

## Chapter 3

# Frozen Ground

### 3.1 introduction

A definition from the National Snow and Ice Data Center:

Permafrost, or permanently frozen ground, is soil, sediment, or rock that remains at or below 0°C for at least two years. It occurs both on land and beneath offshore Arctic continental shelves, and its thickness ranges from less than 1 meter to greater than 1,000 meters. Seasonally frozen ground is near-surface soil that freezes for more than 15 days per year. Intermittently frozen ground is near-surface soil that freezes from one to 15 days per year.

Permafrost underlies 12 to 18 percent of the exposed land surface in the Northern Hemisphere. Seasonally frozen ground regions may cover as much as 55 percent.

Regions characterized by permafrost are grouped into two zones, those where the frozen layer is continuous and those where it is discontinuous. Most continuous permafrost is at least as old as the last glacial maximum. The discontinuous zone embraces areas in which permafrost lies beneath anywhere from 10 to 90 percent of the land surface. Discontinuous permafrost is thought to be much younger than continuous permafrost, having formed since the orbitally-driven high-latitude warming between about 8 and 6 ka.

Permafrost warming has important implications for ecosystems and human infrastructure. Dramatic consequences of warming, such as transitions from forest to bog or thermokarst effects on roads and building foundations, are easily observed. But change detection and monitoring require direct observation and interpretation of permafrost temperature. Indeed, increasing permafrost temperatures in the Arctic are often cited as evidence of global warming (for example, Figures 7.2 and 7.3 in our text). Such presentations are deceptively simple, as soil temperature changes throughout the year, as the subsurface responds to the annual seasonal cycle.

## 3.2 the simplest possible model

Mathematical models of physical processes all begin as statements of conservation (mass, energy, momentum) and boundary conditions that allow those equations to be solved, along with constitutive relationships that describe how material properties influence the behavior of the system. If you want to know the speed at which maple syrup will spread across a counter after you spill it, you need to know something about the friction between the syrup and the counter (a boundary condition) and about the viscosity of the syrup (a material property).

In this lab we will use a simple model of thermal diffusion in soil to help us think about how temperature monitoring can be used to investigate change in frozen ground.

### 3.2.1 thermal diffusion

Diffusion is a fundamental concept for many problems in Earth science. Mathematically, it is the time-change in some conserved quantity (for example, temperature or salinity), driven by a spatial gradient in the magnitude of that quantity. The underlying physical process (molecular, thermal, gravitational), are all related to the second law of thermodynamics. Systems tend toward the lowest possible energy states: piles of sand flatten out over time, contaminants move from regions of high concentration to regions of low concentration, and so on.

Because diffusion involves changes in both time and space, it is described by a partial differential equation. The dependent variable changes with respect to more than one independent variable. Here, we will consider one space dimension.

### 3.2.2 a conservation law

The first law of thermodynamics tells us that the temperature of any particular parcel of space (say a unit volume of soil or of air) changes if the heat flowing into the parcel is different than the heat flowing out of the parcel:

$$\frac{dT}{dt} = -\nabla Q \quad (3.1)$$

where  $T$  represents temperature,  $t$  represents time,  $Q$  represents a vector-valued heat flow and  $\nabla$  (*The symbol  $\nabla$  is called “del” or sometimes “nabla”*) is a vector differential operator that tells us to take the first derivative of  $Q$  in each of the relevant space dimensions.

The borehole measurements are confined to one dimension in space (the vertical). As long as the borehole is not near a feature that will generate significant gradients in the horizontal directions, it is reasonable to simplify our diffusion equation to consider only the vertical dimension, which we will call  $z$ . In this case, equation (3.1) may be written:

$$\frac{dT}{dt} = -\frac{dQ}{dz} \quad (3.2)$$

such that the heat flow is positive in the positive  $z$  direction.

### 3.2.3 a constitutive relation

Heat flow through a material depends on the temperature gradient and a material property  $K$ , the thermal diffusivity. Intuitively, we can think of this as “excess” heat in a relatively warm region diffusing toward adjacent, relatively cooler regions, simply because of the temperature difference. In our one space dimension this is:

$$Q = -K \frac{dT}{dz} \quad (3.3)$$

In the MKS system, the units of  $Q$  are Watts, which have dimension  $\text{MASS} * \text{LENGTH}^2 / \text{TIME}^3$ . The dimension of  $K$  is  $\text{LENGTH}^2 / \text{TIME}$ .

