Biological Modeling of Population Dynamics

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Chapter 1

Preface

This book is an introduction into modeling population dynamics in biology. We will make mathematical models for populations of bacteria, cells, hosts with parasites, and predators with their prey. Models are formulated in terms of ordinary differential equations (ODEs), and we will see that these ODEs often resemble one another. The book covers the material of a course given to undergraduate biology students at Utrecht University, and aims at teaching these students to make and use simple mathematical models in biological research. There are several other textbooks on this subject, and some unique features of this particular book are: (1) an emphasis on “parameter free” models and phase plane analysis, (2) the usage of the epidemiological concept of an $R_0$ (or fitness) to simplify parameter conditions, and (3) a mechanistic “graphical” approach for model development.

The last point is most important. Rather than just explaining the classical models, we will attempt to devise a model ourselves by translating the relevant biological processes, like immigration, birth, death, infection and killing, into intuitive graphs depicting how each process depends on the population densities. These graphs are subsequently translated into simple mathematical functions, and by collecting these functions into a simple system of differential equations we obtain a “mechanistic” mathematical model that explicitly depends on its underlying biological processes. Finally, we will compare our “mechanistic” model with the typically more “phenomenological” classical models covered in other textbooks.

What is the reason for this rather laborious procedure for explaining models to students? I think it is important that biologists can identify each term in a mathematical model with an underlying biological process for which they have some knowledge, or at least some intuition. For example, one often needs biological insight to know how, or even whether, birth, death and interaction rates depend on the population size. The results obtained with a model are likely to depend on these assumptions. By identifying differences between models based upon different assumptions we learn to become critical readers of mathematical models, and learn to be careful with the necessary assumptions one has to make when modeling an interesting biological system.

A second emphasis of this book is on phase plane analysis, which means that we sketch nullclines and trajectories, either by hand or by computer. Phase plane analysis allows one to visualize the potential steady states of a model, and to determine their stability (again by hand or by computer software). Phase plane analysis is a relatively simple technique that is easily accessible to motivated biology students. Most pictures in this book are made an R-software package called Grind, which is good at drawing nullclines, finding steady states, and numerical integration. During
the course students work extensively with Grind (see Chapter 12), and the R-scripts used for making the figures in this book are available on the website tbb.bio.uu.nl/rdb/bm/models/.

Because the parameter values of biological models are typically unknown, there is a strong emphasis in this book on analyzing models with free parameters. This has the enormous advantage that the results will be general, and that we do not run the risk of ignoring possibilities that may occur for different parameter settings. Most pictures in this book therefore have no numbers along the axes (except for zero and one); rather they have parameter expressions for the points of interest. Such expressions in terms of parameters will be simplified using the epidemiological concept reproduction ratio, $R_0$, and the ecological concept “critical resource density”, $R^*$. Simplification typically increases our understanding of the underlying biology.

This course only covers simple caricature models that are designed to capture the essentials of the biological problem at hand. Such simple models can be completely understood, and therefore allow for excellent insight and provide new ideas about the biological problem (May, 2004). Other areas of theoretical biology are about large-scale simulation models that are designed to summarize the existing knowledge about a particular system, like the metabolism of a whole cell, or the nutrient flow in a complete ecosystem. Investigators use such large models for predicting the behavior of the biological system, e.g., when circumstances are changing. Simple caricature models cannot predict what will happen, but importantly they are much better at predicting what could happen. Although large-scale models are not covered in this book, the material covered in this course should be useful for students interested in developing large realistic models. First, small modules within the large models should be developed by the same mechanistic process that we here use for simple models. Second, it is a sobering lesson to let oneself be surprised by the sometimes unexpected behavior of simple toy models, and such a lesson seems essential for developing the required scientific scrutinizing attitude toward large-scale models.

The expected audience of this book is students of biology and ecology. Too many biologists treat a mathematical model as a “black box” that is too difficult to understand. A main objective of this course is to open the black box and teach biology students how to develop simple mathematical models themselves. This allows for a much better understanding, and for a healthy critical attitude toward the existing models in the field. Readers are expected to be familiar with phase space analysis, i.e., should know how to sketch nullclines and derive a Jacobi matrix. The first section of the Appendix provides a short summary on these prerequisites. A complete tutorial on deriving Jacobi matrices is provided in accompanying ebook (Panfilov et al., 2016) that can be downloaded from http://tbb.bio.uu.nl/rdb/books/. The same website provides the answers to the exercises in this book in the file bmAnswers.pdf.

Finally, this book originated from a theoretical ecology course given decades ago by Paulien Hogeweg at Utrecht University. She taught me the strength of phase plane analysis and simple caricature models. After I started teaching this course its contents and presentation have evolved, and have been adapted to the questions, and the comments from numerous students whom attended this course.
Chapter 2

Introduction

This course is an introduction into theoretical biology for biology students. We will teach you how to make and analyze mathematical models, with the ultimate aim that you can critically judge the contributions the assumptions of existing models, and that you can devise useful novel models whenever you need them in your future biological research. Mathematical models are used in all areas of biology, and they are typically formulated in ordinary differential equations (ODEs). We will analyze such models by hand by sketching nullclines and computing steady states, and by letting a computer perform numerical integration and phase plane analysis. A major emphasis of this course is to develop differential equations by following a simple graphical procedure, depicting each biological process as a function of its relevant variable(s). Experience with devising mathematical models will help you to understand and evaluate models proposed by others.

This first chapter introduces some basic concepts underlying modeling with differential equations. You will become familiar with the notion of a “solution”, “steady state”, “half life”, and the “expected life span”. Concepts like solution and steady state are important because a differential equation describes the change of the population size, rather than its actual size. We will start with utterly simple models that are only convenient to introduce these concepts. To keep models general they typically have free parameters, i.e., parameters are letters instead of numbers. Later models in the course are more challenging and more interesting.

2.1 The simplest possible model for a huge problem

Consider the amount of plastic, $P$, floating in the oceans. Since plastic decays very slowly, $P$ increases more or less proportionally with the daily amount of plastic, $k$, that is dumped into the oceans. A current estimate for the world-wide dumping rate is 8 millions tons of plastic per year, i.e., $k = 2.17 \times 10^4$ ton per day. Knowing $k$ we write the following simple mathematical model,

$$\frac{dP}{dt} = k,$$  \hfill (2.1)

which says that the variable $P$ increases at a rate $k$ per time unit (here per day). In this ODE $P$ is a variable that changes over time, and the “dimension” of $P$ is tons of plastic in the oceans. Formally one should write $dP(t)/dt = k$, but for simplicity $P(t)$ is abbreviated to $P$. The parameter $k$ in this Eq. (2.1) here is a constant, with dimension tons of plastic per
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Actually, $k$ should also be increasing over time, as we have been dumping more and more plastics, but for simplicity we here consider a time period over which $k$ is relatively constant (see the last question).

This equation is so simple that one can derive its general solution

$$ P(t) = P(0) + kt, \quad (2.2) $$

where $P(0)$ is the amount of plastic that was already in the ocean at the time we started dumping $k$ tons per day. Plotting $P(t)$ over time therefore gives a straight line with slope $k$, intersecting the vertical axis at $P(0)$. The slope of this line is $k$, which is indeed the derivative defined by Eq. (2.1). Thus, the differential equation Eq. (2.1) gives the “rate of change”, and the solution of Eq. (2.2) gives the “population size at time $t$”. Typically, differential equations are too complicated for solving them explicitly, and their general solutions are not available. In this course we will therefore not consider the integration methods required for obtaining solutions of ODEs. However, having a solution one can easily check it by taking the derivative with respect to time. For example, the derivative of Eq. (2.2) with respect to time is $\frac{d}{dt}[P(0) + kt] = k$, which is indeed the right hand side of Eq. (2.1). Summarizing, the solution in Eq. (2.2) gives the amount of plastic at time $t$, and Eq. (2.1) gives its daily rate of change. Note that if we were to take measures reducing the amount of plastic that streams into the ocean, we would only need to change the value of the parameter $k$. The model remains the same.

We can change the model by making it somewhat more realistic, e.g., by accounting for the fact that plastic in the ocean is decaying slowly, i.e., with a very long half-life. Defining a rate of decay, $d$, the model becomes

$$ \frac{dP}{dt} = k - dP, \quad (2.3) $$

where the parameter $d$ defines the rate at which individual plastic molecules decay. $d$ has a dimension per day (or per unit of time), and therefore is called a “rate”. In the ODE this can be checked by observing that the term $dP$ should have the same dimension “tons per day” as $k$ (otherwise they cannot be subtracted from another). Biological examples of Eq. (2.3) would be red blood cells produced by bone marrow, shrimps being washed onto a beach, daily intake of vitamins, and so on. The $k$ parameter then defines the inflow, or production, and the $d$ parameter is a death rate. Although this seems a very simple extension of Eq. (2.1), it is much more difficult to obtain the solution

$$ P(t) = \frac{k}{d} \left(1 - e^{-dt}\right) + P(0)e^{-dt}, \quad (2.4) $$

which is depicted in Fig. 2.1a. The term on the right corresponds to the exponential loss of the initial value, $P(0)$. The term on the left is more complicated, but when evaluated at long time scales, i.e., for $t \to \infty$, the term $(1 - e^{-dt})$ will approach one, and one obtains the “steady state” $\bar{P} = k/d$. We conclude that the solution of Eq. (2.4) ultimately approaches the steady state $\bar{P} = k/d$, which is ultimate amount of plastic in the oceans when we keep on dumping $k$ tons per day. Note that this predicted steady state value is independent of the initial condition $P(0)$.

Fortunately, we do not always need a solution to understand the behavior of a model. The same steady state can also directly be obtained from the differential equation. Since a steady state means that the rate of change of the population is zero we set

$$ \frac{dP}{dt} = k - dP = 0 \quad \text{to obtain} \quad \bar{P} = \frac{k}{d}, \quad (2.5) $$

which is the same value as obtained above from the solution for $t \to \infty$. Note that a steady state also gives a population size, and therefore provides some insight in the behavior of the
model. For instance, the steady state \( \bar{P} = \frac{k}{d} \) predicts that if we were to half the amount of plastic that we dump in the oceans the world-wide burden of plastic would also half. The decay rate only determines how slowly this halved burden would be approached. If we could double the decay rate by using plastics with a shorter half-life, the steady state would also be halved, and would be approached two-fold faster.

2.2 Exponential growth and decay

Above we have already used the term half-life, and having the model of Eq. (2.3) we can precisely define what we mean by this. Consider the situation that we completely abandon the usage of plastic, and the current amount of plastic, \( P(0) \), is slowly decaying. To study this we do not need to change the model, we just set \( k = 0 \), to be left with \( \frac{dP}{dt} = -dP \). This is the famous equation for exponential decay of radioactive particles, with the almost equally famous solution \( P(t) = P(0)e^{-dt} \), saying that ultimately, i.e., for \( t \to \infty \), the amount of plastic, \( P(t) \), will approach zero. Plotting the natural logarithm of \( P(t) \) as a function of time would give a straight line with slope \(-d\) per day (because \( \ln[P(0)e^{-dt}] = \ln[P(0)] - dt \)). This exponential decay equation allows us to introduce two important concepts: the half-life and the expected life span. The half-life is defined as the time it takes to lose half of the initial population, and is defined by the solution of the ODE:

\[
\frac{P(0)}{2} = P(0)e^{-dt} \quad \text{simplifies into} \quad \ln\frac{1}{2} = -dt \quad \text{or} \quad t = \frac{\ln 2}{d} . \tag{2.6}
\]

Since \( \ln 2 \approx 0.69 \) the half life is approximately \( 0.69/d \) days. Note that the dimension is correct: a half life indeed has dimension time because \( d \) is a rate with dimension day\(^{-1}\). The other concept is expected life span: if radioactive particles or biological individuals have a probability \( d \) to die per unit of time, their expected life span is \( 1/d \) time units. This is like throwing a die. If the probability to throw a four is \( 1/6 \), the expected waiting time to get a four is six trials. Finally, note that this exponential decay model has only one steady state, \( \bar{P} = 0 \), and that this state is stable because it is approached at infinite time. A steady state with a population size of zero is often called a “trivial” steady state.

The opposite of exponential decay is exponential growth

\[
\frac{dN}{dt} = rN \quad \text{with the solution} \quad N(t) = N(0)e^{rt} , \tag{2.7}
\]

where the parameter \( r \) is known as the “natural rate of increase”. The solution can easily be checked: the derivative of \( N(0)e^{rt} \) with respect to \( t \) is \( rN(0)e^{rt} = rN(t) \). Biological examples of this equation are the growth of mankind, the exponential growth of a pathogen in a host, the growth of a tumor, and so on. Similar to the half life defined above, one can define a doubling time for populations that are growing exponentially:

\[
2N(0) = N(0)e^{rt} \quad \text{gives} \quad \ln 2 = rt \quad \text{or} \quad t = \ln[2]/r . \tag{2.8}
\]

This model also has only one steady state, \( \bar{N} = 0 \), which is unstable because any small perturbation above \( N = 0 \) will initiate unlimited growth of the population. To obtain a non-trivial (or non-zero) steady state population size in populations maintaining themselves by reproduction one therefore needs density dependent birth or death rates. This is the subject of the next chapter.
In replicating biological populations, this natural rate of increase of $dN/dt = rN$ should obviously be a composite of birth and death rates. A more natural model for a biological population that grows exponentially therefore is

$$\frac{dN}{dt} = (b - d)N \quad \text{with solution} \quad N(t) = N(0)e^{(b-d)t}, \quad (2.9)$$

where $b$ is a birth rate with dimension $t^{-1}$, and $d$ is the death rate with the same dimension. Writing the model with explicit birth and death rates has the advantage that the parameters of the model are strictly positive (which will be true for all parameters in this course). Moreover, one now knows that the “generation time” or “expected life span” is $1/d$ time units. Since every individual has a birth rate of $b$ new individuals per unit of time, and has an expected life span of $1/d$ time units, the expected number of offspring of an individual over its entire life-span is $R_0 = b/d$ (see Chapter 6). We will use this $R_0$ as the maximum “fitness” of an individual, i.e., the life-time number of offspring expected under the best possible circumstances. In epidemiology the $R_0$ is used for predicting the spread of an infectious disease: whenever $R_0 < 1$ a disease will not be able to spread in a population because a single infected host is expected to be replaced by less than one newly infected host (Anderson & May, 1991); see Chapter 6.

Biological examples of Eq. (2.9) are mankind, the exponential growth of algae in a lake, and so on. Similarly, the natural rate of increase $r = b - d$ yields a “doubling time” solved from $2N(0) = N(0)e^{rt}$ giving $t = \ln[2]/r$ time units. A famous example of the latter is the data from Malthus (1798) who investigated the birth records of a parish in the United Kingdom, and found that the local population had a doubling time of 30 years. Solving the natural rate of increase $r$ per year from $30 = \ln[2]/r$ yields $r = \ln[2]/30 = 0.0231$ per year, which is sometimes expressed as a growth rate of 2.31% per year. More than 200 years later the global human growth rate is still approximately 2% per year. Simple exponential growth therefore seems a fairly realistic model to describe the growth of the quite complicated human population over a period of several centuries.

In this book we will give solutions of differential equations whenever they are known, but for most interesting models the solution is not known. We will therefore not explain how these solutions are obtained (see textbooks like the one by Adler (1997) for an overview of methods of integration). You can also use symbolic software like Mathematica to find the explicit solution of some of the differential equations used here.

Finally, it is important to realize that most models introduced in this book require a number of “unrealistic assumptions”: (1) all individuals within a population are equal, (2) each populations is well-mixed and can therefore be described with a single density, (3) population sizes are so large that we never have populations containing less than one member, and (4) typically parameters are constants that do not vary over time. We will see that such “unrealistic” models nevertheless help us to think clearly about the biology described by the model (May, 2004).

### 2.3 Summary

An ordinary differential equation (ODE) describes the rate of change of a population. The actual population size is given by the solution of the ODE, which is generally not available. To find the population size one can compute the steady state(s) of the model (the ODE), and/or solve the ODEs numerically on a computer, which gives the model behavior. Steady states are derived by setting the rate of change to zero, and solving for the actual population size.
2.4 Exercises

Figure 2.1: Population growth. Panel (a) depicts the solution of Eq. (2.4). Panels (b) and (c) depict exponential growth on a linear, and a logarithmic vertical axis, respectively. A differential equation describes the slope of the solution for each value of the variable(s), i.e., in Panel (b) the slope of the $N(t) = N(0)e^{rt}$ curve for each value of $N(t)$ is $\frac{dN}{dt} = r$. This figure was made with the model intro.R.

Doubling times and half-lives are solved from the solution of the exponential growth (or decay) equation $N(t) = N(0)e^{rt}$. The fitness, $R_0$, of a population is the expected number of offspring of one individual over one generation, under the best possible circumstances.

