happens by increasing feedbacks, processes, temporal or spatial details. It is important to stress that no matter the sophistication of ecosystem models, the challenge is to build a model capable of dealing with species composition changes. The focus of current models is on quantitative changes in the background of a relatively fixed structure. The large uncertainty in the model outcomes that partly result from the poor knowledge about model parameters and partly from the complexity of the systems being modelled was discussed by Hannah et al. (2010). These authors suggest the need to move towards ensemble simulations to overcome some of these limitations and handle system stochastic-

Fig. 12.10 (continued) ammonification, denitrification, etc.) and their links are represented in parallel with pelagic and benthic food webs. These have a circular form to emphasize the importance of closing the terms associated with gains and losses of the different functional groups (P primary producers, H herbivores, C carnivores, D detritivores, B bacteria/decomposers). Dots in the grid represent the hypothetical distribution of a high trophic level species. The 3D grid necessary for water column processes includes: (1) inputs from glaciers and rivers (water, nutrients, suspended matter, etc.); (2) exchanges with the atmosphere (in the form of precipitation, evaporation, radiation, wind momentum transfer, carbon dioxide, oxygen, etc.); (3) exchanges with the open ocean (water, momentum transfer, nutrients, suspended matter, dissolved gases, plankton, nekton); (4) water circulation (represented in the grid by the three velocity components u, v and w) (cf. -Svnthesis)

ity. However, these types of simulations are a great challenge with very complex models demanding a great deal of computer power.

The conceptual model presented here is a sort of "idealization" rooted in the concept of "ecosystem". It by no means implies that all the mentioned complexity is necessary to obtain meaningful results. It merely seeks to suggest a model environment that, in direct interaction with field and experimental work, can address some of the current concerns related with a changing Arctic Ocean, whilst building on recent advances in ecology and modeling. Such an "ideal" model would make it possible to evaluate the relative importance of HTL on ecosystem biogeochemistry – a question that remains largely unanswered in quantitative terms, up to our best knowledge, although that it has been addressed in recent years (e.g. Lavery and Roudnew 2014; Doughty et al. 2015). Such a model could be used to analyse the impacts of warming on the LTL, HTL and their feedbacks, and it would be useful for addressing management and conservation issues. These aspects may become more relevant in the near future, considering the ongoing development of fisheries in the Arctic under the new ice regime. However, the development of such a model is limited by the availability of calibration and validation data. Here, it is important to stress that data-limiting problems are not just related to the model state variables but also to the simulated rates. These rates depend on parameters that should be better constrained, which could be achieved though experimental studies.

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