### 3.2.4 all together

Combining equations (3.2) and (3.3) yields the thermal diffusion equation in one dimension.

$$\begin{aligned} \frac{\partial T}{\partial t} &= -\frac{\partial}{\partial z} \left( -K \frac{\partial T}{\partial z} \right) \\ \frac{\partial T}{\partial t} &= K \frac{\partial^2 T}{\partial z^2} \end{aligned} \quad (3.4)$$

Equation (3.4) uses partial derivatives because now our dependent variable  $T$  is a function of two independent variables,  $z$  and  $t$ .

### 3.2.5 solution to equation 3.4

Without some unwarranted assumptions, the diffusion equation must be solved numerically, according to some specified boundary conditions on  $T(z, t)$  and a thermal diffusivity for the frozen soil. No worries, this is a relatively straightforward task. For now, let’s think about those boundary conditions.

We can think of our model domain as being a straight line, descending from the ground surface to some depth within the permafrost (perhaps along a borehole). In order to solve equation 3.4, we must specify either  $T(z, t)$  or  $\partial T / \partial z$  at the upper and lower ends of that domain.

The annual surface temperature cycle  $T(z_s, t)$ , perhaps measured at a nearby weather station or at the top of a borehole, is a good candidate for the upper surface condition. The lower boundary condition is a bit trickier. Here, we may take advantage of the fact that temperature remains fairly constant, at the mean annual temperature, over the course of the year at some depth below the surface (this depth may be observed in a borehole or estimated using theory). Alternatively, we

may chose to use the geothermal gradient, if we know it, and specify a condition on  $\partial T/\partial z$  at the lower end of the model domain.

The thermal diffusivity, the ratio of thermal conductivity to heat capacity, depends on the composition of the soil (mineral and organic content) and its ice content. This can be determined experimentally in the laboratory or computed using borehole temperature data. The thermal diffusivity for dry sand is  $2.8 \times 10^{-7} \text{ m}^2 \text{ s}^{-1}$ . Mauro (2004) computed permafrost diffusivities in the range of 0.9 to  $1.9 \times 10^{-7} \text{ m}^2 \text{ s}^{-1}$  using temperatures recorded at sites in the Italian Alps and Northern Victoria Land, Antarctica.

### 3.3 borehole temperature records from Alaska

Soil temperature records are developed by augering a borehole into the soil and installing a set of thermistors at fixed depths within the hole. Thermistors are resistors for which the relationship between change in temperature and change in resistance is known. In modern installations, the thermistors are connected to a data logger at the surface. Back in the good old days, data were recorded manually, using a hand-held voltmeter. As you might expect, long-standing, continuous permafrost temperature records are rare. The reference for the data included with this lab is Osterkamp (1999).

Two borehole temperature records are stored in the MATLAB file `PTrecords.mat` at the class website. The variables with a prefix `T_` store year, day of year, and temperatures (degrees Celsius) measured at specified depths (meters). The variables with a prefix `d_` contain the corresponding depths. The `fb` data are from an installation at Franklin Bluffs, on the North Slope of Alaska and the `gi187` data are from an installation at the University of Alaska, Fairbanks Geophysical Institute. The former is a relatively shallow record, extending 0.86 meters below the surface while the latter extends to a depth of 93.75 meters. In each record, a value of 999.9 is used to indicate missing data.

### 3.4 investigating the data

#### 3.4.1 a simple start

A good first step is to visually inspect the data by plotting time series in one way or another. There are a lot of data here, daily records from 1986 to 2003 at Franklin Bluffs and from 1987 to 1995 at the Fairbanks site. We probably don't want to plot *all* of the data. You are provided with a simple MATLAB function `f_PTplot.m` that generates an initial view of the data by plotting all observation times at a few depths, all depths on every day for one year, and all depths once every 30 days in each observation year. The function requires four variables to be passed to it, the temperature data array, the depth data array, a starting figure number (two figures are drawn) and a title string for the plots.