2.4 Exercises

Question 2.1. Red blood cells
Red blood cells are produced in the bone marrow at a rate of $m$ cells per day. They have a density independent death rate of $d$ per day.

a. Which differential equation from this chapter would be a correct model for the population dynamics of red blood cells?

b. Suppose you donate blood. Sketch your red blood cell count predicted by this model in a time plot.

c. Suppose a sportsman increases his red blood cell count by receiving blood. Sketch a time plot of his red blood cell count.

Question 2.2. Pesticide on apples
During their growth season apples are frequently sprayed with pesticide to prevent damage by insects. By eating apples you accumulate this pesticide in your body. An important factor determining the concentration of pesticide is their half life in the human body. An appropriate mathematical model is

$$\frac{dP}{dt} = \sigma - \delta P,
$$

where $\sigma$ is the daily intake of pesticide, i.e., $\sigma = \alpha A$ where $A$ is the number of apples that you eat per day and $\alpha$ is the amount of pesticide per apple, and $\delta$ is the daily rate at which the pesticide decays in human tissues.

a. Sketch the amount of pesticide in your body, $P(t)$, as a function of your age, assuming you eat the same number of apples throughout your life.

b. How much pesticide do you ultimately accumulate after eating apples for decades?

c. Suppose you have been eating apples for decades and stop because you are concerned about
the unhealthy effects of the pesticide. How long does it take to reduce your pesticide level by 50%?

d. Suppose you start eating two apples per day instead of just one. How will that change the model, and what is the new steady state? How long will it now take to reduce pesticide levels by 50% if you stop eating apples?

e. What is the decay rate if the half-life is 50 days?

**Question 2.3. Bacterial growth**

Every time you brush your teeth, bacteria enter your blood circulation. Since this a nutritious environment for them they immediately start to grow exponentially. Fortunately, we have neutrophils in our blood that readily kill bacteria upon encountering them. A simple model would be:

$$\frac{dB}{dt} = rB - kNB,$$

where $B$ and $N$ are the number of bacteria and neutrophils per ml of blood, $r$ is the growth rate of the bacteria (per hour), and $k$ is the rate at which bacteria are killed by neutrophils.

a. What is the doubling time of the bacteria in the absence of neutrophils?

b. Neutrophils are short-lived cells produced in the bone marrow, and chemotherapy can markedly reduce the neutrophil counts in the peripheral blood. What is the critical number of neutrophils that is required to prevent rampant bacterial infections after chemotherapy?

c. What is the dimension of the parameters $r$ and $k$?

d. The $kBN$ term is called a mass-action term because it is proportional to both the bacterial and the neutrophil densities. A disadvantage of such a term is that each neutrophil is assumed to kill an infinite number of bacteria per hour if the bacterial density $B \to \infty$ (please check this). Later in the course we will use saturation functions to allow for maximum killing rates per killer cell. An example of such a model would be

$$\frac{dB}{dt} = rB - \frac{kNB}{h+B},$$

where the total number of bacteria killed per hour approaches $kN$ when $B \to \infty$ (please check this). What is now the dimension of $k$?

e. What is now the critical number of neutrophils that is required to prevent bacterial infections after chemotherapy? Can you sketch this?

f. What is the dimension of $h$, and how would you interpret that parameter?

**Question 2.4. Physics**

The linear ODEs used for the plastic model should be familiar to those of you who studied the famous equations for velocity and acceleration:

$$\frac{dx}{dt} = v \quad \text{and} \quad \frac{dv}{dt} = a,$$

where $x$ is the total distance covered, $v$ is the velocity, and $a$ is the time derivative of the velocity, which is defined as the “acceleration”. Integrating $dv/dt$ gives $v(t) = at + v(0)$, where the integration constant $v(0)$ is the velocity at time zero, and integrating $dx/dt = at + v(0)$ gives $x(t) = \frac{1}{2}at^2 + v(0)t$.

a. Check the dimensions of $v$ and $a$.

b. In Eq. (2.1) we considered the case where we dump a fixed amount, $k$, of plastic in the oceans on a daily basis. Now consider the more realistic case where $k(t)$ becomes a variable that increases linearly over time, i.e., write that $dk/dt = a$, where $a$ is the slope with which $k(t)$ increases. Starting at a time when $k(0)$ tons of plastic was dumped per day, we write the solution $k(t) = at + k(0)$. What is the new ODE for the total amount of plastic in the oceans, and what is its solution?

c. Do you expect the amount of plastic in the oceans to approach a (new) steady state?
Chapter 3

Density dependence

Population change size by various biological processes, like migration, production, replication (birth), death and differentiation. Biological models tend to be complicated, and typically non-linear, because these processes often depend on the population size(s). This is a form of feedback that is called density dependence. In this chapter we will develop a number of models for the growth of a population, where at least one of these processes is regulation by the density of that population. Considering single populations the models in the chapter will consist of only one ODE (i.e., they are one-dimensional), and what we will do is define functions describing how these biological processes depend on the population density. Using biological knowledge and intuition we will first sketch a reasonable curve describing this relationship (see Fig. 3.1). This curve is subsequently described with a simple mathematical function, and since we are aiming for non-dimensional functions, we can multiply such a function with the appropriate parameter of the model (and keep the dimensions of the model correct). This ultimately results in a model with density-dependent interaction terms each corresponding to a well-defined biological process. We will analyze the model by identifying steady states and by numerical integration. These results can then be compared with data and the corresponding classical models in the literature.

We have seen in Chapter 2 that non-replicating populations that are maintained by a fixed source term, and have a density-independent death rate, e.g., Eq. (2.3), will ultimately approach a stable steady state where the source balances the death. If such a population is perturbed it will return to the same steady state at a rate determined by the death rate (the inverse of this rate is called the “return time”, which we will address later in Chapter 4). This demonstrates that stable population densities can come about without having any regulation or feedbacks in the system. This is not true for the replicating population that we considered in Chapter 2 because the only steady state of Eq. (2.9) is $N = 0$. Whenever $b > d$, i.e., if the fitness $R_0 > 1$ (see Chapter 6), this equilibrium is unstable (see Chapter 4). If $R_0 < 1$ the equilibrium is stable, and the population will ultimately go extinct (i.e., for $t \to \infty$ the solution $N(t)e^{(b-d)t} \to 0$ when $d > b$). One could argue that Eq. (2.9) also has a steady state when $b = d$, but this is a untenable condition because the birth rate and the death rate would have to stay exactly the same over long time scales.
3.1 Negative density dependence

At high population densities the availability of essential resources is typically low, and this is expected to result in a lower fecundity and/or higher death rates (see Fig. 3.1). This is called negative density dependence since both processes reduce the net population growth rate. Numerous examples from microorganisms and ecology illustrate that fecundity tends to decline with the population density; see Figs. 3.1 and 3.2 (and Walker et al. (2009)). Similarly the contact inhibition of proliferation of cells growing in a monolayer, or as a tissue, plays a role in limiting the population size until the resource “space” is filled up (Wieser & Oesch, 1986). At high population densities one also expects the death rates of cells or organisms to be high (although several microorganisms have evolved mechanisms to survive long periods of starvation (Phaiboun et al., 2015)). Let us start by adding negative density-dependence to the birth and death processes of our models.

Density dependent death

If the death rate were to increase with the population size, the simplest model would be to have a linear increase of the per capita death rate with the population size (see Fig. 3.1a). A linear increase need not be realistic, as one could argue that death rates increase steeply at high densities, or alternatively that the death rate should approach a maximum at the highest densities. Choosing for a linear increase of the per capita death rate would therefore be “natural” first choice because it is a compromise between the two alternatives, and is definitely the simplest possible extension of the density-independent death rate, $d$, in Eq. (2.3) and Eq. (2.9).

By adding a linear increase to the normal death rate, $d$, we obtain a simple mathematical function, $F(N) = d + cN$, for the graph in Fig. 3.1a, where $d$ is the normal death rate that is approached when the population size is small, and where $c$ is the slope with which the death rate increases with $N$. Since $cN$ should be a rate that can be added to the death rate $d$, the dimension of $c$ should be per time unit per individual, and the dimension of $F(N)$ is a rate that should replace the $d$ parameter in Eq. (2.3) and Eq. (2.9). It is therefore much simpler to define a non-dimensional function, $f(N)$, that we can multiply with the original death rate, $d$, i.e., $df(N) = F(N)$, or

$$f(N) = \frac{F(N)}{d} = 1 + \frac{cN}{d} = 1 + \frac{N}{k},$$

(3.1)
3.1 Negative density dependence

where \( k = \frac{d}{c} \) has same dimension as \( N \). Now we can preserve the original death rate of the model, and multiply the parameter \( d \) in Eq. (2.3) and Eq. (2.9) with \( f(N) \). Thanks to this simplification the exact interpretation of the new density-dependence parameter, \( k \), is the population size at which the death rate had doubled (i.e., when \( N = k \) the per capita death rate is \( 2d \)). This is an intuitive parameter with a simple dimension that one can easily explain to an audience, and estimate from experimental data (see Fig. 3.2a). Finally, because \( f(N) = 1 \) when \( N \to 0 \) the minimum per capita death rate, \( d \), and maximum generation time, \( d^{-1} \), remain exactly the same.

For the replicator population of Eq. (2.9), the full model becomes

\[
\frac{dN}{dt} = \left[ b - d\left(1 + \frac{N}{k}\right) \right] N .
\] (3.2)

At low population sizes the expected life span of the individuals remains \( 1/d \) time units, and they always have a birth rate \( b \) per time unit. Since the \( R_0 \) is a maximum fitness, it is computed for an individual under optimal conditions, which here means \( N \to 0 \). The fitness of individuals obeying Eq. (3.2) therefore equals \( R_0 = b/d \). To search for steady states of Eq. (3.2) one sets \( \frac{dN}{dt} = 0 \), cancels the trivial \( N = 0 \) solution, and solves from the remainder

\[
b - d = \frac{dN}{k} \quad \text{that} \quad \bar{N} = k \frac{b - d}{d} = k(R_0 - 1)
\] (3.3)

is the non-trivial steady state population size. In ecology such a steady state is called the “carrying capacity”. A negative feedback in the form of a linearly increasing density-dependent death rate is therefore sufficient to deliver a carrying capacity. Here, the carrying capacity depends strongly on the fitness of the population, i.e., doubling \( (R_0 - 1) \) doubles the steady state population size.

For a population that is maintained by a source, i.e., \( \frac{dN}{dt} = s - dN \), the full model becomes

\[
\frac{dN}{dt} = s - d\left(1 + \frac{N}{k}\right) N , \quad \text{with steady states} \quad \bar{N} = \frac{-dk \pm \sqrt{dk(dk + 4s)}}{2d} .
\] (3.4)

Because the square root term is positive and larger than \( dk \), the positive root of this quadratic equation corresponds to a meaningful steady state, and the negative root has to be ignored. Because this population has no birth rate the \( R_0 \) is not defined.

Density dependent birth

Now that we have learned how one can add density-dependent effects to the death terms of a model, we turn to adding negative density-dependence to the birth or source terms of Eq. (2.9) and Eq. (2.3). For the replicator model the per capita birth rate should decrease with the population size (evidence supporting a decreasing birth rate in two “natural” populations is shown in Fig. 3.2). The simplest functional relationship between a decreasing per capita birth rate and the population size is again a linear one, and the graph in Fig. 3.1b can mathematically be described as \( F(N) = b - cN \), where \( b \) is the birth rate at low population densities and \( c \) is the slope of the line. Simplifying this into a non-dimensional function we write

\[
f(N) = F(N)/b = 1 - \frac{cN}{b} = 1 - \frac{N}{k} ,
\] (3.5)

and multiply the original birth rate parameter, \( b \), by this non-dimensional function such that the model becomes

\[
\frac{dN}{dt} = \left[ b\left(1 - \frac{N}{k}\right) - d \right] N .
\] (3.6)
The dimension of the parameter $k$ is again biomass, or individuals, and its exact interpretation now is that $k$ defines the population size where the birth rate becomes zero (which is again intuitive and measurable). Because $f(N)$ will become negative whenever $N > k$, which would deliver a negative birth rate, it is technically better to define $f(N) = \max(0, 1 - N/k)$, where the function $\max()$ returns the maximum of its arguments. Because the steady state will always correspond to a density with a non-zero birth rate, we proceed with Eq. (3.5) for reasons of simplicity.

Since at low densities $f(N) \to 1$, the interpretation of the parameter $b$ remains the maximum birth rate, implying that the fitness of individuals obeying Eq. (3.6) remains $R_0 = b/d$ (which is a natural result because at sufficiently low population size the density-dependence should have no effect). The steady states of Eq. (3.6) are $N = 0$ and solving 

$$b - d = b \frac{N}{k} \quad \text{yields} \quad \bar{N} = k \left(1 - \frac{d}{b}\right) = k \left(1 - \frac{1}{R_0}\right).$$

A negative feedback in the form of a linear density-dependent per capita birth rate therefore also allows for a carrying capacity. When $R_0 \gg 1$, this carrying capacity approaches the value of $k$, and becomes fairly independent of the fitness (which differs from the result obtained with density-dependent death).

Similarly, the source term in a $dN/dt = s - dN$ model could suffer from the negative density-dependence. An example would be the production of red blood cells in the bone marrow, which is increased when interstitial cells in the kidney increase their production of erythropoietin (EPO) when they suffer from too low oxygen levels. Although the effect of EPO is probably non-linear we could start with multiplying $s$ with Eq. (3.5) to obtain

$$\frac{dN}{dt} = s \left(1 - \frac{N}{k}\right) - dN \quad (3.8)$$

where the production rate (e.g., cells day$^{-1}$) decreases linearly with the red blood cell density $N$. The interpretation of $k$ remains the population size at which the production is zero. For red
3.2 Logistic growth and our assumptions

Having a derived a number of models for population growth we should start comparing them with existing models. The density-dependent models for replicating populations, Eq. (3.2) and Eq. (3.6), are both of the form \( \frac{dN}{dt} = \alpha N - \beta N^2 \), where \( \alpha \) and \( \beta \) are parameter combinations of the original birth and death rates, \( b \) and \( d \), and the density-dependence parameter \( k \) (see the exercises). Both models are therefore mathematically identical to the classical “logistic equation”:

\[
\frac{dN}{dt} = rN(1 - N/K), \quad \text{with solution} \quad N(t) = \frac{KN(0)}{N(0) + e^{-rt}(K - N(0))},
\]

(3.10)

with a natural rate of increase of \( r = b - d \), and a carrying capacity that is directly defined by the parameter \( K \) (these equations are identical because \( \alpha = r \) and \( \beta = r/K \) in the logistic growth model). The behavior of the three models is therefore the identical: starting from a small initial population the growth is first exponential, and will approaches zero when the population size approaches the carrying capacity (see Fig. 3.3a). Starting from a large initial population, i.e., from \( N(0) > K \), the population size will decline until the carrying capacity is approached. Logistic growth is often employed to describe population growth in many biological disciplines (ranging from ecology, epidemiology, virology to cell biology), and by deriving Eq. (3.10) ourselves we have learned that is is indeed an excellent choice for populations having
Density dependence

(a)

(b)

Figure 3.4: Populations with density-dependence either on the production (i.e., obeying Eq. (3.8); red lines), or on the death rate (i.e., obeying Eq. (3.4); blue lines). The horizontal black line in Panel (b) denotes the steady state level (i.e., the two panels are scaled differently). In Panels (b) we add noise sampled from a normal distribution with mean zero and 2.5% standard deviation to the population size $N(t)$ of both models at random selected time points. This figure was made with the model `source.R`.

A linear density-dependence on their *per capita* birth and/or death rate. Eq. (3.10) is more convenient than the models we derived ourselves because the carrying capacity is defined by just one of its parameters, but because Eq. (3.10) has no explicit death rate, we cannot define a life span, and hence the $R_0$ is not defined. One can easily extend Eq. (3.10) to allow for a non-linear density-dependence, e.g.,

$$\frac{dN}{dt} = rN(1 - (N/K)^m),$$

where the meaning of $r$ and $K$ remain the same and $m$ can be used to define a concave or convex dependence of the *per capita* growth rate on the population density (Fig. 3.3c).

The two density-dependent models for populations that are maintained by a source, i.e., Eqs. (3.4) and (3.8), are mathematically not identical, and their steady states are defined by quite different parameter expression. Thus, the effect of changing a parameter like the source, $s$, on the steady state of the population depends on our choice of which biological process depends (most strongly) on the population density. In Fig. 3.4 we depict the behavior of both models in the presence and absence of noise. The two models are given the same source and death rates, and the $k$ value of the model with density-dependent death is set to such a value that both models have the same steady state (see the R-script `source.R`). Thus, at low densities the two populations have the same initial growth rate, and at high densities they approach the same steady state (see Fig. 3.4a where the red line depicts the population with density-dependent production, and the blue curve is the population with density-dependent death). We observe that the population with density-dependent death approaches the steady state somewhat earlier than the population with density-dependent production. In the presence of noise, i.e., by frequently adding or removing a randomly drawn small value to $N$ (with 2.5% standard deviation), we observe that the (red) population with density-dependent production is somewhat more sensitive to noise than the (blue) population with density-dependent death (Fig. 3.4b). The difference between the two models is small, and depends on the value of the density-dependence parameter, $k$, i.e., when $k \gg s/d$ the models will approach the same behavior, and the smaller $k$ the more different the behavior. Although the difference is small, we have to conclude that the sensitivity of the steady state to changes in the external circumstances, e.g., noisy changes in parameter...
values and/or population densities, depends on the biological choices we make when developing
the model. Thus, whenever possible, we better employ our biological knowledge when devising a
model, and if it remains unknown which biological process depends most on the density, it is best
to develop several models to test the sensitivity of the results on these assumptions (Ganusov,
2016). Because, the same is true for the assumption on the linear shape of \( f(N) \), we expand our
analysis of the shape of \( f(N) \) in the next section.

### 3.3 Non-linear negative density-dependence

Above we have considered *per capita* birth and death rates that were linear functions of the
population density. Although this is generally taken to be sufficient, as one typically models
replicating populations with logistic growth, it would in most cases be more realistic to let
production, birth and death rates only be density-dependent when the resources become limiting,
i.e., at the high population densities (see the blue concave curve in Fig. 3.3c). Populations
that grow spatially by extending their boundaries would be an exception because are already
faced with high competitor densities at low population numbers (and even then their density
dependence is not expected to be linear; see the exercises). Thus, we need functions that allow
us to define non-linear relationships, and it would be convenient to have functions that are non-
dimensional. Above we already used the function \( f(N) = 1 - \left(\frac{N}{k}\right)^m \), and in the appendix we
provide a few more families of such non-dimensional functions (see Page 137). Here we highlight
the very convenient Hill and exponential functions, i.e.,

\[
\begin{align*}
    f(x) &= \frac{x^n}{h^n + x^n} \quad \text{and} \quad f(x) = 1 - e^{-\ln[2]x/h} . \\
\end{align*}
\]

Both functions, \( f(x) \), are non-dimensional, and can be used to formulate saturated and/or
sigmoid positive and negative feedback effects. The functions in Eq. (3.12) are zero when \( x = 0 \),
increase with \( x \), they are half-maximal when \( x = h \), and they approach their maximum,
\( f(x) = 1 \), when \( x \to \infty \). Because these functions are dimensionless, and remain bounded between zero
and one, i.e., \( 0 \leq f(x) < 1 \), one can easily multiply any parameter in a model (corresponding
to some biological process) with \( f(x) \). Having increasing functions \( 0 \leq f(x) < 1 \), one can easily
define decreasing similarly convenient functions by defining \( g(x) = 1 - f(x) \) (see Page 137).

#### Non-linear negative density-dependent birth

For a replicating population with density dependent growth we can now generalize Eq. (3.5)
into

\[
\frac{dN}{dt} = (bf(N) - d)N ,
\]

and use one of the several candidates for the decreasing density dependent functions, \( f(N) \), e.g.,

\[
\begin{align*}
    f(N) &= 1 - \frac{N}{2k} , \quad f(N) = \frac{1}{1 + N/k} , \quad f(N) = \frac{1}{1 + [N/k]^2} \quad \text{and} \quad f(N) = e^{-\ln[2]N/k} , \\
\end{align*}
\]

which are all depicted in Fig. 3.5. Because the birth rate should probably remain close to
maximal as long as the population size is sufficiently small, and is only expected to decrease
when competition kicks in, the sigmoid function of Eq. (3.14c) seems most realistic. Data
supporting linear density dependent growth functions are depicted in Fig. 3.2. Each of the
four models has a single non-trivial steady state (see Table 3.1) and this steady state is always
Density dependence

Figure 3.5: Density dependent birth rates based upon Eq. (3.14). The declining red curves in Panels (a)–(d) correspond to per capita birth rate, \( b f(N) \), where the density dependence is defined by one of the four functions in Eq. (3.14). The horizontal black lines depict the density independent per capita death rate of Eq. (3.13). The intersects therefore correspond to steady states.

\[
\begin{align*}
\text{Function} & \quad f(0) \quad f(k) \quad f(\infty) \quad R_0 \quad \text{Carrying capacity} \\
\frac{dN}{dt} &= \left[ b - d - \delta f(N) \right] N \\
\end{align*}
\]

Table 3.1: Different properties of several functions for density dependent growth in \( \frac{dN}{dt} = (bf(N) - d)N \).

Non-linear density-dependent death

One could use an increasing Hill-function to define a per capita death rate that increases with the population density, i.e., write

\[
\frac{dN}{dt} = \left[ b - d - \delta f(N) \right] N ,
\]

where \( \delta \) is an additional death rate that is due to competition, and comes on top of the normal death rate experienced at low densities (when \( f(N) \to 0 \)). A steep sigmoid Hill-function would allow one to define a population density, \( h \), at which the competition starts to severely increase the death rate, until the maximum per capita death rate, \( d + \delta \) is approached. Since it remains
3.4 Positive density dependence

Now that we learned to use saturation functions we are ready to start modeling positive feedbacks. Replicating populations not only face competition at high densities, they may also suffer from a lack of conspecifics at low densities. Examples would be sexual reproduction where individuals need to encounter partners or gametes (Berec et al., 2007), growing tumors that by inducing angiogenesis increase their own growth rate, cooperating predators like wolves or spoonbills, and microorganism that improve their own environment (Kramer et al., 2009).

Modeling population growth with sexual reproduction basically means that we have to extend our model with density dependent birth and/or death with an additional function describing the probability (or rate) at which individuals are expected to encounter mates. A mechanistic approach would be to define a function, \( g(N) \), for the probability that there is at least one mate in a particular neighborhood, and multiply the birth rate with that probability. This can be defined as a Poisson process, where \( g(N) = 1 - e^{-\lambda N} \) is one minus the probability that there are no males in the neighborhood of a particular female. Knowing that such an exponential function closely resembles the increasing Hill-function \( g(N) = N/(h + N) \) (see Fig. 13.5), we can also use this somewhat more phenomenological model, and define \( h \) as the population density where
Figure 3.7: Positive density-dependence on the reproduction leads to an Allee effect. Panel (a) shows that a population based up Eq. (3.17a,ba) has a critical density (depicted by the horizontal line) above which it increases until the carrying capacity is approached, and below which it declines. The heavy red line in Panel (b) depicts the per capita birth rate as a function of the population density, and the horizontal black line depicts the per capita death rate. Densities at which these line intersect are steady state (because the birth rate balances the death rate). The steady state at a low density is the unstable critical density and the one at a high density is the stable carrying capacity. This figure was made with the model allee.R.

We study the effect of a positive density-dependence by numerically solving Eq. (3.17a,ba) with \( g(N) = N/(h + N) \), starting with either a low, or a somewhat higher, initial population density (Fig. 3.7a). The small population declines and goes extinct and the largest population expands and approaches carrying capacity. The horizontal black lines depicts the critical density that the population needs to expand, and populations that would accidentally drop below this density are expected to go extinct. The per capita birth rate is depicted by the red line in Fig. 3.7b. At low densities the birth rate is small because it is difficult to find mates (i.e., \( g(N) \) is small and \( f(N) \simeq 1 \)), and at high densities it is low because of competition (i.e., \( f(N) \) is small and \( g(N) \simeq 1 \)). The horizontal black line depicts a density-independent death rate, and we see that this lines intersects the birth-rate curve at two population densities. The lower density is the unstable steady state above which the population can grow (see Eq. (3.17a,ba)), and the higher density is the carrying capacity. Because the net per capita population growth is negative at low densities this is called a “strong” Allee effect, which implies that a population of zero individuals is a stable steady state. Eq. (3.17a,ba) therefore has three steady states, of which \( N = 0 \) and \( N = K \) (where \( K \) is the carrying capacity) are stable. Having alternative steady states is due to the fact that this model has a positive feedback (May, 1977).
3.5 Summary

The growth of populations typically involves feedbacks that are called density dependence (or homeostasis). Negative density-dependence allows for a carrying capacity, i.e., a stable steady state population size, and such a negative density-dependence can be implemented as a feedback on the production rate, the birth rate, and/or the death rate. The most convenient approach to implement feedback functions in mathematical models is to define non-dimensional functions describing a particular biological feedback, and to multiply the corresponding parameters of the model with such a function. The most general model describing the growth of a replicating population is the Logistic growth equation. Density-dependence can have a linear or non-linear shape, and can be positive or negative. A Hill-function is convenient tool for defining increasing or decreasing non-linear functions. Positive feedbacks allow for multiple steady states.

3.6 Exercises

Question 3.1. Carrying capacity
What do you expect for the individual well-being in a human population that is approaching its carrying capacity:

a. Do you expect the individual birth rate to be small or large?
b. Do you expect the individual death rate to be small or large?
c. In which population would you prefer to live: a small expanding population, or in one that is approaching carrying capacity?
d. Optimists like Julian Simon advised the American government by saying that “every human being represents hands to work, and not just another mouth to feed” (Cohen, 1995). We can investigate this proposal by arguing that the carrying capacity $K$ in Eq. (3.10) increases with the population size. Test a simple example, e.g., $K = k \sqrt{N}$, and see how this influences the result. Do you still expect a carrying capacity where the individual well-being is at its minimum?

Question 3.2. Freitas
B cells are lymphocytes that can produce antibodies. They circulate via blood and lymph. Novel (naive) B are produced in the bone marrow by pre-B cells that divide, mature, and egress. Agenes et al. (1997) at the Pasteur Institute were breeding mice with different numbers of pre-B cells in the bone marrow to study how the number of circulating naive B cells (e.g., those in the spleen) depends on this source from the marrow. They found the following:

![Graph showing the relationship between number of pre-B cells in bone marrow and number of B cells in spleen.](image-url)
A simple model for the naive B cell population is $dB/dt = m - dB$ where $m$ is the bone marrow production, and $1/d$ is the average life span of naive B cells. We have learned above that the rate of naive B cell production, $m$, is proportional to the number of pre-B cells in the bone marrow, e.g., $m = \alpha P$, where $P$ is the number of pre-B cells that was being changed in the mice. The investigators allowed the mice to mature and we can therefore assume that their observations correspond to the steady state, $\bar{B}$, of our simple model.

a. Is the simple model compatible with the data?

b. If not, how would you extend the model?

c. Do the data require homeostasis, i.e., density dependent regulation?

d. Is $dB/dt = m - dB$ accounting for homeostasis?

Question 3.3. Overfishing herring

For simplicity assume that the dynamics of the herring population in the North Sea can be described by a simple logistic growth model, i.e., $dN/dt = rN(1 - N/K)$. Although this is clearly a gross oversimplification we will learn something insightful from this exercise.

a. Sketch the population growth $dN/dt = f(N)$ as a function of the population size $N$.

b. What is the maximum of the function $f(N)$?

c. What is the long-term optimal population size for the fishermen, and what would then be the maximum harvest (i.e., the maximum number of fish captured per unit of time)?

d. Next include this maximum harvest explicitly in the model to model a situation where we have adopted this policy for a long time.

e. Sketch the growth of the population as a function of its size for this new situation, and show that this quota is too large.

f. What would be a more durable quota for fishing herring?

Question 3.4. Biofilm

Bacteria in often reside in self-organized environments known as biofilms. The bacterial cells become embedded in a matrix of self-produced extracellular polymeric substances, which act like a biological “glue” enabling the microbes to colonize a wide range of surfaces. Once integrated into biofilms, bacterial cells can better withstand environmental challenges. Production of a protective biofilm by the bacteria therefore classifies as positive density dependence, and one way to to implement this into an equation for bacterial growth would be to write a hill function, $F$, for the positive effect of the biofilm on the birth rate, e.g.,

$$\frac{dB}{dt} = [bF(B) - d(1 + eB)]B,$$

where $F(B) = B/h + B$ and where we also allow for a carrying capacity by having negative density dependence in the death rate. When $B = h$ the effect of the biofilm on the birth rate is half-maximal.

a. Sketch the per capita birth rate and the per capita death rate in one graph.

b. Sketch the population birth rate and death rate in one graph. Hint: realize that these are of the form $y = \frac{ax^2}{b + x}$ and $y = ax + bx^2$, respectively, and that the former approaches $y = \frac{a}{b}x^2$ when $x \to 0$, and $y = ax$ when $x$ is large, and that the latter approaches $y = ax$ when $x \to 0$, and $y = bx^2$ when $x$ is large. If you need further assistance in drawing these functions use the biofilm.R model on the website.

c. How many steady states do you expect for these bacteria, and which of them are stable? How would you call this?

d. Can you write a similar model where the biofilm reduces the death rate?

Question 3.5. Stem cells

Consider a population of stem cells that dividing and dying at at fixed rate. The stem cells are located on a surface (or substrate) at the border of a tissue, and this substrate provides the stem cells a signal that inhibits their differentiation. Thus, as long as the cells remain in contact with
3.6 Exercises

the substrate they remain stem cells, and cells that detach differentiate and mature into the cell type defining the tissue. Let there be room on the substrate for about $K$ cells, i.e., let there be $K$ “binding sites”. When a stem cell divides, one of the daughter cells will remain attached to the surface, while the other daughter will only stay attached when the site next to it is empty. Describing the number of stem cells on the surface with the variable $S$, the probability that this site is empty is approximately $\frac{K-S}{K}$.

a. Write a model for this population of stem cells. Do we need density dependent birth or death rates to have a stable carrying capacity?

b. What is the carrying capacity, and why is it smaller than the number of sites $K$?

c. What would be the corresponding equation for the differentiated cells?

d. Sketch the production rate of differentiated cells as a function of the number of stem cells.

Question 3.6. Generalized logistic growth

We have seen in this chapter that the famous Logistic growth model of Eq. (3.10) is obtained when the per capita birth and/or death rate depend linearly on the population size. In Eq. (3.11) we have generalized the Logistic growth model by raising the density-dependent term to the $m$th power.

a. Verify that Eq. (3.10) is indeed obtained when both the per capita birth and the death rate depend linearly on the population size.

b. What would underlying the per capita birth rate function be when the $m$th power is due to density-dependent birth? Would this be realistic for $m = 0.5$ and $m = 2$, and for any value of $m$?

c. What would underlying the per capita death rate function be when the $m$th power is due to density-dependent death? Would this be realistic for $m = 0.5$ and $m = 2$, and for any value of $m$?

Question 3.7. Red blood cells (partly Grind)

Red blood cell (RBC) production in the bone marrow is increased when erythrocyte numbers in the periphery are low. Mechanistically, this works via the hormone erythropoietin (EPO) that is produced by renal epithelial cells when the blood delivers insufficient oxygen to them. This process has been modeled extensively, and one typically assumes a sigmoid curve for the RBC production rate, which declines from a high maximum at low RBC densities to a $n$-fold lower minimum at high RBC densities (Belair et al., 1995; Schirm et al., 2013). On average the human body produces $3 \times 10^9$ new erythrocytes per kg of body weight per day, and let us assume that under normal conditions this requires only a minor effect of EPO, i.e., let us assume that the normal production is close to the minimum, e.g., $10^9$ cells kg$^{-1}$ d$^{-1}$. Additionally, we know that the life expectancy of RBC is about 120 days. Because the bone marrow of the long bones becomes fatty in the elderly, the total amount of bone marrow that is producing erythrocytes decreases with age, which means the maximum production rate declines. Nevertheless, the number of peripheral red blood cells remains fairly constant when we age.

a. Define a function, $f(B)$, for the RBC production rate in the bone marrow, assuming that EPO can increase the production rate about 10-fold.

b. Write a mathematical model (an ODE) describing the number of RBC in the blood.

c. What is the expected steady state RBC density in people that cannot produce EPO? Run the model in Grind to compute the steady state in the presence of EPO.

d. Does this model explain the observation that erythrocyte numbers are fairly independent of the age of an individual?

Question 3.8. Regression to the mean (computer)

To establish whether or not populations are regulated by density dependent effects it is typically best to measure per capita birth and death rates at different population densities, and plot these
Density dependence as a function of the population size (e.g., Fig. 3.2). Alternatively, one can take a long time series of sequential population densities, $N_t$, and study how the per capita rate of change between subsequent time points, i.e., $(N_{t+\Delta} - N_t)/N_t$, depends on the previous population density, $N_t$. Although the second method comes with a well-known problem (Shenk et al., 1998), it is nevertheless still being used to detect density-dependence in time-series data (Freckleton et al., 2006). The problem is illustrated by the following R-script (called normal.R on the website):

```r
n <- 100; data <- rnorm(n,1,0.1); hist(data)
N <- data[1:(n-1)]; r <- (data[2:n]-N)/N
plot(N,r,type="p")
lm(r~N,as.data.frame(cbind(N,r)))
```

Artificial data is generated by drawing $n = 100$ times from a normal distribution with $\mu = 1$ and $\sigma = 0.1$, and the per capita rate of increase, $r$, is computed by subtracting two subsequent data points, and dividing by the former. The relationship is plotted and quantified by linear regression (by a call to `lm()`).

a. What do you expect for the relationship between $r$ and $N_t$ in this random data set?

b. What do you find, and how can this be?

c. Can a time-series provide solid evidence for density dependent effects? The Freckleton et al. (2006) paper provides an excellent discussion on this topic.