For the Franklin Bluffs data:

```
>> f_PTplot(T_fb, d_fb, 1, 'Franklin Bluffs')
```

### 3.5 Questions

1. Run f\_PTplot for both data sets. What happens late in the Fairbanks record?
2. What differences in the soils at these two sites can you infer from the temperature records?
3. Describe how you might use these data to detect a temperature trend over time.

#### graduate students

4. The Franklin Bluffs data set extends down less than one meter into the subsurface. How could it be used to estimate the temperature trend at, say, 20 meters depth? *Be careful, there are several steps in this answer.*

### 3.6 References

Hewitt, C.D. and J.F.B. Mitchell, 1998, A Fully Coupled GCM Simulation of the Climate of the Mid-Holocene, *Geophys. Res. Lett.*, 25, 361-364.

Mauro, G., 2004, Observations on permafrost ground thermal regimes from Antarctica and the Italian Alps, and their relevance to global climate change, *Global and Planetary Change*, 40, 159-167.

Guglielmin Mauro Osterkamp, T. 1999, updated 2004. Borehole temperatures from the North Slope of Alaska, 1977-2002. Boulder, CO: National Snow and Ice Data Center. Digital media.



## Chapter 4

# simple models of marine biogeochemistry

### 4.1 introduction

#### 4.1.1 big ideas

Marine ecosystems are vast and diverse, ranging from productive near-shore environments to relatively barren deep sea-floor environments. In the ocean, productivity is limited by the availability of nutrients and light (in contrast, terrestrial ecosystems are often limited by the availability of water). As on land, the fundamental energy source for most of the marine food web is photosynthesis. Marine phytoplankton are the the most numerous *primary producers* on Earth. Individual species are adapted to a large range of temperature, salinity, and sea ice conditions.

Photosynthesis is limited to the *photic (or euphotic) zone*, the part of the shallow ocean through which sunlight penetrates. The depth of the photic zone varies from a few meters or less in very turbid conditions to about 200 meters in the open ocean. The biomass of the photic zone varies significantly across the ocean, depending primarily on nutrient content of the water. Nutrient availability in turn depends on ocean circulation (for example, upwelling of nutrient-rich deep water), wind-driven turbulence, proximity to terrestrial nutrient sources, seasonal cycles (for example, sea ice and river ice), and other processes.

Polar marine organisms are adapted to large seasonal changes in their environments, including solar radiation, temperature, salinity, nutrient availability, and (of course) sea ice. Contrary to what one might expect, polar marine ecosystems are diverse. While a few key species provide the majority of food to polar marine predators, the planktonic base of the pelagic energy supply is as diverse as the planktonic base in lower latitude, more equable environments.

Interaction between bathymetry, ocean circulation, and ice cover (both marine and terrestrial) determines the range of polar marine habitats. The Arctic (and sub-Arctic) region is characterized by extensive shallow continental shelf environments and a relatively confined ocean basin while

Antarctic habitats are mainly open-ocean and deep continental shelf. It is the presence and seasonal variation in sea ice that sets these habitats apart from their lower-latitude counterparts.

Arctic and sub-Arctic sea ice has both perennial and annual components. The former is restricted to the Arctic Ocean basin. Seasonal sea ice expands over continental shelves in the Arctic Ocean, extends to about 70° S in the Atlantic, while in the north Pacific it extends as far as 44° N around northern Japan, covering most of the continental shelf (an exception is the relatively deep southwestern Bering Sea). Sea ice melting and freshwater input from terrestrial rivers yield a strong haline stratification within the Arctic Ocean.

Despite the similarities in climate forcing, northern and southern polar food webs are not mirrors of each other. In the north, the key prey for vertebrates are benthic organisms and fish while in the south, crustaceans transfer the bulk of the energy from lower to higher trophic levels. Interactions among trophic levels in polar oceans, in particular the nature of forcing among trophic levels, is a subject of considerable discussion and strongly-held opinion (some ecologists would argue that marine trophic interactions are poorly understood in general, due to depopulation of large predator species by human predation).

#### 4.1.2 Arctic productivity

The central Arctic Ocean is characterized by relatively low productivity. The shallow ocean is relatively nutrient poor because strong haline stratification limits upward transport of nutrients from deep water. Nevertheless, in contrast to most of the shallow ocean, productivity under perennial sea ice is not nutrient limited but is light limited instead.