**Question 3.9. The Fisher equation (Grind)**

To model a population that is growing logistically on a one-dimensional spatial domain one can just add a diffusion term,

$$ \frac{dN}{dt} = rN \left(1 - \frac{N}{K}\right) + D \frac{\partial^2 N}{\partial x^2} , $$

where the parameter $D$ is a diffusion constant. This equation was introduced by the famous Ronald Fisher in 1937 to describe the spatial spread of an advantageous allele. To study such a PDE numerically one needs to discretize it into something like

$$ \frac{dN_i}{dt} = rN_i \left(1 - \frac{N_i}{K}\right) + D(N_{i-1} + N_{i+1} - 2N_i) , \quad \text{for } i = 1, 2, \ldots, n $$

where $i$ defines a location of a (small) compartment in space, and $D$ describes the movement of individuals between neighboring compartments.

a. This model is available in the website as the file fisher.R. Study how such a vector of equations can be defined in R, and realize that we have wrapped the boundaries, i.e., individuals move from $N_1$ to $N_n$ and vice versa.

b. What is the behavior of the model?

c. What do you expect will happen if the model is extended with an Allee effect?

**Question 3.10. Cell division takes time (Grind)**

A simple model for a population of proliferating cells is $dN/dt = (p - d)N$, which defines cells that are dividing at a rate $p$ and dying at a rate $d$. Both rates are density independent. Like all ODEs, this model assumes that cellular division and death times are exponentially distributed, which actually means that most cells divide and die instantaneously. Since the process of cell division is composed of various “time consuming” phases, i.e., DNA has to be synthesized, and chromosomes have to properly align, cell division cannot occur instantaneously, and takes a minimal amount of time. The quite famous Smith-Martin model (Smith & Martin, 1973) accounts for this by implementing a fixed time delay between an exponentially distributed “trigger” to initiate division, and the time at which the cell actually divides. This model
3.6 Exercises

successfully describes the growth of tumor cells in vitro. Smith & Martin (1973) write: “Some time after mitosis all cells enter a state (A) in which their activity is not directed towards replication. A cell may remain in the A-state for any length of time, throughout which its probability of leaving A-state remains constant. On leaving A-state, cells enter B-phase in which their activities are deterministic, and directed towards replication.” Adding, an exponentially distributed death rate (which is here not different between the A-state and B-phase), the model can be written as a delay-differential equation (DDE):

\[
\frac{dA(t)}{dt} = 2pA(t-\Delta)e^{-d\Delta} - (p + d)A(t) \quad \text{and} \quad \frac{dB(t)}{dt} = pA(t) - dB(t) - pA(t-\Delta)e^{-d\Delta},
\]

where \(\Delta\) is the length of the B-phase, and hence \(e^{-d\Delta}\) is the fraction of cells surviving the B-phase. The total number of cells at time \(t\) is defined as \(N(t) = A(t) + B(t)\), and starting with a quiescent population \(N(0) = A(0)\) it will take at least \(\Delta\) time steps before the first new cells are born. Ganusov et al. (2005) have analyzed the Smith-Martin model, and derive that after an initial phase the total number of cells, \(N(t)\), approached a growth rate, \(r\), that can be solved from the equation

\[
2pe^{-(d+r)\Delta} - (r + p + d) = 0,
\]

which for \(\Delta = 0\) indeed delivers \(r = p - d\). The Smith-Martin model, with a function call solving Eq. (3.19) numerically is available as the file \texttt{sm.R}.

Because DDEs are difficult to solve numerically, and because fixed time delays need not be realistic, it can sometimes be better to replace the time delay by defining a large number, \(n\), of “dummy” intermediate populations, \(B_i\), with a transition rate, \(\frac{\Delta}{n}\), such that the expected length of the delay remains \(\Delta\) time steps, irrespective of \(n\). For large \(n\) this model approaches a “smooth” time delay of \(\Delta\) time steps (smooth here means without a discontinuity). An alternative formulation of the Smith-Martin model would therefore be

\[
\frac{dA}{dt} = \frac{2n}{\Delta}B_n - (p + d)A, \quad \frac{dB_i}{dt} = pA - \left(d + \frac{n}{\Delta}\right)B_i \quad \text{and} \quad \frac{dB_i}{dt} = \frac{n}{\Delta}(B_{i-1} - B_i) - dB_i,
\]

for \(i = 2, 3, \ldots n\). This model is available as the function \texttt{er1()} (for Erlang distribution) in the file \texttt{sm.R}.

a. What is the ODE for total number of cells in the Smith-Martin model at early time points, i.e., for \(t < \Delta\)? Would that be different in the model with a flexible delay?

b. What is \(dA/dt\) in the Smith-Martin model at early time points, i.e., for \(t < \Delta\), when we start with a quiescent population, i.e., \(N(0) = A(0)\)? Verify your answer by running the Smith-Martin model and the \texttt{er1()} model for a short period of time.

c. What is the expected time between divisions in the Smith-Martin model, and what would be the corresponding division rate in the corresponding d\(N/dt = (p - d)N\) model? Is this faster or slower than the division rate, \(r + d\), predicted by Eq. (3.19)? Why?

d. What is the asymptotic behavior of the Smith-Martin model? How different is it from the simple d\(N/dt = (p - d)N\) model, and how does this depend on the relative length of the A-stage (1/p) and the B-phase (\(\Delta\))?

Question 3.11. Life stages

Consider an insect population consisting of larvae (\(L\)) and adults (\(A\)). Adults give birth to larvae (in an asexual manner), and these larvae later mature into adults. Adults have a density independent mortality, i.e., a given expected life span. Larvae compete with adults and have a mortality that is dependent on the density of adults (use a simple term for this).

a. Make a model consisting of two ODEs for the growth of such a population.
b. Draw nullclines and determine the stability of all steady states.
c. Assume that the dynamics of the larvae is much faster than that of adults, i.e., make a “quasi steady state” assumption for the larvae.
d. Write the new ODE for the adults. Does this equation look familiar to you?
e. What model would one get if we instead make the quasi steady state assumption for the adults?
f. Which of the two assumptions do you think is most realistic?

**Question 3.12. Tumor growth**

Consider a small melanoma growing as a flat disk. Assume that the tumor cells are dividing only at the tumor boundary because of a lack of blood supply inside, and that cell death occurs uniformly throughout the tumor mass. A first approximation would be that the total biomass is proportional to the area of this circle, i.e., $A = c\pi r^2$, where $r$ is its radius and $c$ is a constant scaling from area to biomass. Since reproduction takes place at the border, realize that the circumference of the circle is given by $2\pi r$. Thus, if $N$ is the total number of cells in the tumor, the number of cells at the surface is proportional to $\sqrt{N}$.

a. Write a growth model for the total number of cells in the tumor.
b. What are the steady states?
c. Sketch the per capita growth as a function of the tumor mass. Does this look okay?
Chapter 4

Stability and return time

In the previous chapter we have seen several numerical examples of populations approaching a steady state. Such a stable steady state is an attractor of the system, and in most examples this corresponded to the carrying capacity of the population. We have also argued that for replicating populations the trivial steady state, \( N = 0 \), is unstable whenever the maximal per capita birth rate exceeds the minimal per capita death rate, i.e., whenever \( R_0 > 1 \), because the population will expand following a positive perturbation. Technically, we need the solution of the ODE to see which attractor is approached when \( t \to \infty \), but in this chapter we will determine the stability of a steady state by simplifying the differential equation around a steady state. By doing so we will be able to define the “return time” of a stable steady state as the typical time it would take the population to return to the steady state after a small disturbance. Steady states with a long return time are sensitive to perturbations and are said to have a low resilience. Populations having several stable steady states, e.g., those with an Allee effect (see Eq. (3.17a,b)), will have an unstable steady state defining the boundary between the basins of attraction of the alternative attractors.

4.1 Stability defines by the local slope of the growth function

In the previous chapter we emphasized that is typically most convenient to sketch biologically defined per capita functions for birth and death rates, and subsequently multiply these with the population size to obtain a function defining the net growth, \( dN/dt = f(N) \), of the population. Having defined such a growth function one can plot it as a function of the population size, i.e., plot \( f(N) \) as a function of \( N \) (see Fig. 4.1). The values \( \bar{N} \) of \( N \) at which \( f(N) = 0 \) then define the steady states because \( dN/dt = 0 \). The growth function the classical logistic model, \( f(N) = rN(1 - N/K) \), is a parabola that is zero when \( N = 0 \) or \( N = K \), and has its maximum at \( N = K/2 \) (see the blue line in Fig. 4.1a). To check the stability of the non-trivial steady state, \( \bar{N} = K \), one can study what happens when the steady state population size is somewhat increased. Increasing \( N \) from its non-trivial steady value \( \bar{N} \) results in a negative value of \( f(N) \), implying that the population will decrease after it was increased by a perturbation. Similarly, a decrease of the population size will result in an increase, because \( f(N) > 0 \) when \( N \lesssim K \). This suggests that the steady state is stable because \( f(N) \) provides a negative feedback on small perturbations around the steady state.

We can generalize this approach by plotting several of the growth functions introduced in the
previous chapter. For example, for the generalized logistic growth model, \( f(N) = rN(1 - (N/K)^m) \), the steady states remain to be localized at \( \bar{N} = 0 \) and \( \bar{N} = K \), and the only qualitative changes is that the maximum is shifted to the right for \( m = 2 \) and to the left for \( m = 1/2 \) (see Fig. 4.1a). The carrying capacity \( \bar{N} = K \) therefore remains a stable steady state. For the non-replicating population with a density dependent production, i.e., \( f(N) = s(1 - N/k) - dN \) from Eq. (3.8), we observe that \( f(N) \) is a straight line starting at \( f(0) = s \), and intersecting the horizontal axis as \( \bar{N} = K = \frac{sk}{s + dk} \) (see the red line in Fig. 4.1b). The growth function of Eq. (3.4), i.e., \( f(N) = s - d(1 + N/k)N \) is depicted as a blue line in Fig. 4.1b, and is a parabola having its maximum at \( N = -k/2 \) and intersecting the horizontal axis at

\[
\bar{N} = K = \frac{-dk \pm \sqrt{dk(dk + 4s)}}{2d}.
\]

By the same approach we infer that the steady state of the two non-replicating populations is also stable because of a negative feedback that decreases population growth when the population were to increase.

Importantly, note that we only need the local slope \( \partial_N f(N) \) in the point \( N = \bar{N} \) to infer the stability of the steady state (where we use the “partial”, \( \partial \), notation to explicitly define what derivative we take, e.g., \( \partial_x x^2 = 2x \), \( \partial_y xy = x \), and \( \partial_N N(t) = dN(t)/dt \)). Thus, we see that a steady state of an equation, \( dN/dt = f(N) \), is stable whenever \( f'(\bar{N}) < 0 \) (where we use the shorthand \( f' \) to denote a derivative, and \( f'(\bar{N}) \) for the derivative in the steady state). Similarly, one can see that a steady state is unstable when \( f'(\bar{N}) > 0 \) because that corresponds to a positive feedback where an increase in the population from its steady state value leads to a further increase of the population because \( dN/dt = f(N) > 0 \). An example of an unstable steady state is the origin of Fig. 4.1a, where \( f(N) \) has a positive slope in the trivial steady state \( \bar{N} = 0 \).

### 4.2 Linearization

The fact that one can read the stability of a steady state by the local slope, or derivative, of the growth function is not a lucky coincidence. Mathematically one can linearize any continuous function \( f(x) \) around any particular value, e.g., \( \bar{x} \), by its local derivative \( \partial_x f(\bar{x}) \) in that point:

\[
f(x) \simeq f(\bar{x}) + \partial_x f(\bar{x})(x - \bar{x}) = f(\bar{x}) + f'\bar{x}h,
\]

where \( h = x - \bar{x} \) is a small distance in the \( x \)-direction, and \( f' = \partial_x f(x) \) is the derivative of \( f(x) \) with respect to \( x \) at the value \( x = \bar{x} \) (see Fig. 13.4 in the Appendix, and the accompanying Ebook (Panfilov et al., 2016)). For example, one can linearize the function \( f(x) = 2x^2 \) by its derivative \( f'(x) = 4x \), and approximate the value of \( f(x) \) at \( x = 3.1 \) by writing, \( f(3.1) \simeq f(3) + 4 \times 3 \times 0.1 = 2 \times 9 + 1.2 = 19.2 \), and see that this is close to the true value \( f(3.1) = 19.22 \).

To apply this to our stability analysis one rewrites \( f(N) \) into \( f(\bar{N} + h) \) where \( \bar{N} \) is the steady state population size and \( h \) is considered to be a small disturbance of the population density from the steady state, i.e., \( h = N - \bar{N} \). Following Eq. (4.1) one rewrites \( dN/dt \) into

\[
\frac{dN}{dt} = f(N) \simeq f(\bar{N}) + \partial_N f(\bar{N})(N - \bar{N}) = 0 + \lambda h,
\]

because \( f(\bar{N}) = 0 \), and where we have defined \( \lambda = \partial_N f(\bar{N}) \) as the local derivative of \( f(N) \) at \( N = \bar{N} \), and \( h = N - \bar{N} \) as the distance to the steady state. Because the sum of two derivatives is the derivative of the sum, and \( \bar{N}/dt = 0 \), we can apply the following trick

\[
\frac{dN}{dt} = \frac{dN}{dt} - \frac{d\bar{N}}{dt} = \frac{d(N - \bar{N})}{dt} = \frac{dh}{dt},
\]

(4.3)
4.3 Return time

The stability of a steady state is determined by the local derivative (slope) of the growth function at the steady state. We plot the population growth rate, \( \frac{dN}{dt} = f(N) \), as a function of the population size \( N \). Panel (a) depicts the generalized logistic growth model, \( f(N) = rN[1 - (N/K)^m] \) for \( m = 0.5 \) (green), \( m = 1 \) (blue), and \( m = 2 \) (red). The blue line is the characteristic logistic parabola. Panel (b) shows the population growth of Eq. (3.8), modeling density dependent production, i.e., \( f(N) = s(1-N/k) - dN/N \) as a red line, and that of Eq. (3.4), i.e., \( f(N) = s - d(1+N/k)N \) as a blue line.

The \( k \) parameters of the latter two models have been scaled such that both models have the same steady state \( K \). The carrying capacities depicted in Panel (a) are all stable because \( \partial N f(N) = \lambda = -mr < 0 \) when \( \bar{N} = K \). Indeed, increasing the population size in the carrying capacities results in \( f(N) < 0 \), which is a negative feedback. In Panel (a) the trivial steady states are unstable because \( \partial N f(N) = \lambda = r > 0 \) when \( \bar{N} = 0 \). At the steady state \( \bar{N} = K \) in Panel (b), \( \lambda = -d - s/k < 0 \) for the straight red line corresponding to Eq. (3.8), and \( \lambda = -d(1-2K/k) < 0 \) for the blue parabola corresponding to Eq. (3.4). \( N = 0 \) is not a steady state in Panel (b). Note that the dimension of the slopes, \( \lambda \), are time\(^{-1} \) in each case. This figure was made with the model \texttt{logist.R}.

to obtain

\[
\frac{dh}{dt} = \lambda h \quad \text{with solution} \quad h(t) = h(0)e^{\lambda t}, \tag{4.4}
\]

for the behavior of the distance, \( h \), to the steady state. Thus, whenever the local tangent \( \lambda \) at the equilibrium point is positive, small disturbances, \( h \), grow. Whenever \( \lambda < 0 \) they decline, and the equilibrium point is stable.

This readily confirms the intuitive approach explained in Fig. 4.1 where we used the slope, \( \lambda = f'(N) \), to determine whether or not a steady state is stable. For example, for the logistic equation, \( f(N) = rN(1 - N/K) \), one obtains \( \lambda = r - 2rN/K \). At the carrying capacity, i.e., at \( N = K \), the local tangent is \( \lambda = -r \), and at \( N = 0 \) we obtain \( \lambda = r \) (see Fig. 4.1a), confirming that \( N = K \) is a stable steady state, and that \( N = 0 \) is an unstable steady state. Similarly, for the non-replicating populations in Fig. 4.1b, we obtain that at the carrying capacity where \( f(K) = 0, \lambda = -d - s/k < 0 \) for the straight red line corresponding to Eq. (3.8), and \( \lambda = -d(1-2K/k) < 0 \) for the blue parabola corresponding to Eq. (3.4). Since both slopes are negative, local perturbations of size \( h(0) \), die out at a rate defined by Eq. (4.4).
Figure 4.2: The return time to a steady state depends on the parameters and the density-dependent functions. Panels (a) and (b) depict a classical $r$-selected and $K$-selected population where the natural rate of increase of the $r$-selected species (in red) is 10-fold larger than that of the $K$-selected species (in blue). In Panel (a) we add noise sampled from a normal distribution with mean zero and 5% standard deviation to the population size $N(t)$ of both models at randomly selected time points, and observe that the red $r$-selected species varies considerably less and remains closer to the carrying capacity. In Panel (b) we draw random values for the carrying capacity from a normal distribution with 5% standard deviation at randomly selected time points, and observe that the red $r$-selected species varies considerably more, as it more rapidly approaches the new carrying capacities. Panel (c) depicts the generalized logistic growth model of Eq. (3.11) for $m = 0.5$ (green), $m = 1$ (blue), and $m = 2$ (red), where we add noise sampled from a normal distribution with mean zero and 5% standard deviation to the population size $N(t)$ of both models at randomly selected time points, and observe that the (red) species with the steepest slope $\lambda$ at the carrying capacity has the shortest return time. This figure was made with the models logist3.R.

4.3 Return time

Note that the slopes in Fig. 4.1 do have a different steepness, i.e., that the $\lambda$s differs. Since $\lambda$ in Eq. (4.4) define the rate at which perturbations die out, the stability of a steady state can be expressed as a “Return time”

$$T_R = -\frac{1}{\lambda},$$

i.e., the more negative $\lambda$ the faster perturbations die out. Note that the dimension of $T_R$ are correct: because $\lambda$ is a rate with dimension “time$^{-1}$”, $T_R$ indeed has the dimension “time”. For example, consider the return time of the logistic growth equation around its carrying capacity. Above we derived that at $\bar{N} = K$ the tangent $\lambda = -r$. This means for return time of the logistic growth equation that $T_R = 1/r$, i.e., the larger $r$ the shorter the return time. Thus, populations that grow fast are more resistant to perturbations, which sounds intuitive.

The paradigm of $r$-selected and $K$-selected species in ecology is built upon this $T_R = 1/r$ (see Fig. 4.2a for an example). Although an $r$-selected species with a 10-fold higher rate of increase than a $K$-selected species varies less when we put additive white noise on the population size (Fig. 4.2a), the $r$-selected species varies more when we make the carrying capacity, $K$, a noisy parameter (see Fig. 4.2b). Biologically this would correspond to having a fluctuations in the environment allowing for better and worse periods with a higher or smaller maximum population size. Due to its faster growth rate an $r$-selected species traces these fluctuations, whereas a slower growing species lags behind and “averages” more over these periods.

Thus, the natural rate of increase, $r$, in the logistic equation plays an important role in the resilience of the carrying capacity to perturbations. The three growth functions of the generalized
4.4 Basins of attraction

In the previous chapter we saw that positive density-dependence can give rise to an Allee-effect, meaning that a population needs to be sufficiently large before it can grow. The growth function of that model is depicted in Fig. 4.3a, which confirms that this population has three steady states where \( f(\bar{N}) = 0 \). The local derivative, \( \lambda \), has a positive slope at the critical population size, demonstrating that this is an unstable steady state. Since starting values below this unstable
Stability and return time

state all approach the stable point $N = 0$, and trajectories starting above it all approach the carrying capacity, the unstable point separates the “basins of attraction” of the two stable steady states. This concept of a basin of attraction is further illustrated by the example function in Fig. 4.3b. Note that the return time has no bearing on a basin of attraction: return times are only defined in the neighborhood of a steady state where the linearization remains a good approximation. The concept of “resilience” does cover the size of a basin of attraction. Steady state with a small basin of attraction have low resilience because perturbations may push the population into approaching an alternative attractor.

4.5 Summary

Plotting the population growth function $\frac{dN}{dt} = f(N)$ as a function of the population size, $N$, reveals the steady states, and from the slope in the steady state one can determine the stability of the steady state. A steady state is stable when the local derivative, $f'(\bar{N}) = \lambda$, of the growth function is negative, and it is unstable whenever $\lambda > 0$. When the slope is computed by linearization one obtains a parameter expression that can be used to define the return time, $T_R = -\frac{1}{\lambda}$, quantifying how rapidly the population re-approaches the steady state following a small disturbance. Basins of attraction are defined by unstable steady states, and steady states with a small basin of attractions are not resilient because disturbances that breach the basin of attraction bring the population to an alternative attractor.

4.6 Exercises

Question 4.1. Density dependent death
Consider a replicating population where most of the death is due to competition with other individuals, i.e., let $f(N) = cN$ in a model where $\frac{dN}{dt} = (b - f(N))N$.

a. Sketch the per capita death rate as a function of $N$.

b. Sketch the per capita net growth rate as a function of $N$

c. Compute the steady states.

d. Why is the $R_0$ not defined?

e. What is the return time in the non-trivial steady state?

Question 4.2. Return time
Compute the return time around the carrying capacities of:

a. the “logistic growth” models with an explicit density-dependent birth of death rate, i.e., $\frac{dN}{dt} = bN[1 - N/k] - dN$ and $\frac{dN}{dt} = bN - dN[1 + N/k]$. Does the return time depend on the birth or the death rate?

b. of the non-replicating population $\frac{dN}{dt} = s - dN$.

c. Why are the return times independent of $k$ and $s$?

d. Would adding negative density dependence to the model of the non-replication population, e.g., $\frac{dN}{dt} = s(1 - N/k) - dN$, shorten the return time?

Question 4.3. Whales
Develop a simple model for a population of whales in the oceans. Because at low population densities the females face difficulties find a male, it is essential to include the likelihood of finding a mate in your model.
a. Write an appropriate ODE.

b. Sketch the birth and death rates as a function of the population size (you may want to use the file whales.R).

c. Sketch the net growth of the whale population as a function of the population size, and indicate the basins of attraction of the steady states.
Chapter 5

Killing and consumption

In Chapter 3 we have written models for density-dependent population growth by allowing the birth rate to decline as a function of the population density, and/or the death rate increase with the population density. Such models tend to be simplifications because density-dependent effects typically operate indirectly via other variables, and not by direct contacts between the individuals. For example, we have written a model for density-dependent production of red blood cells with a production term that decreases as a function of the density of red blood cells. In reality this depended on the production of EPO produced by cells in the kidney, which in turn depended on their oxygenation, which finally depended on the red blood cell density. Another example is the density-dependent growth of a population of bacteria, which typically operates via the depletion of resources, or via the production of toxins, at high bacterial densities. An example where direct competition would be mechanistic is the slowing down of cell-division by “contact inhibition” when cells become surrounded by other cells in growing cell cultures or organs.

To explicitly allow for the factors mediating the density-dependence we have to extend our models with variables representing these factors. Classical examples are bacteria or algae requiring and consuming nutrients. Because at high population densities the resource availability decreases by this consumption, one naturally obtains a density-dependence that will ultimately limit the total population size. A simple example would be a population of cells growing in a closed environment, requiring a certain nutrient for successful cell division. If this nutrient becomes freely available upon cell death, one could write a conservation equation for the resource, \( R_T = R + cN \), where \( R_T \) is the fixed total density of resource in the closed environment, \( cN \) is the amount of resource contained in the \( N \) cells of the population, and \( R \) is the amount of resources that is freely available. Writing the rate of cell-division as a saturation function of the available resource density, one would obtain something like,

\[
\frac{dN}{dt} = \frac{bRN}{h + R} - \delta N = \frac{b(R_T - cN)N}{h + R_T - cN} - \delta N = bN\left(1 - \frac{h}{h + R_T - cN}\right) - \delta N ,
\]

where \( b \) is the maximum division rate, \( h \) the resource density at which the cells divide at half their maximal rate, and \( \delta \) is the death rate of the cells. For this simple case we therefore re-obtain an ODE where the population birth is limited directly by the population density, but note that none of the models in Chapter 3 resembles Eq. (5.1).

To generally extend our model with a dynamic resource that is limiting population growth, we need to write an ODE for the resource, with a production and a loss term, we need to define a
Killing and consumption

functional form for the consumption rate, and we need to define how the birth and/or death rate of the population depends on the amount of resources consumed. We will treat each of these terms separately, and, whenever needed, sketch simple functions to define the form of interaction terms.

5.1 Bacteria in chemostats

First consider bacteria growing in a chemostat with a fixed influx of fluid containing nutrients, and a constant outflow of fluid containing nutrients and bacteria. In the absence of bacteria one would write $dR/dt = s - wR$, where $R$ (for resource) is the concentration of the nutrient in the chemostat, $s$ is the rate of influx (e.g., in moles per hour), and $w$ is the rate of efflux (then also per hour). Some time after initializing the chemostat, the nutrient concentration approaches the steady state $\bar{R} = s/w$.

When the maximum nutrient levels remain sufficiently low, e.g., if the source $s$ is small, one can safely assume that the rate at which bacteria take up nutrients remains proportional to $R$, i.e., a sketch of the per capita consumption rate as a function of $R$ would be a straight line through the origin with slope $a$. Writing $N$ for the density of bacteria, and $a$ for the rate of uptake of nutrients per bacterium per hour, one would write

$$\frac{dR}{dt} = s - wR - aRN. \quad (5.2)$$

If the division rate of the bacteria is limited by nutrients, and if this were to remain proportional to their per capita uptake, $aR$, at these low nutrient levels, one would write

$$\frac{dN}{dt} = caRN - (w + d)N = caRN - \delta N, \quad (5.3)$$

where $caR$ is the per capita birth rate (increasing linearly with $aR$), $w$ remains the rate of wash-out from the chemostat, $d$ is the death rate of the bacteria (per hour), and $\delta = w + d$. Seeding a chemostat at steady state, $\bar{R} = \frac{s}{w}$, with some bacteria will lead to bacterial growth whenever their $R_0 = \frac{caR}{\delta} = \frac{ca}{aw} > 1$.

The properties of this 2-dimensional model can be analyzed by sketching nullclines and computing the steady state(s). Starting with the latter we observe that in the presence of bacteria, the steady state resource density is solved by setting $dN/dt = 0$ in Eq. (5.3). Cancelling the trivial $N = 0$ solution that we already considered above, this leads to $\bar{R} = \frac{\delta}{ca}$. This calculation also reveals that the $dN/dt = 0$ nullcline consists of two straight lines in the phase plane, one corresponding to the line $N = 0$, and the other to the line $R = \frac{\delta}{ca}$. To proceed with the steady state we solve $N$ from $dR/dt = 0$ in Eq. (5.2),

$$N = \frac{s}{aR} - \frac{w}{a} \quad \text{and, after substituting } R = \frac{\delta}{ca}, \quad \bar{N} = \frac{sc}{\delta} - \frac{w}{a}. \quad (5.4)$$

The former expression gives the $dR/dt = 0$ nullcline, and the latter the “carrying capacity” of the bacteria in a chemostat with source $s$ and loss rate $\delta = w + d$. The model therefore has two steady states: the trivial $(\bar{R}, \bar{N}) = (\frac{s}{w}, 0)$ and the non-trivial $(\bar{R}, \bar{N}) = (\frac{\delta}{ca}, \frac{sc}{\delta} - \frac{w}{a})$.

To study the stability of these steady state we perform phase plane analysis. Since the $dR/dt = 0$ nullcline is expressed a function $N = f(R)$, and the $dN/dt = 0$ nullclines are simple straight lines at fixed $R = \bar{R}$ or $N = 0$ values, we define the vertical axis of the phase plane by the bacteria...
and the horizontal axis by the resource (see Fig. 5.1) The dR/dt = 0 nullcline, N = \( \frac{s}{ca} - \frac{w}{a} \), has a vertical asymptote when R = 0, a horizontal asymptote \( N = -\frac{w}{a} \) when \( R \to \infty \), and intersects the horizontal axis at the trivial resource density, \( R = s/w \) (see Fig. 5.1a). For the vector field one could start close to the origin, \((R, N) \simeq (0, 0)\), where dR/dt > 0 because \( s > wR \) and dN/dt < 0 because \( caR < \delta \) (see the arrows in the bottom-left corner). Flipping the horizontal arrows at the dR/dt = 0 nullcline, and the vertical arrows at the dN/dt = 0 nullcline, the vector field can be completed for every qualitatively different region in the phase space. One may double-check that dR/dt < 0 and dN/dt > 0 in the upper-right corner, where \( s < dR - aRN \) and \( caR > \delta \). Finally, note that the location of the bacterial nullcline, \( R = R^* = \frac{\delta}{ca} \), corresponds to the critical resource required for bacterial growth (Tilman, 1980, 1982), and that the nullclines will only intersect when \( \frac{s}{w} > R^* \).

In Fig. 5.1a the steady state \( (\frac{s}{w}, 0) \) without bacteria is unstable because the vertical vectors are pointing away from it (actually, it is a saddle-point because the horizontal vectors are pointing towards it). Indeed, introducing bacteria into this state is expected to lead to bacterial growth (because \( \frac{s}{w} > R^* \)). To determine the stability of the non-trivial steady state we have to linearize the system to compute the Jacobi matrix. We write the two ODEs in Eq. (5.2) and (5.3) as two normal functions, \( f(R, N) = s - wR - aRN \) and \( g(R, N) = caRN - \delta N \), determine their partial derivatives, and subsequently substitute the steady state values:

\[
J = \begin{pmatrix}
\frac{\partial R f}{\partial R} & \frac{\partial N f}{\partial N} \\
\frac{\partial R g}{\partial R} & \frac{\partial N g}{\partial N}
\end{pmatrix}
|_{(R,N)} = \begin{pmatrix}
-w - a\bar{N} & -a\bar{R} \\
ca\bar{N} & ca\bar{N} - \delta/c
\end{pmatrix} = \begin{pmatrix}
-\alpha & -\beta \\
+\gamma & 0
\end{pmatrix},
\]

where \( \alpha, \beta \) and \( \gamma \) are arbitrary positive values. Since the trace of this Jacobi matrix, \( \text{tr} = -\alpha < 0 \), and its determinant, \( \text{det} = 0 - \beta\gamma = \beta\gamma > 0 \), both eigenvalues will be negative (i.e., have a negative real part). We therefore conclude that the non-trivial steady state is stable (see the accompanying Ebook (Panfilov et al., 2016)). Note that we can also read of the signs of this Jacobian from the vector field. The local effect of \( R \) on dR/dt = f(R, N) is given by the negative arrow on the right side of the steady state, the negative effect of \( N \) on dR/dt = f(R, N) is given by the negative arrow above the steady state, the positive effect of \( R \) on dN/dt = g(R, N) is given by the positive arrow on the right side of the steady state, and the null effect of \( N \) on dN/dt = g(R, N) is revealed by the fact that \( g(R, N) = 0 \) above the steady state. A population
Saturated consumption

Actually it has been known for a long time (Monod, 1949) that the division rate of bacteria approaches a maximum at high nutrient densities. This has been modeled with a simple Hill function, \( f(R) = \frac{R}{h+R} \), which in this literature has been coined as the Monod saturation function. Assuming that the rate at which bacteria divide is proportional to the rate at which they take up nutrients, one would write

\[
\frac{dR}{dt} = s - wR - \frac{aRN}{h+R} \quad \text{and} \quad \frac{dN}{dt} = \frac{caRN}{h+R} - (w+d)N = \frac{caRN}{h+R} - \delta N .
\]  

At the expense of one new parameter, \( h \), representing the resource density at which the per capita consumption rate is half maximal, we now have a model that is also realistic at high resource densities. The fitness \( R_0 \) of the bacteria can now be defined in two ways. First, one could invoke the maximum resource density, \( R = s/w \), to compute a maximum division rate \( \frac{caR}{h+caR} \). With an expected residence time of \( 1/\delta \) this would correspond to an \( R_0 = \frac{ca}{\delta} \). Second, one could go for a much simpler definition of \( R_0 \) by making use of the fact that the division rate approaches a maximum, \( ca \), at infinite resource densities, which provides an \( R_0 = \frac{ca}{\delta} \). The latter \( R_0 \) is elegantly simple and will be used to clean up the expression of the steady states.

Analyzing the behavior of the model by computing steady states and nullclines, we first observe that setting \( dN/dt = 0 \), and cancelling the trivial \( N = 0 \) solution, again provides the steady state of the resource, \( \frac{d\tilde{R}}{dt} = \frac{h\delta}{\delta + ca - \delta} = \frac{h}{\delta + ca - \delta} \), where \( R_0 = \frac{ca}{\delta} \). The \( dN/dt = 0 \) nullclines therefore remain to be two straight lines, one at \( N = 0 \) and the other at the non-trivial \( R = \bar{R} \) (see Fig. 5.2). To find the steady state of the bacteria we substitute \( R \) in the \( dR/dt = 0 \) equation with
5.2 Replicating resources

Next consider a population consuming a replicating resource (that itself would approach a steady state in the absence of consumption). This could be zooplankers grazing algae, or killer cells that divide after removing tumor cells. In Chapter 3 we have learned that logistic growth is a general for a replicating resource with linear density dependent birth and/or death rates. Thus, starting simple by adopting logistic growth for the resource, and with the same mass-action consumption as above, one would write

\[ \frac{dR}{dt} = rR(1 - R/K) - aRN , \quad \frac{dN}{dt} = caRN - \delta N . \]  \hspace{1cm} (5.9)
This is the famous Lotka-Volterra model that was proposed independently by Lotka (1913) and Volterra (1926) as an ecological predator-prey model. Note that the ODE for the consumers is identical to Eq. (5.3). We will see later that epidemiological models for an infection spreading in a population of susceptible hosts can also be described with Eq. (5.9) (when \( R \) are susceptible and \( N \) infected hosts, \( a \) is an infection rate, and \( c = 1 \)). Interpreting \( R \) has the size of a tumor (or an infection), \( caR \) as a per capita cell division rate, and \( N \) as the number of immune effector cells, the same model has also been used for modeling an immune response to a replicating threat.