Seasonal sea ice has two important effects on primary production. First, the ice cover reduces light penetration, limiting photosynthesis. Second, spring melting releases freshwater, microorganisms, and trace elements (especially iron) into the surface layer. The fresh water input lowers salinity in the near surface, producing a stable (haline) stratification that in turn holds nutrients near the surface. Together, these effects accelerate the spring bloom. Under favorable conditions, short, intense, phytoplankton blooms follow in the wake of seasonally retreating sea ice. Where this primary productivity exhausts the nutrient supply, products of the bloom sink out of the surface layer, transferring energy from the pelagic to the benthic environment.

The Barents and Chukchi Seas, gateways to the Arctic Ocean, are more productive than are shelf seas within the ocean basin. This is because water moving through these regions originates from deep, nutrient-rich water masses. In the Pacific, water flowing through the Bering Strait originates from the deep water masses of the southwestern Bering Sea. As the water moves toward and through the shallow strait, iron is added by mixing with shelf water sea ice melt products. The shallow depth of the shelf in this region allows much of the primary biomass to settle out to the sea floor, where it is used by a rich benthic fauna (which in turn becomes an energy source for benthic specialists at higher trophic levels, for example eiders, grey whales and walrus). Relatively strong currents and wind mixing through the region result in vigorous nutrient recycling between the water column and sediments. In contrast, the Barents Sea is deeper and thus, relatively more phytoplankton biomass is retained in the water column (which in turn supports a large populations of planktivorous fish).

Latitudinal temperature gradients in the Bering Sea drive gradients in the species composition of the marine ecosystem. In the southern (subarctic) region of the sea, most of the benthic biomass is consumed by bottom-dwelling *demersal* fish and *epifaunal* invertebrates. The northern extent of these organisms is limited by very cold bottom temperatures. With distance north, benthic-feeding mammals and birds take over as primary consumers.

As Earth's climate changes, ecosystem composition must change as well. At high latitudes, both warming and changes in the sea ice extent and seasonality are expected to have important consequences on marine ecosystems. Understanding marine ecosystem function is complicated by very efficient human predation on certain species. Nevertheless, trends may be observed via monitoring projects and insights into system processes may be made by investigating responses to specific climate events.

### 4.1.3 an unusual event in the Bering Sea

Late in the summer of 1997, the surface of the eastern Bering Sea turned from dark blue to aquamarine. The dramatic transformation was the result of a massive bloom of the coccolithophore *Emiliana huxleyi*, well after the spring bloom. Coccolithophores are phytoplankton with tests composed of calcium carbonate discs that usually comprise only a small proportion of the Bering Sea phytoplankton community. This was the first such event on record but such blooms have been common since that summer.

Diatoms, silicate-test forming phytoplankton usually dominate the Bering Sea primary producer community. These organisms are adapted to relatively cool, turbulent (nutrient rich) conditions. Coccolithophores favor more temperate conditions and don't compete well in nutrient-rich environments. Weather records for 1997 show that following a large storm event, conditions in the eastern Bering Sea were unusually warm and calm leading up to the coccolithophore bloom.

## 4.2 ecosystem modeling

Ecosystem models are mathematical representations of change in populations over time that that rely on parameterizations of interactions among ecosystem components. These models may include geochemical components (sources and sinks of nutrients). The intent is to capture processes and interactions in the aggregate rather than to simulate the fates of individual organisms (or indeed, even all species). This approach is necessary due the complexity of species (individual) interactions and limited knowledge regarding the details of most food webs.

Ecosystem models start with the definition of a set of state variables that represent key components of a system. From there, the models range from simple inspections of population growth to coupled equations representing many tropic levels, as well as and geochemical and geophysical processes. In every case, biological functions are parameterized, as are interactions with non-biological system components.

### 4.2.1 population growth

The simplest models we can develop are *zero dimensional* models for time change in single populations. In a zero dimensional model we assume that the dependent variable is “well mixed” in the region of interest. The only independent variable is time. This is thus an *initial value problem*. We know the initial state of our system (a population size) and wish to know how it changes with respect to the independent variable (time).