Because the Lotka-Volterra model is used so widely in Theoretical Biology we will analyze it in detail. Starting with the steady states we observe that in the absence of consumers the resource will either be zero, or approach the steady state \( \bar{R} = K \). In the presence of consumers one solves \( \ddot{R} = \frac{\delta}{ca} \) by setting \( dN/dt = 0 \), and substituting this into

\[
\dot{r}(1 - R/K) - aN = 0 \quad \text{delivering} \quad \dot{N} = \frac{r}{a}\left(1 - \frac{\delta}{caK}\right) \tag{5.10}
\]

for the non-trivial steady state of the consumers. The \( dN/dt = 0 \) nullcline consists of the now familiar straight lines \( N = 0 \) and \( R = \frac{\delta}{ca} \), and the \( dR/dt = 0 \) isocline is defined by \( R = 0 \) and \( N = \frac{r}{c}(1 - \frac{\delta}{ca}) \). Depicted in a phase space with \( N \) on the vertical axis and \( R \) on the horizontal axis, the nullcline of the resource is a declining straight line, intersecting the vertical axis at \( N = r/a \) and the horizontal axis at \( R = K \) (see Fig. 5.3a). The location of the non-trivial consumer nullcline again defines the critical resource density, \( R^{*} \), required for net growth of the consumers, and the non-trivial steady state only exists when \( R^{*} < K \) (see Fig. 5.3a).

The model has maximally three steady states,

\[
(\bar{R}, \bar{N}) = (0,0), (K,0) \quad \text{and} \quad \left(\frac{\delta}{ca}, \frac{r}{a}\left[1 - \frac{\delta}{caK}\right]\right) \tag{5.11}
\]

The vector field in Fig. 5.3a reveals that the first two are unstable (saddle-points). Defining \( f(R,N) = dR/dt \) and \( g(R,N) = dN/dt \), computing the four partial derivatives, the Jacobian of the non-trivial steady state is defined as

\[
J = \begin{pmatrix}
\frac{\partial f}{\partial R} & \frac{\partial f}{\partial N} \\
\frac{\partial g}{\partial R} & \frac{\partial g}{\partial N}
\end{pmatrix}_{|(\bar{R},\bar{N})} = \begin{pmatrix}
\left(r - \frac{2rK}{ca} \bar{R} - a\bar{N} & -aR \\
ca\bar{N} - \bar{R} & -\frac{\delta}{caK} - \frac{\delta}{c} \frac{\delta}{caN}
\end{pmatrix} = \begin{pmatrix}
-\alpha & -\beta \\
+\gamma & 0
\end{pmatrix}
\tag{5.12}
\]

where \( \alpha, \beta \) and \( \gamma \) are arbitrary positive values. Since the trace of this Jacobian matrix, \( \text{tr} = -\alpha < 0 \), and its determinant, \( \det = \beta\gamma = \beta\gamma > 0 \), both eigenvalues will be negative (i.e., have a negative real part), and that the non-trivial steady state is stable. Note that the trajectory in Fig. 5.3b is spiraling inwards, meaning that for the parameters that were used to make this figure the steady state is a stable-spiral point (and that the eigenvalues are a complex pair with a negative real part).

The \( R_{0} \) of the resource is not defined because the logistic growth term collapsed birth and death into a net growth rate. Since \( dN/dt \) has separate birth and death terms, one can calculate an \( R_{0} \) for the predator. Because the per capita birth rate of the consumers, \( caR \), is proportional to the prey density, we have to substitute the maximum prey density \( R = K \) into the birth rate, \( caR \) (because the \( R_{0} \) is calculated for the best possible circumstances; see Chapter 6). Doing so one arrives at \( R_{0} = \frac{caK}{\delta} \), and for this fitness \( R_{0} = 1 \) can indeed be used as an invasion criterion because the predator can only grow when \( caK > \delta \). The expression of the fitness, \( R_{0} = \frac{caK}{\delta} \), and the location of the consumer nullcline, \( R^{*} = \frac{\delta}{ca} \), resemble each other. This can be used to express \( R^{*} \) in terms of the \( R_{0} \), i.e., \( R^{*} = K/R_{0} \), which says that the degree by which a predator exhausts its prey population is completely determined by its \( R_{0} \). A predator with an \( R_{0} = 10 \) is therefore expected to deplete the prey density to 10% of its carrying capacity.
5.2 Replicating resources

Generalizing the Lotka-Volterra model

The Lotka-Volterra model assumed that the density-dependent terms of the resource are linear. What to expect for the consumption of replicating resources having a non-linear density-dependence? A simple approach to test this is to use the generalized form of the Logistic-growth equation (see Chapter 3), and write a “generalized” Lotka-Volterra model

$$\frac{dR}{dt} = rR(1 - \frac{R}{K})^m - aRN, \quad \frac{dN}{dt} = caRN - \delta N,$$  \hspace{1cm} (5.13)

which has identical $dN/dt = 0$ nullclines. The non-trivial $dR/dt = 0$ nullcline, $N = \frac{r}{\delta}(1 - \frac{R}{K})^m$, is concave when $m > 1$ and convex when $m < 1$ (see Fig. 5.4). Because, this does not affect the nature of the steady states in the phase plane, i.e., the local vector field in the neighborhood of the steady states remains the same, we conclude that similar model behavior is expected when resources have a non-linear density-dependence.

Generally the shape of the $dR/dt = 0$ nullcline for a resource having a mass-action consumption term reflects the per capita growth rate of the resource. Consider the more general form

$$\frac{dR}{dt} = [f(R) - aN] R,$$  \hspace{1cm} (5.14)

where $f(R)$ is an arbitrary function defining the per capita growth rate of $R$, and observe that the non-trivial nullcline can be written as $N = \frac{f}{a}(R)\frac{R}{c}$. Thus, whenever the per capita growth rate of $R$ is a monotonically declining function of $R$, we expect a declining “Lotka-Volterra like” nullcline of the resource in the phase space, provided we can cancel $R$ from the consumption term (here the mass-action, $aN$, term). We therefore expect more complicated nullclines for saturated consumption terms, e.g., $\frac{aNR}{K+R}$, from which we cannot cancel $R$. This is explored in Chapter 7.

When to expect the vertical $dN/dt = 0$ nullcline that we obtained throughout this chapter? The Lotka-Volterra model assumes that the birth rate of the consumers increases linearly with the per capita consumption, $aR$. This need not be true as a consumer’s birth rate may be a saturation function of its consumption; at a certain level of consumption the birth rate may slow.
down due to “diminishing returns”. Such a relationship, e.g., a per capita birth rate of
\[ g(aR) = \beta \frac{aR}{H + aR} = \beta \frac{R}{h + R}, \]  
(5.15)
where \( \beta \) is the maximum birth rate and \( h = H/a \), would correspond to
\[ \frac{dN}{dt} = \left[ \frac{\beta R}{h + R} - \delta \right] N, \]
(5.16)
with an \( R_0 = \beta/\delta \). Since, one can cancel the \( N = 0 \) solution after setting \( dN/dt = 0 \), we would still obtain a vertical nullcline (at \( R = \frac{h}{R_0 - 1} \)). Rewriting Eq. (5.16) in a more general form like
\[ \frac{dN}{dt} = [\beta f(R) - \delta] N, \]
(5.17)
one indeed obtains a vertical predator nullcline for any function \( f(R) \). Summarizing, a vertical predator nullcline is obtained whenever one can cancel the consumer, \( N \), from the consumer’s \( dN/dt = 0 \) equation. The nullcline will no longer be vertical when the consumer, \( N \), remains present in the term between the square brackets of Eq. (5.17). This will be the case when the functional response is predator dependent, i.e., when one replaces \( f(R) \) by \( f(R,N) \), or when the death rate is density dependent, e.g., when \( \delta \) is replaced by \( \delta(1 + \epsilon N^m) \). Whenever this leads to a negative density-dependence, the predator nullcline will typically be slanted to the right, which changes the effect of the consumer on itself from zero to negative (see Fig. 5.5e). The graphical Jacobian of the non-trivial steady state of a Lotka-Volterra model with a negative density-dependence of the consumer will therefore be
\[ J = \begin{pmatrix} - & - \\ + & - \end{pmatrix} \quad \text{with} \quad \text{tr} < 0 \quad \text{and} \quad \text{det} > 0. \]
(5.18)
The steady state remains stable, and most of the conclusions drawn in this chapter seem robust to allowing for direct competition among the consumers. In the next section we will see that allowing for positive density-dependence among the consumers, e.g., by cooperative killing, is also expected to lead to a stable steady state whenever the resource has sufficient negative density-dependence (see Fig. 5.5f).

**Horizontal and vertical nullclines**

The Lotka-Volterra model is sometimes written in a structurally unstable form without a carrying capacity of the resource:
\[ \frac{dR}{dt} = rR - aRN, \quad \frac{dN}{dt} = caRN - \delta N, \]
(5.19)
which has the normal vertical \( dN/dt = 0 \) nullcline at \( R = \frac{\delta}{ca} \) and a horizontal \( dR/dt = 0 \) nullcline at \( N = \frac{r}{a} \) (see Fig. 5.5b). This model is mathematically elegant but has limited biological relevance. The reason is that any small change of the model will lead to a qualitatively different type of behavior. The model is therefore said to be “structurally unstable”, and should not used it in biological research. Mathematicians use the model in teaching examples because the model is so elegantly simple. The non-trivial steady state is given by the perpendicular intersection of the nullclines, i.e. \( (\bar{R}, \bar{N}) = (\frac{\delta}{ca}, \frac{r}{a}) \), and the Jacobian of this steady state is
\[ J = \begin{pmatrix} r - a\bar{N} & -a\bar{R} \\ ca\bar{N} & ca\bar{R} - \delta \end{pmatrix} = \begin{pmatrix} 0 & -\delta/c \\ cr & 0 \end{pmatrix}. \]
(5.20)
Figure 5.5: The Lotka Volterra model with horizontal and slanted nullclines. Red lines depict the \( \frac{dR}{dt} = 0 \) nullclines, blue lines the \( \frac{dN}{dt} = 0 \) nullclines, and black lines trajectories. In Panels (a-c) the non-trivial consumer nullcline is a vertical line at \( R = \frac{\delta}{ca} \) (because \( \epsilon_N = 0 \) in Eq. (5.22)), and in Panels (d) and (f) the non-trivial resource nullcline is a horizontal line at \( N = \frac{r}{\epsilon} \) (because \( \epsilon_R = 0 \)). Panel (a) depicts the classical Lotka-Volterra model with a resource nullcline that is slanted downwards (due to their negative density-dependence, \( \epsilon_R > 0 \), allowing for a carrying capacity). In Panel (b) the resource nullcline is horizontal and the consumer nullcline vertical. In Panel (c) the resource nullcline is slanted upwards (positive density-dependence, \( \epsilon_R < 0 \)). In Panel (d) the consumer nullcline is slanted leftwards (positive density-dependence, \( \epsilon_N < 0 \)). In Panel (e) the consumer nullcline is slanted rightwards (\( \epsilon_N > 0 \)). In Panel (f) illustrates that sufficient negative density-dependence of the resource, \( \epsilon_R > 0 \), can compensate for positive density-dependence of the consumer, \( \epsilon_N < 0 \), and allow for a stable steady state (if the trace is negative). The graphical Jacobian of the non-trivial steady state is provided in the upper right corner, the determinant of these matrices is always positive and the sign of the trace is indicated. The perpendicular nullclines in Panel (b) intersect in a steady state with neutral stability, \( \text{tr} = 0 \) and \( \det > 0 \), and the behavior of the model is cycles of neutral stability that are defined by the initial condition (bullets). This Figure was with the model `lotka0.R`.

Because \( \text{tr}(J) = 0 \) the steady state has a “neutral” stability. The eigenvalues of this matrix are

\[
\lambda_{\pm} = \pm \sqrt{-\delta r} = \pm i \sqrt{\delta r};
\]

see Page 142. Because the eigenvalues have no real part the system is not structurally stable: any small change of the system will slightly change the angle at which the nullclines intersect, and make the equilibrium either stable or unstable. The behavior of this model are cycles of neutral stability: any perturbation of the population densities leads to a new cycle (see Fig. 5.5b).

Generally, one should be careful with perfectly horizontal or vertical nullclines because they result in Jacobi matrices with a zero on the diagonal, and they are typically the result of ignoring (perhaps minor) density-dependent effects. The non-trivial steady state will have the
biologically ill-defined neutral stability when the trace of the Jacobian is zero, i.e., when all
diagonal elements are zero. Since biological populations are typically expected to have at least
some effect on themselves, one should check the robustness of the results by slightly altering
the slope of both horizontal and vertical nullclines. Generally, one tests for structural stability
by making small changes to a model: the model is robust when small changes do not affect its
results. Here we study the effect of the slope of the non-trivial nullclines of Eq. (5.19), by adding
a small density-dependence to both ODEs,
\[
\frac{dR}{dt} = rN - aRN - \epsilon R^2 \quad \text{and} \quad \frac{dN}{dt} = caRN - \delta N - \epsilon N^2.
\] (5.22)

We have seen above that neutral stability is obtained in the absence of density-dependence, i.e.,
when \(\epsilon_R = \epsilon_N = 0\), leading to perpendicular nullclines (Fig. 5.5b). Negative density-dependence,
\(\epsilon > 0\), leads to a stable steady states (Fig. 5.5a and e), and positive density-dependence, \(\epsilon < 0\),
tends to destabilize (Fig. 5.5c and d). This analysis shows that the non-trivial steady state is
stable whenever at least one of the two populations has a negative density-dependence. When
either the resource or the consumer has a negative density-dependence, and the other population
a positive density-dependence, the sign of the trace will depend on the relative strength of the
density-dependent effects.

Returning to the classical Lotka-Volterra model model with a carrying capacity of the resource,
i.e., with \(\epsilon_R > 0\), we observe in Fig. 5.5f that a small positive density-dependence of the consumer
will lead to the graphical Jacobian
\[
J = \begin{pmatrix}
-p & -q \\
r & s
\end{pmatrix}
\] with \(\text{tr} = -p + s\) and \(\text{det} = ps + qr > 0\).

This steady steady state will be stable when \(s < p\), i.e., whenever the positive density-dependence
of the consumer is sufficiently small (see Fig. 5.5f). We conclude that a vertical consumer
nullcline is robust in a Lotka-Volterra model with a carrying capacity of the resource because
slanting the consumer nullcline slightly leftwards or rightwards does not affect the stability of
the steady state.

Resource densities are determined by consumption only

An unexpected consequence of the vertical consumer nullclines located at \(R = \frac{\delta}{ca}\) is that the
equilibrium density of the resource is determined by the parameters of the consumer, i.e., \(\delta, c\) and
\(a\) only, and is independent of its own parameters, \(s, w, r\) and/or \(K\) (see Fig. 5.6). This implies
that the effect of increasing the inflow of resource (e.g., nutrients), or increasing the carrying
capacity of the resource, increases the steady state of the consumer, and not that of the resource.
In ecology this is sometimes referred to as the “Paradox of enrichment” (Rosenzweig, 1971),
because euthrophication (enrichment) of 2-dimensional aquatic ecosystems comprised of algae,
\(R\), that are consumed by zooplankton, \(N\), leads to an increase of the zooplankton densities, and
not of the densities of the algae. Similar effects have been observed in 2-dimensional bacterial
food chains (Kaunzinger & Morin, 1998). This unexpected property of these models is due to
the fact that the consumers, \(N\), cancel from the \(dN/dt = 0\) equation upon solving steady states,
or sketching nullclines. Hence it is the steady state of the resource, \(\bar{R}\), that is solved when
setting \(dN/dt = 0\). Which steady state is solved from which equation not only depends on the
form of the equations, but also on the number of equations (see Chapter 8). As a consequence
predictions for how populations are expected to change upon changing one of the parameters may
crucially depend on the design of the model (De Boer, 2012). Since we do not know beforehand
Figure 5.6: Enrichment of the resource increases the steady state of the consumer only. The red lines depict the $dR/dt = 0$ nullcline and blue lines the $dN/dt = 0$ nullcline. In Panel (a) we consider the chemostat for two different influx rates, $s_1$ and $s_2$, of the resource. The trajectory corresponds to starting in the steady state with the low influx, $s_1$, and increasing the influx to the higher $s_2$. In Panel (b) we consider a Lotka-Volterra model for two different carrying capacities, $K_1$ and $K_2$ of the resource. The trajectory corresponds to starting in the steady state with the low $K_1$, and increasing the influx to the high $K_2$. Enrichment transiently increases both resource and consumer densities, but at the new steady state only the consumer is increased. Panel (a) was made with model `chemo.R` and Panel (b) with `lotka.R`.

which variable is solved from which equation, the general procedure for solving a steady state of a model with several ODEs, is to start with the most simple equations, and use the steady state values that they deliver for solving the more complex equations.