Change in a population must, at a minimum, be related to its birth rate. Such a model for the number  $X$  of individuals in a population would state:

$$\frac{dX}{dt} = rX \quad (4.1)$$

in which  $r$  represents the growth rate and  $t$  represents time. This is called the Malthusian growth model, for the Reverend Thomas Malthus, who made use of its underlying principle in his 1789 *An Essay on the Principle of Population, as it affects the Future Improvement of Society with remarks on the Speculations of Mr. Godwin, M. Condorcet, and Other Writers*, an early and influential book on population. The limitation here is fairly clear.

We can improve our population model by embracing the notion of a survival rate. Supposing we make two assertions, 1) the reproductive rate is proportional to the population size (as above) and 2) the reproductive rate is proportional to resource availability. The second assertion imposes competition in our population for a finite set of resources. Mathematically, our model of population  $X$  is:

$$\frac{dX}{dt} = rX \left( 1 - \frac{X}{K} \right) \quad (4.2)$$

in which  $K$  represents the *carrying capacity*. This is an application of the *logistic function*, for which an exact analytic solution can be found (using an initial value for  $X$  at  $t = 0$ ). Values for the parameters  $r$  and  $K$  may be determined empirically for specific cases. “ $r/K$  selection theory” was popular in the 1970’s.

Predator-prey models, first developed by Alfred Lotka (an American mathematician who proposed that the selection applied in evolution is one which favors the maximum useful energy transformation) and Vito Volterra (who was booted out of the Italian academy for refusing to sign a loyalty oath in 1931) are common. The Lotka-Volterra (or Volterra-Lotka, if you are Italian) equations for interaction between a predator species  $Y$  and a prey species  $X$  are:

$$\frac{dX}{dt} = \alpha X - \beta XY \quad (4.3)$$

$$\frac{dY}{dt} = \gamma \beta XY - \delta Y \quad (4.4)$$

in which  $\alpha$  represents the prey species growth rate,  $\beta$  represents the predation rate of  $Y$  upon  $X$ ,  $\gamma$  represents the efficiency with which the predator uses resources contained in its prey,  $\delta$  represents

the mortality rate of the predator species, and  $t$  represents time. This is a set of coupled first-order ordinary differential equations.

### 4.2.2 competition

These basic equations may be modified to account for more complicated interactions, for example, competition, commensalism, and mutualism between species. Suppose two species compete for the same resource but do not prey upon each other. In this case we could write a set of coupled ordinary differential equations:

$$\frac{dX_1}{dt} = rX_1(1 - N_1 + \gamma_{12}X_2) \quad (4.5)$$

$$\frac{dX_2}{dt} = rX_2(1 - N_2 + \gamma_{21}X_1) \quad (4.6)$$

in which the subscript identifies the species and the parameter  $\gamma$  represents the effect of one species on the other with respect to resource availability (that is,  $\gamma_{12}$  represents the effect of population 2 on population 1). The equations could be simplified if the two species are ecologically identical (the  $\gamma$ 's would have a value of one). Outcomes of these models may depend importantly on initial conditions.

Despite the apparent simplicity of the logistic function and the Lotka-Volterra model, both can be (and have been) used to gain important insights into ecosystems. Inter-specific competition is a tricky business and we could while away a lot of time devising uses for the equations already at our disposal. To make progress with our phytoplankton though, we must move on. This is because there are important geochemical processes at work that must be captured in some fashion.

## 4.3 simple ocean biogeochemistry

Marine biogeochemical modeling is a rich and diverse research field. Research topics range from the origin of Earth's atmosphere to future climate change to the search for insight into time-transient contemporary phenomena.

Any model of primary production must at least include two dependent variables, one for mineral nutrients and one for phytoplankton. Such a model would follow the form of either equation 4.1 or equation 4.2. Of course, we know that our shallow ocean is not as simple as this, we must embrace nutrient cycling through a food web, nutrient cycling in the water column, sedimentation, and ocean circulation. With those processes in mind, our coupled model should include at least four dependent variables: mineral nutrients  $N$ , phytoplankton  $P$ , zooplankton  $Z$ , and detritus  $D$ . Models with these four components and a set of parameterized processes linking them together are called "NPZD" models. The NPZD model may be zero dimensional (treating the mixed layer as homogenous so that the only independent variable is time) or higher (with at least one dimension is space).