### 5.3 Summary

Consumer-resource models with a mass-action killing term tend to have a stable steady state where the consumer determines the density of the resource. Plotting the consumer on the vertical axis and the resource on the horizontal axis, the consumer nullcline is typically a vertical line located at the critical resource density, $R^*$, required for growth of the consumers, whereas the resource nullcline is a declining line intersecting the horizontal axis in the carrying capacity of the resource. Lotka Volterra type nullclines are obtained with replicating resources, and when the killing obeys a mass-action term. The shape of the nullcline of the resource then reflects the per capita growth of the resource. Saturated killing terms have little effect on the phase plane with resources that are maintained by a source, and are expected to have a major effect when the resource is maintained by replication.

### 5.4 Exercises

**Question 5.1. Sketch the per capita birth rate**

In Eq. (5.1) we considered a case of a population of cells in a closed environment containing a fixed amount, $R_T$, of nutrients. The cells consume nutrients as “building blocks” upon cell division,
and the rate of cell division was a saturation function, \( \frac{bR}{K + R} \), of the free nutrient availability, \( R = R_T - cN \), where \( c \) is the amount of nutrient contained in a single cell.

a. Sketch the per capita birth rate as a function of the population density \( N \) (hint: you may need to use the file `birth.R`).

b. Which of the density dependent function from Chapter 3 would corresponds best with this concave shape?

**Question 5.2. Neutrophils**

Let us return to the neutrophil project of Chapter 2 and complicate the model by giving the bacteria a carrying capacity, \( K \), and allowing neutrophils to arrive from the bone marrow:

\[
\frac{dB}{dt} = rB(1 - B/K) - kNB + R \quad \text{and} \quad \frac{dN}{dt} = s - dN ,
\]

where \( k \) is the mass-action killing rate, \( s \) the source of neutrophils from the bone marrow, and \( d \) is the death rate of neutrophils. Note that in this model the neutrophil dynamics are independent of the bacteria.

a. Sketch the nullclines and determine the stability of all steady states.

b. What is the parameter condition for which neutrophils control bacterial infections?

c. In Chapter 2 we argued that neutrophils should have a maximum killing rate, and we wrote \( \frac{dB}{dt} = rB(1 - B/K) - \frac{kNB}{K + B} \), where neutrophils maximally kill \( kh \) bacteria per unit of time. Sketch the nullclines and determine the stability of all steady states of the model extended with this saturated killing rate.

d. Which steady state now defines the condition for which neutrophils control small bacterial infections?

e. Next extend the ODE for the bacteria with an Allee effect, e.g., because they need to form a biofilm, and draw the nullclines with the third model in the file `neutrophils.R`. Does this make a difference?

f. In reality neutrophils are rapidly released from a reservoir in the bone marrow during an inflammatory immune response. The model `neutrophils2.R` adds an equation for the bone marrow, and if you have time you may want to study that model.

**Question 5.3. Lotka-Volterra models**

We have claimed that the Lotka-Volterra model is very general for the situation where a self-replicating population is controlled by a population that exerts its control by a mass-action term, and which is stimulated to replicate as a function of this control term.

a. Write an ODE model for a tumor that is controlled by natural killer cells that replicate when they encounter and kill tumor cells.

b. Write an epidemiological model for a population of susceptible individuals that grow logistically in the absence of the infectious agent, with new infections occurring when infected individuals encounter susceptible individuals.

c. Can you think of simple improvements of these models?

**Question 5.4. Desert**

Consider the following model for a vegetation \( V \) in a desert. The growth of the vegetation is limited in the amount of water \( W \) in the soil:

\[
\frac{dW}{dt} = a - bWV - cW \quad \text{and} \quad \frac{dV}{dt} = dWV - eV ,
\]

where \( a \) is the rainfall dependent water uptake in the soil, \( b \) is the extra water uptake and evaporation by the vegetation, \( c \) is the normal evaporation, \( d \) is the water dependent growth of the vegetation,
and \( e \) is the death rate of the vegetation.

For this exercise consider steady state situations.

a. How much water does the soil contain if there is no vegetation?

b. Suppose the rainfall increases two-fold because of a change in climate. How much water would the soil contain if there is still no vegetation?

c. How much water would the soil contain if there is a vegetation?

d. How much water would the soil contain if the rainfall increases two-fold in the presence of a vegetation?

e. Draw the nullclines, and determine the stability of the steady states.

f. How would the increased rainfall change these nullclines?

**Question 5.5. Phages and bacteria (Grind)**

Levin et al. (2013) and Jiang et al. (2013) describe several experiments in which they culture bacteria *in vitro* and infect them with phages to study the evolution of resistance. Some of their data are available on the website, and we ask you to fit the data to two different versions of their model. The first model is the system of delay differential equations (DDEs) that they present in their paper (Levin et al., 2013), which consists of a resource, \( R \), sensitive bacteria, \( B_0 \), resistant bacteria, \( B_1 \), infected bacteria, \( M \), and phages, \( P \), and where have kept their notation of the parameters (i.e., \( \delta \) is the infection rate, and \( v \) is the maximum consumption rate, and \( e \) is the amount of resources contained in a single bacterium),

\[
\begin{align*}
\frac{dR(t)}{dt} &= -\frac{evR(t)}{K + R(t)} \left( B_0(t) + (1 - s)B_1(t) \right), \\
\frac{dB_0(t)}{dt} &= \frac{vR(t)}{K + R(t)} B_0(t) - \delta B_0(t)P(t), \\
\frac{dB_1(t)}{dt} &= \frac{vR(t)}{K + R(t)} (1 - s)B_1(t), \\
\frac{dM(t)}{dt} &= \delta B_0(t)P(t) - \delta B_0(t - \lambda)P(t - \lambda), \\
\frac{dP(t)}{dt} &= b\delta B_0(t - \lambda)P(t - \lambda) - \delta P(t)[B_0(t) + B_1(t)]
\end{align*}
\]

where we explicitly indicate that variables either depend on time, \( t \), or on the time delay, \( t - \lambda \), that they use to model the eclipse phase. Infected bacteria therefore burst after \( \lambda = 0.4h \) to give rise to \( b \) phages, where \( b \) is the burst size. The \( \delta P(t)[B_0(t) + B_1(t)] \) term in the last equation is the absorption of phages to bacteria, i.e., phages are absorbed by resistant bacteria, but cannot infect them. This model is provided on the website as the file `Levin.R` with a parameter setting copied from Levin et al. (2013) (note that we have added the selection coefficient, \( s \), to allow for a fitness cost of the resistance mechanism). The two data sets in Figure 2 of the Levin et al. (2013) paper are available on the website as the files `LevinPG13Fig2B0.csv` and `LevinPG13Fig2.csv`. The first one depicts the growth of (sensitive) bacteria in the absence of phages, and the second one provides the total densities of the bacteria and the phages after infection.

a. Read the equations carefully and make sure that you understand the time delay.

b. Plot the data with the `Levin.R` script, and make sure you understand them.

c. Fit the first data set to check their estimate for the consumption rate, \( v \). It makes no sense to check the \( e \) and \( k \) parameters because we have no information on the resource densities.

d. Use your improved estimate of the consumption rate to fit the model to the infection data. Do you obtain a good fit, and what do you think of their parameter estimates?

e. Time delays are notoriously difficult to solve numerically, and the DDE solver of the `deSolve` library is doing an excellent job here. We could nevertheless check whether or not the data suggest that this fixed time delay of \( \lambda = 0.4h \) is truly required, by changing the last two
Killing and consumption

\[
\frac{dM(t)}{dt} = \delta B_0(t)P(t) - \frac{M(t)}{\lambda} \quad \text{and} \quad \frac{dP(t)}{dt} = \frac{bM(t)}{\lambda} - \delta P(t)[B_0(t) + B_1(t)],
\]

where \( \lambda \) still defines the average length of the eclipse phase, which is now exponentially distributed. This model is included in the Levin.R file under the function odeModel, and an example on how to fit the ODE model to the data is shown in the second half of the file.

Do the data require a fixed time delay? Is it wise to allow for a fitness cost?

f. Are there any other parameters that you would have added to the model?

**Question 5.6. Return time**

This is a challenging exercise that will show that one can also determine the return time around a steady state of a model composed of several ODEs, as it is defined by the dominant eigenvalue, i.e., \( T_R = \frac{1}{\lambda_{max}} \). We recommend that you make this exercise by carefully reading the answer. In the answer we compute the return time of the non-trivial steady state of the Lotka Volterra model and study how this depends on the mechanism of the density dependence of the prey. For reasons of simplicity we consider the case where the non-trivial steady state is a stable spiral point (and not a stable node), and first compute the return time of a general form of the Lotka Volterra model, e.g.,

\[
\frac{dR}{dt} = rR - \gamma R^2 - aRN \quad \text{and} \quad \frac{dN}{dt} = caRN - \delta N.
\]

a. Compute the return time of this general form.

b. What is the return time when we explicitly make the birth rate density dependent (e.g., replace \( rR - \gamma R^2 \) with \( bR[1 - R/k] - dR \))? Is the birth or the death rate determining the return time?

c. Address the same questions for a Lotka Volterra model with a density dependent death rate of the prey.

d. Interpret your results.
Chapter 6

The basic reproductive ratio $R_0$

In this book we frequently use the fitness, $R_0$, of a population to simplify steady state values, and the expressions for nullclines, which has facilitated their biological interpretation. Analyzing competition we will see in Chapter 9 that the population with the largest $R_0$, and not necessarily the one with the largest carrying capacity, is typically expected to win the competitive exclusion. In our consumer-resource models we observed that the depletion of resource species is (at least partly) determined by the $R_0$ of the consumer. We have defined $R_0$ as a fitness, namely as the maximum number of offspring that is produced over the expected lifespan of an individual, in a situation without competition or predation, i.e., as the mean lifetime reproductive success of a typical individual (Heffernan et al., 2005). The $R_0$ plays a central role in epidemiology, where it is defined as the expected number of individuals that is successfully infected by a single infected individual during its entire infectious period, in a population that is entirely composed of susceptible individuals (Anderson & May, 1991; Diekmann et al., 1990). Epidemics will grow whenever $R_0 > 1$. In order to provide a more general understanding of the basic reproductive ratio, $R_0$, this Chapter reviews some of the classical epidemiological approaches to define and calculate $R_0$.

6.1 The SIR model

The most classical model in epidemiology is the “SIR” model, for Susceptible, Infected, and Recovered individuals, e.g.,

\[
\frac{dS}{dt} = s - dS - \beta SI , \quad \frac{dI}{dt} = \beta SI - (\delta + r)I , \quad \text{and} \quad \frac{dR}{dt} = rI - dR , \quad (6.1)
\]

where $s$ defines the source of susceptibles, $d$ is their death rate, $\beta$ is an infection rate, $\delta$ the death rate of infected individuals (with $\delta \geq d$), $r$ is a recovery rate, and where recovered individuals have the same death rate as susceptibles. Let us consider a time scale of days, i.e., all death rates are per day. If the time scale at which susceptible individuals are produced and die is much slower than that of the epidemic one can simplify the first ODE into $dS/dt = -\beta SI$. Additionally, note that in this version of the SIR model the subpopulation of recovered individuals does not feed back onto the dynamics of the other two subpopulations, which means that they need not be considered when analyzing the establishment of an epidemic. Also note that setting $r = 0$ defines the “SI” model of an endemic infection that no one recovers from. Finally, one sometimes
writes Eq. (6.1) as
\[
\frac{dS}{dt} = s - dS - \frac{\beta SI}{N}, \quad \frac{dI}{dt} = \frac{\beta SI}{N} - (\delta + r)I, \quad \text{and} \quad \frac{dR}{dt} = rI - dR,
\] (6.2)
where \(N = S + I + R\) to define that the infection rate is proportional to the fraction of infected individuals.

The disease-free steady state of Eq. (6.1) is defined as \(\bar{S} = s/d\) and \(\bar{I} = \bar{R} = 0\), and the endemic equilibrium is defined as
\[
\bar{S} = \frac{\delta + r}{\beta}, \quad \bar{I} = \frac{s}{\delta + r} - \frac{d}{\beta}, \quad \text{and} \quad \bar{R} = \frac{r}{d} \bar{I} = \frac{rs}{d(\delta + r)} - \frac{r}{\beta},
\] (6.3)
which can only be present when \(\bar{I} > 0\), i.e.,
\[
\frac{s}{\delta + r} > \frac{d}{\beta} \quad \text{or} \quad \frac{s}{d} \frac{\beta}{\delta + r} > 1.
\] (6.4)

The \(R_0\) of Eq. (6.1) is defined by the rate, \(\beta S\), at which new cases are produced per infected individual over its entire infectious period of \(1/(\delta + r)\) days, in a fully susceptible population \(\bar{S} = s/d\), \(R_0\) is therefore defined as
\[
R_0 = \beta \bar{S} \frac{1}{\delta + r} = \frac{s}{d} \frac{\beta}{\delta + r}.
\] (6.5)
Since the epidemic will only spread if an infected individual is replaced by more than one secondary case, we require \(R_0 > 1\), which indeed corresponds to the threshold derived in Eq. (6.4). This also means that we could have derived the same condition from the Jacobian of the disease-free steady state, i.e., for the 2-dimension “SI” model with \(\bar{I} = 0\),
\[
J = \begin{pmatrix} -d & -\beta \bar{S} \\ 0 & \beta \bar{S} - \delta - r \end{pmatrix},
\] (6.6)
with eigenvalues \(\lambda_1 = \beta \bar{S} - \delta - r\) and \(\lambda_2 = -d\). The parameter condition \(R_0 > 1\) indeed corresponds to the transcritical bifurcation point, \(\lambda_1 = 0\), at which the endemic steady state becomes positive.

Note that \(R_0\) is dimensionless, i.e., it is the expected number of secondary cases per infectious period. Since \(R_0\) is not a rate, it cannot define how fast the epidemic is expanding. Indeed the initial rate at which an epidemic is expected to grow is here defined by
\[
\frac{dI}{dt} = \beta \bar{S}I - (\delta + r)I = \left(\frac{\beta s}{d} - \delta - r\right) I = r_0 I,
\] (6.7)
where the rate \(r_0\) is the initial per capita net growth rate of the infected individuals. Observe that this growth rate, \(r_0\), corresponds to the dominant eigenvalue of the Jacobi matrix in Eq. (6.6), and that applying the “invasion criterion” \(r_0 > 0\), i.e., \(\frac{\beta s}{d} > \delta + r\) or \(\frac{s}{d} \frac{\beta}{\delta + r} > 1\), is again the same as requiring \(R_0 > 1\). The net growth rate, \(r_0\), over the entire infectious period, \(L = 1/(\delta + r)\), should obviously be related to the \(R_0\), i.e.,
\[
R_0 = 1 + r_0L = 1 + \frac{r_0}{\delta + r} = \frac{s}{d} \frac{\beta}{\delta + r} \quad \text{or} \quad r_0 = \frac{R_0 - 1}{L} = (R_0 - 1)(\delta + r)
\] (6.8)
where the 1 is required to compensate for the fact that \(R_0\) is defined by the new cases only, whereas the rate \(r_0\) includes the death rate.
Finally, defining the disease free steady state as a carrying capacity, $K = s/d$, one can see that the ultimate degree of depletion of the susceptibles is fully determined by the $R_0$, i.e., in Eq. (6.3) we see that $\bar{S} = K/R_0$. Summarizing, $R_0$ is a valuable and meaningful concept in epidemiology; there are several methods to compute an $R_0$, where the one that calculates the number of secondary cases produced during the infectious period of an infected individual seems the most intuitive.