A basic list of relevant processes could include:

- sources
  - terrestrial input/sea ice
  - mixing between shallow and deep ocean (upwelling/convection)
- cycling
  - phytoplankton productivity
  - phytoplankton mortality
  - phytoplankton grazing by zooplankton
  - zooplankton mortality
  - zooplankton metabolic losses
  - phytoplankton metabolic losses
- sinks
  - detritus settling to the deep ocean
  - predation on zooplankton by higher trophic levels
  - mixing between shallow and deep ocean (downwelling/convection)

This is not a short list, and it contains a hidden danger: those higher trophic levels. But before we consider that issue, let's develop a set of process-based relationships among the dependent variables. Construction of a flow chart of interactions is straightforward way to make progress (Figure 3.1).

### 4.3.1 zero-dimensional model

The next step is to consider the dimensionality of our model. The simplest case is to assume a well-mixed shallow layer and write the governing equations with only one independent variable, time  $t$ .

The expressions for the four dependent variables in our ocean mixed layer are

$$\begin{aligned} \frac{dN}{dt} &= (\mu_p(1-\gamma)L_I(t,P)L_NP + \mu_zZ + \mu_dD) \\ &\quad + (\tau(P+Z+D)) \end{aligned} \tag{4.7}$$

$$\begin{aligned} \frac{dP}{dt} &= (\mu_p(1-\gamma)L_I(t,P)L_NP - G_PZ - m_pP) \\ &\quad + (-\tau P) \end{aligned} \tag{4.8}$$

$$\frac{dZ}{dt} = (a_pG_PZ + a_dG_DZ - m_sZ - \mu_zZ)$$

$$\begin{aligned}
& + (-\tau Z) & (4.9) \\
\frac{dD}{dt} = & ((1 - a_p) G_P Z - a_d G_D Z + m_p P + m_z Z + \mu_d D) \\
& + \left( \tau D - \frac{v_d}{h} D \right) & (4.10)
\end{aligned}$$

in which the variables and processes are as defined in tables 4.3.1 and 4.3.1 and the functions  $L_I$ ,  $L_N$ ,  $G_P$ , and  $G_D$  are yet to be defined. The first set of terms on the right-hand side of each equation describe processes in the mixed layer while the second term represents a source or sink, that would be applied as a boundary condition in a higher-dimension model.

The function  $L_I(t, P)$  describes the light limitation of photosynthesis. The dependence on population size  $P$  represents the effect of shade cast by the phytoplankton themselves. In a higher-dimension model,  $L_I$  would also depend on depth in the water column.

The parameterization of biochemical processes requires some assumptions about how organisms find their food sources. The simplest relationships we can write, following Michaelis-Menten kinetics, assume free diffusion of nutrients and random interactions between organisms and their nutrients. The function  $L_N$  parameterizes nutrient limitation on phytoplankton growth. With our simple assumptions, this would be written:

$$L_N = \frac{N}{k_N + N} \quad (4.11)$$

The half-saturation constant  $k_N$  is the concentration at which the growth rate is equal to half the maximum growth rate. This constant varies from species to species.

The functions  $G_P$ , and  $G_D$  describe zooplankton grazing rates on phytoplankton and detritus. Following Michaelis-Menten kinetics, these may be defined:

$$G_P = \frac{g_z P^2}{k_z + P^2} \quad (4.12)$$

$$G_D = \frac{g_z D^2}{k_z + D^2} \quad (4.13)$$

Other formulations are possible.

Higher trophic level organisms are not included in our set of four dependent variables so we have no way to compute their population. This is a point of concern because we have no way to compute a population-dependent predation rate. Instead, we must come up with a function to represent that hidden process.

Upward and downward mixing of nutrients across the boundary between shallow and deep water should be included in equation 4.7. This requires an estimate of the deep ocean dimension relative to the shallow ocean dimension (so that deep concentration may be determined).

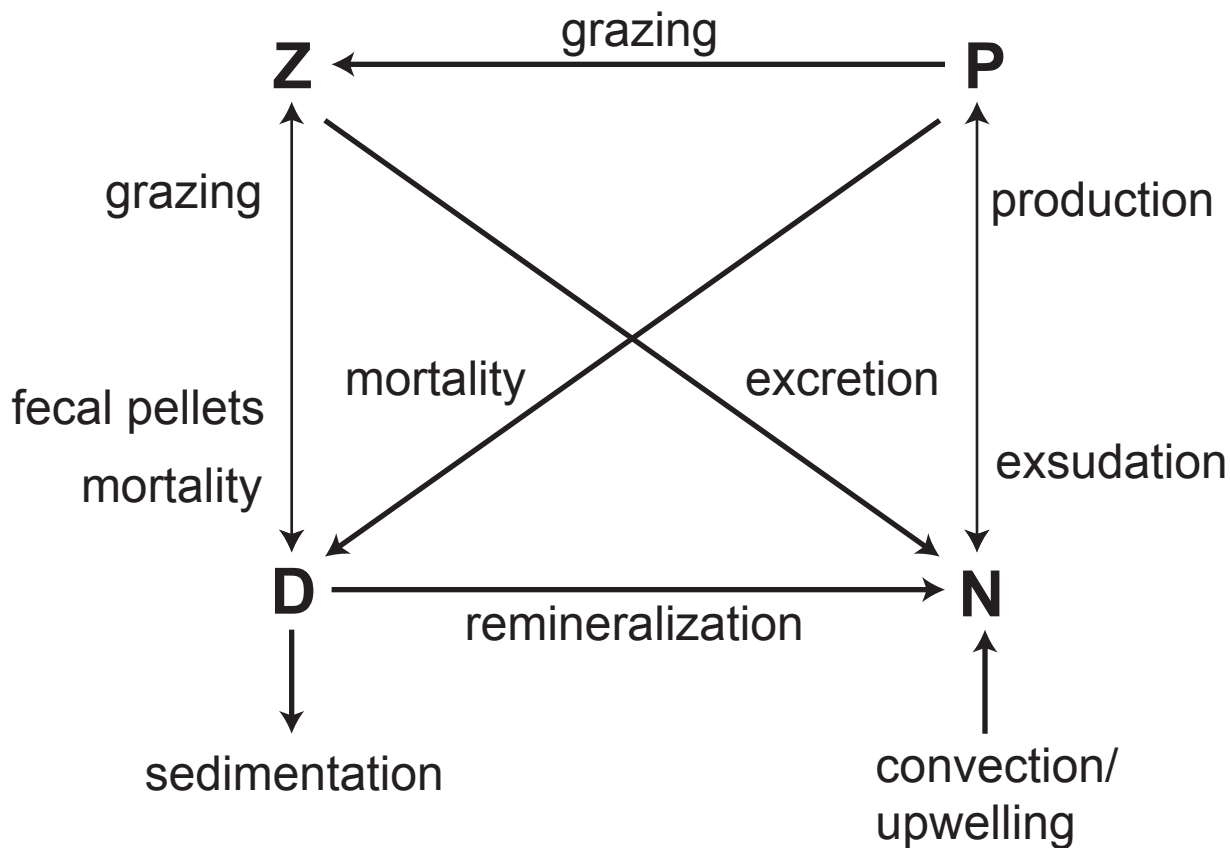


Figure 4.1: Interactions among components of the NPZD model.

parameter	variable name	units
half saturation constant	$k_n$	$\text{mmol N m}^{-3}$
maximal grazing rate	$g_z$	$\text{day}^{-1}$
half-saturation constant for grazing	$k_z$	$\text{mmol N m}^{-3}$
assimilated fraction of phytoplankton	$a_p$	
assimilated fraction of detritus	$a_d$	
zooplankton excretion rate	$\mu_s$	$\text{day}^{-1}$
phytoplankton mortality rate	$m_p$	$\text{day}^{-1}$
zooplankton mortality rate	$m_z$	$\text{day}^{-1}$
detritus remineralization rate	$\mu_d$	$\text{day}^{-1}$
detritus sedimentation speed	$v_z$	$\text{m day}^{-1}$
mixed layer thickness	$h$	$\text{m}$
phytoplankton maximal growth rate rate	$\mu_p$	$\text{day}^{-1}$
phytoplankton exsudation fraction	$\gamma$	
sediment remineralization rate	$\tau$	$\text{day}^{-1}$

Table 4.1: parameters for the NPZD model

process	parameterization
phytoplankton production	$\mu_p L_I L_N P$
phytoplankton exsudation	$\gamma \mu_p L_I L_N P$
grazing on phytoplankton	$G_p Z$
grazing on detritus	$G_d Z$
phytoplankton mortality	$m_p P$
zooplankton mortality	$m_z Z$
zooplankton excretion	$\mu_z Z$
rem mineralization in water column	$\mu D$
zooplankton fecal pellets	$(1 - a_p) G_p Z + (1 - a_d) G_d Z$

Table 4.2: processes in the NPZD model

## 4.4 computation

### 4.4.1 ordinary differential equations posed as initial value problems

Initial value problems are ones in which we know the initial state of a system and wish to compute how the system changes as the value of the independent variable changes. The independent variable might be time, a space dimension, or another quantity. Starting from a known (initial) value of the dependent variable, a numerical method (or analytical solution if one is available) is used to compute successive values of the dependent variable. The job of the numerical method is to approximate the differential equation over each interval.

The general form of our equation is:

$$\frac{dy}{dt} = f(y, t) \quad y = y_0, t = t_0 \quad (4.14)$$

where  $f(t, y)$  is some mathematical function and  $(t_0, y_0)$  is an initial condition. Beginning from the initial  $y_0$  at  $t_0$ , some numerical scheme is used to approximate  $f(t, y)$  over intervals between the specified values of  $t$ . Over the interval from  $t_j$  to  $t_{j+1}$  we write this:

$$y_{j+1} = y_j + \int_{t_j}^{t_{j+1}} g(t) dt \quad (4.15)$$

in which  $g(t)$  represents  $f(t, y)$  over the finite interval. The definite integral is unknown, but calculable. The challenge is to perform that calculation as accurately and as efficiently as possible.

The “model domain” is the range of the independent variable over which we wish to solve the differential equation. The differential equation we wish to solve must be continuous over the model domain. At least two tasks are required to define the model domain.

- A range of values for the independent variable must be selected (*for example, start and stop times*).

- That range must be divided into discrete intervals within which the function is estimated (the integral in equation (4.15)).

The interval size, or “step size,” may be specified and then used to discretize the domain or the number of intervals may be specified and used to compute a corresponding step size. The discrete values of the independent variables are often called “nodes” in the model domain. If there are  $N$  intervals, then there are  $N + 1$  nodes in the domain.

Don’t panic.

#### 4.4.2 numerical scheme for a two-species competition model

The competition model for two species defined by equations 4.18 and 4.19 is a set of coupled ordinary differential equations. A variety of numerical techniques are available for coupled ODEs. Which one you choose depends on the nature of the equations, in particular whether or not they span a range of characteristic time scales. We will develop the simplest possible solution, an Euler single-step, but keep in mind that it is not the best method for every problem.

The Euler single-step method makes the very simple assumption that  $g(t)$  is constant over the interval  $\{t_j : t_{j+1}\}$  and equal to  $f(t_j, y_j)$ . In this case, equation 4.15 becomes:

$$y_{j+1} = y_j + \Delta t f(t_j, y_j) \quad (4.16)$$

in which  $\Delta t$  is the step size

$$t_{j+1} = t_j + \Delta t. \quad (4.17)$$

In the language of numerical modeling, we would call this forward-stepping solution an explicit scheme. It is named for the Swiss mathematician Leonard Euler (1707-1783).

Applying this scheme to our set of equations, we can compute the two dependent variables at any time step  $t_{j+1}$

$$X_{1\ j+1} = X_{1\ j} + \Delta t \{rX_{1\ j}(1 - N_1 + \gamma_{12}X_{2\ j})\} \quad (4.18)$$

$$X_{2\ j+1} = X_{2\ j} + \Delta t \{rX_{2\ j}(1 - N_2 + \gamma_{21}X_{1\ j})\} \quad (4.19)$$

with appropriately defined initial conditions on  $X_1$  and  $X_2$ . The Euler single step is easy to implement (you could do this with a piece of paper and a pencil if you wanted to) but requires relatively small time step size for a good result.

Runge-Kutta techniques are often used to solve sets of coupled ODEs. These methods offer better accuracy and stability than simpler, lower order, methods like the Euler single step. They are more complicated to implement but many computational software packages, such as MATLAB, offer implementations of these schemes.