### 6.2 The SEIR model

The definition of the $R_0$ becomes more complicated in systems where the infection involves several stages. Adding a stage of exposed individuals, $E$, that are not yet infectious, one obtains the SEIR model

$$\begin{align*}
\frac{dS}{dt} &= s - dS - \beta SI, \\
\frac{dE}{dt} &= \beta SI - (\gamma + d)E, \\
\frac{dI}{dt} &= \gamma E - (\delta + r)I, \\
\frac{dR}{dt} &= rI - dR, \\
\end{align*}$$

(6.9)

where the exposed individuals become infectious at a rate $\gamma$ (and have the same death rate as the susceptibles). A general method for deriving the $R_0$ for multi-stage models is the “next generation method” devised by Diekmann et al. 1990, and involves the definition of a matrix collecting the rates at which new infections appear in each compartment, and a matrix defining the loss and gains in each compartment. This method is general but its explanation would be too involved for the short summary in this chapter (if you are interested read any of the following: Heffernan et al. 2005 or Diekmann et al. 2012; 1990). Eq. (6.9) is simple enough to define the $R_0$ by the more intuitive “survival” method. The initial rate at which an infected individual produces novel infections remains $\beta \bar{S}$, and this will occur over an infectious period of $1/(\delta + r)$ time steps, but since not all exposed individuals become infectious (i.e., only a fraction $\gamma/(\gamma + d)$ are expected to survive and become infectious), we need to multiply with this fraction and obtain

$$R_0 = \frac{s}{d} \frac{\beta}{\delta + r} \frac{\gamma}{\gamma + d}.$$

(6.10)

Solving $\bar{E} = \frac{\delta + r}{\gamma} I$ from $dE/dt = 0$, and substituting that into $dI/dt = 0$ delivers $\bar{S} = \frac{\gamma + d}{\gamma} \frac{\delta + r}{\beta}$, which when substituted in $dS/dt = 0$ gives

$$\bar{I} = \frac{s}{\beta \bar{S}} - \frac{d}{\beta} = \frac{\gamma}{\gamma + d} \frac{s}{\delta + r} - \frac{d}{\beta},$$

(6.11)

which can only be positive when

$$\frac{\gamma}{\gamma + d} \frac{s}{\delta + r} > \frac{d}{\beta} \quad \text{or} \quad \frac{s}{d} \frac{\beta}{\delta + r} \frac{\gamma}{\gamma + d} > 1 \quad \text{or} \quad R_0 > 1,$$

(6.12)

confirming that the $R_0$ derived by the survival method again corresponds to the parameter threshold at which the epidemic steady state becomes positive. The initial growth rate, $r_0$, of an epidemic in the SEIR model now depends on two ODEs, $dE/dt$ and $dI/dt$, and can still be computed because these ODEs are linear around the disease-free steady state $\bar{S} = s/d$. Solving these ODEs and applying the invasion criterion $dI/dt > 0$, or deriving the dominant eigenvalue of the Jacobian of the disease-free equilibrium, would therefore be alternative means to calculate the $R_0$ of this SEIR model. Summarizing, there are various ways to one can compute an $R_0$ for infections involving multiple stages, where the next generation method (Diekmann et al., 1990, 2012) is the most general (but is not explained here).
6.3 Fitness in consumer-resource models

In this book we have similarly defined the $R_0$ of resource and consumer populations to facilitate the biological interpretations of otherwise more complicated expressions. For instance re-consider the Lotka-Volterra model with explicit birth and death rates for the resource,

$$\frac{dR}{dt} = bR(1 - R/k) - dR - aRN \quad \text{and} \quad \frac{dN}{dt} = caRN - \delta N , \quad (6.13)$$

with a carrying capacity $\bar{R} = K = k(1 - d/b)$. Using the survival method, the $R_0$ of the resource is defined by the maximum number of offspring, $b$ per day (note that the $(1 - R/k)$ term can only decrease the birth rate), over its expected life span of $1/d$ days, i.e., $R_{0R} = b/d$. One can also easily see that the resource population can only invade when the maximum birth rate, $b$, exceeds the death rate, $d$, i.e., when $b/d > 1$, and define the $R_0$ this way (like above for the SIR model). Given this $R_0$ of the resource the carrying capacity can be written as $K = k(1 - 1/R_{0R})$ (see Chapter 3).

Similarly, the $R_0$ of the consumer is its maximum birth rate, $ca\bar{R}$, times its expected life span, $1/\delta$, i.e., $R_{0N} = caK/\delta$. Likewise, see that the maximum consumer birth rate, $caK$, should exceed its death rate, $\delta$, implying that $R_{0N} = caK/\delta > 1$. Hence, one can again derive the $R_0$ parameters of this model in several ways. The $R_0$ of the consumer can be used to simplify the expression for the non-trivial steady state of the resource, which is solved from $dN/dt = 0$, i.e., $\bar{R} = \delta ca$, and can now be expressed as $\bar{R} = K/R_{0N}$. This reveals the biological insight that the depletion of the resource population is proportional to the $R_0$ of the consumer (like in the SIR model), which even means that one can estimate the $R_0$ from an observed level of depletion.

We have also considered models where the birth rate of the consumer is a saturation function of its consumption, e.g.,

$$\frac{dR}{dt} = bR(1 - R/k) - dR - aRN \quad \text{and} \quad \frac{dN}{dt} = \frac{\beta RN}{h + R} - \delta N , \quad (6.14)$$

with the same equation, $R_0$, and carrying capacity of the resource. Now the $R_0$ of the consumer can either be defined as $R_0 = \beta/\delta$, because $\beta$ is a maximum birth rate of the consumer at infinite resource densities, or —more classically— as $R_0 = \frac{\beta K}{\delta h + K}$, which uses the consumer birth rate at carrying capacity of the resource for the maximum consumer birth rate. Since we aim for simplifying mathematical expressions, the simpler $R_0 = \beta/\delta$ is typically the most useful definition. When $h \ll K$ the two definitions of $R_0$ approach one another. If not, an invasion criterion would correspond to the more complicated $R_0$, because consumers can only invade into a resource population at carrying capacity when $\frac{\delta K}{\delta h + K} > \delta$. The simpler form of the consumer fitness, $R_0 = \beta/\delta$, instead allows us to simplify the expression for the steady state of the resource, which is again solved from $dN/dt = 0$, i.e., $\bar{R} = \frac{\delta h}{\beta - \delta} = \frac{h}{R_0 - 1}$, revealing that the depletion of the prey still increases with the $R_0$ of the predator, but that this is no longer proportional the either of the $R_0$s.

6.4 Exercises

Question 6.1. SARS
Consider a deadly infectious disease, e.g., SARS, and write the following model for the spread
6.4 Exercises

of the disease:

\[
\frac{dI}{dt} = \beta I - \delta I ,
\]

where \( I \) is the number of human individuals infected with SARS, \( \beta \) is the number of new cases each infected individual causes per day, and \( 1/\delta \) is the number of days an infected individual survives before he/she dies of SARS. Since an infected individual here is expected to live for \( 1/\delta \) days, and is expected to cause \( \beta \) new cases per day, the \( R_0 \) of this disease is \( \beta/\delta \).

\[ \text{a.} \quad \text{It has been estimated that on average a SARS patient causes } R_0 = 3 \text{ new cases, during a typical disease period of two weeks (Lipsitch et al., 2003). Most patients die at the end of these two weeks. How long does it take with these parameters to reach the point where } 3 \times 10^9 \text{ individuals (i.e., half of the world population) are infected? Note that at this time point the healthy uninfected pool is less than half of the world population because many people will have died (i.e., your simple estimate is a worst case estimate).} \]

\[ \text{b.} \quad \text{Do you think this is a realistic estimate? How would you extend the model to make it more realistic?} \]

**Question 6.2. SIR model**

In Eq. (6.2) we define a frequency dependent SIR model where susceptible individuals meet an expected number of other individuals per day, and where the infection rate is proportional to the fraction of infected individuals.

\[ \text{a.} \quad \text{What is the } R_0 \text{ of this model, and what is the initial growth rate, } r_0, \text{ of the epidemic?} \]

\[ \text{b.} \quad \text{Sketch the 2-dimensional nullclines of a frequency dependent SI version of this model (by setting } R = 0). \]

\[ \text{c.} \quad \text{Do these identify potential problems, and how would your repair them?} \]

**Question 6.3. Measles (Grind)**

The model of Eq. (6.2) was used to describe epidemics of measles in Niamey (Niger), and this question is based upon one of the excellent online practicals by Aaron A. King (http://kinga.github.io/short-course/), and the paper by Grais et al. 2008. The data was collected in three communities in Niamey, here called A, B and C, and represent weekly samples on the number of infected individuals in each community. On the website we provide the original data (niamey.csv) and three separate text files for each community. Because the dynamics of a measles epidemic have a time scale of weeks, whereas the birth and death rates of the people in Niamey have a time scale of years, we will fit the data to Eq. (6.2) after setting \( s = d = 0 \) using the model sir.R in Grind. For simplicity we will also assume that measles is relatively benign, and hence that \( \delta = 0 \), and trace an unknown population of susceptible individuals, \( S(0) \) (probably mostly children), and describe the epidemic in this sub-population (i.e., at the end most of these children will be in the recovered class). Finally, we assume that you know that infection by measles in a healthy child takes about a week, i.e., \( 1/r = 1 \text{ week} \).

\[ \text{a.} \quad \text{Read the niameyA.txt data into Grind and plot it on a logarithmic scale.} \]

\[ \text{b.} \quad \text{To have an informed guess for the infection rate, } \beta, \text{ and the initial number of infected individuals, } I(0), \text{ we follow Aaron King’s suggestion to first study the exponential growth phase of the infection (i.e., the first 8 weeks). This can be done by linear regression on the log-transformed data (i.e., } \text{fitlm} \log(I) \text{ time, data=subset(data, time<=8)})) \text{, which delivers an offset defining ln}[I(0)] \text{ and a slope defining } r_0 = \beta - r \text{ (see the previous exercise). Use these two estimates to set } I(0) \text{ and the initial guess for } \beta. \]

\[ \text{c.} \quad \text{Subsequently, fit the data starting with } S(0), \beta, \text{ and } r \text{ as free parameters. Do you obtain a good fit? Are all parameters identifiable? What happens if you fix } r = 1 \text{ w}^{-1}? \]

\[ \text{d.} \quad \text{In the last two lines of the sir.R file we estimate confidence intervals on the parameters by bootstrapping the data a 500 times. (Bootstrapping means fitting many samples of the data by randomly picking data points from the set; see Section 13.8). Do you get reasonable bounds on the parameters? Are the parameters correlated (see the output of the } \text{pairs}()
function)?

e. What would happen if you fit the same data with Eq. (6.1), where the infection rate depends on the absolute number of individuals?
Chapter 7

Functional response

Most models in the previous chapter were based upon a mass-action killing term. One of these resource-consumer models suggested that qualitatively different resource nullclines are expected for more complicated killing terms. In biology mass-action interaction terms are often a simplification that is valid only at low population densities. Mass-action terms can become very large when either of the involved populations becomes large, and, as a consequence, the per capita rate of the other population may become unrealistically large. For example, the rate at which bacteria are infected by phages should not become extremely fast when the average number of phages surrounding a single bacterium becomes extremely large. Productive infection takes time because the phages have to attach, enter the cell, and interact with the intracellular machinery of the bacteria, and this “handling” time is not accounted for if infection is modeled with a mass-action infection term (unless every subprocess, such as the attachment and entry, are implemented as subsequent steps in the model).

Saturation functions provide a semi-mechanistic short-cut for limiting the interaction rate at high population densities, and in earlier chapters we have used Hill functions and exponential functions to allow for maximum birth rates at high resource densities. A famous paper by Holling in 1959 (Holling, 1959) defined a number of such saturation functions, by using his secretary, whom was picking up artificial “resource” items, as an experimental consumer. These functions were coined “functional responses”, and Holling (1959) defined three non-linear responses:

$$f(R) = a \min\left(1, \frac{R}{2h}\right), \quad f(R) = a \frac{R}{h + R} \quad \text{and} \quad f(R) = a \frac{R^2}{h^2 + R^2},$$

(7.1)

which are called the Holling type-I, II, and III functions, respectively (see Fig. 7.1). All three functions approach a maximum corresponding to the maximum amount of resource a consumer can catch within a certain time unit. Holling’s motivation for this maximum was the “handling time”: even at an infinite resource density the consumer cannot consume the resource infinitely fast because of the time required to handle, eat, and digest the resource (e.g., his blind-folded secretary had to find an item with her hands, pick it up, and store it). There is indeed a simple way to derive Eq. (7.1b). Let $n = atR$ be the number of prey items picked up by the secretary, $a$ her attack rate, $t$ the amount of time available for searching, and $R$ the number of prey-items on the table. The time available for searching, $t$, is the total time of the experiment, $T$, minus the time spend on handling the items found, $bn$. Substituting, $t = T - bn$ into $n = atR$ gives

$$n = a(T - bn)R \quad \text{or} \quad n = \frac{aTR}{1 + abR} = \frac{a'R}{h + R},$$

(7.2)
where \( a' = T/b \) and \( h = \frac{1}{ab} \), i.e., her handling time \( b \) per item defines the maximum, \( a' \), and part of the saturation constant, \( h \).

Eq. (7.1) shows that the Holling type-II and type III responses are conventional Hill functions. Thus, we know that \( a \) is the maximum consumption rate, and that \( h \) is the resource density at which the function consumption is half maximal. Synonyms of the type-II and III responses are the “Monod saturation” (Monod, 1949; Holling, 1959), and the “sigmoid” functional response, respectively. Both will be discussed at length in this chapter. The type-I response is linear until the per capita consumption rate equals the maximum of \( a \) per time unit, an extension of this will be discussed in one of the exercises.

### 7.1 Monod functional response

We start simple by considering a Monod saturated per capita killing rate of a logistically replicating resource, \( R \), by a consumer, \( N \),

\[
\frac{dR}{dt} = rR(1 - R/K) - \frac{aRN}{h + R} = rR(1 - R/K) - \frac{a'RN}{1 + R/h},
\]  

(7.3)

where \( a \) is the maximum number of resource consumed (and/or killed) per consumer per unit of time, \( h \) is the resource density at the consumption rate is half-maximal, and \( a' = a/h \) is a mass-action killing rate. The latter form of the equation reveals that when the saturation constant, \( h \), is large this model approaches the Lotka-Volterra model (here large would mean \( h \gg K \)). The \( dR/dt = 0 \) isocline can be found by setting Eq. (7.3) to zero, and solving

\[
R = 0 \quad \text{and} \quad N = \frac{r}{a} \left(1 - \frac{R}{K}(h + R)\right),
\]  

(7.4)

where the latter is a parabola crossing \( N = 0 \) at \( R = K \) and \( R = -h \), and having its maximum value at \( R = (K - h)/2 \). In Fig. 7.2 this nullcline is depicted for positive population densities. When \( h < K \), the resource nullcline is a parabola with an unstable part having vectors pointing away from it in the region where \( R < \frac{K - h}{2} \) (see Fig. 7.2a–c). When \( h \geq K \) the resource nullcline is a monotonically declining function resembling that of the (generalized) Lotka-Volterra model.
7.1 Monod functional response

Figure 7.2: Qualitatively different phase spaces of the Monod saturated model of Eq. (7.3) and (7.5). The red parabola is the resource nullcline intersecting the horizontal axis at \( R = K \), and the vertical axis at \( N = rh/a \). The blue vertical consumer nullcline is located at \( R^* = h/(R_0 - 1) \). Black lines are trajectories starting just above the carrying capacity of the resource. In Panels (a-c) we set \( h \ll K \) such that the maximum of the parabola that is located at \( R = (K - h)/2 \), occurs approximately half-way the carrying capacity. In Panel (a) \( R^* > K \), making the carrying capacity of the resource is the only attractor. In Panel (b) \( R^* > (K - h)/2 \), making the non-trivial steady state stable. In Panel (c) \( R^* < (K - h)/2 \), making the non-trivial steady state unstable, and giving rise to a stable limit cycle, corresponding to periodic behavior. In Panel (d) \( h = K \), which puts the top of the parabola at \( R = 0 \) and makes the \( dR/dt = 0 \) nullcline monotonically declining. This figure was made with the model monod.R.

(see Fig. 7.2d). For the consumer it is typically assumed that the per capita birth rate is proportional to its per capita consumption,

\[
\frac{dN}{dt} = \frac{caRN}{h + R} - \delta N ,
\]

which is identical to the consumer equation in Eq. (5.6), and therefore has the same \( R_0 = \frac{ca}{\delta} \) and nullcline at \( R = \frac{h}{R_0 - 1} \). This nullcline again defines the resource density, \( R^* \), that the consumers require to expand, i.e., on the right-hand side of the nullcline the vector-field points upwards.

In ecology this Monod-saturated model is sometimes referred to as the Rosenzweig-McArthur model. For a given setting of the parameters, it can have three steady states: two trivial states \((\bar{R}, \bar{N}) = (0, 0)\) and \((K, 0)\), and a non-trivial co-existence state that is present when \( R^* < K \). Fig. 7.2 depicts qualitatively different phase spaces of the model. In Fig. 7.2a the consumer cannot maintain itself because \( R^* > K \), i.e., even the maximum resource density \( K \) is insufficient. As a
Figure 7.3: Bifurcation diagrams illustrating the effect of increasing the carrying capacity, \( K \) (starting at a \( K_0 > 0 \)). Heavy red lines represent stable steady states, light blue lines unstable steady states, and black points minima and maxima of a stable limit cycle. Panel (c) depicts the trajectory of Fig. 7.2c as a time plot (\( R \): red and \( N \): blue). This figure was made with the model `monod.R`.

consequence, \((\bar{R}, \bar{N}) = (K, 0)\) is a stable steady state (see the vector field in Fig. 7.2a). Indeed systems containing too little nutrients are expected to have such a low carrying capacity of the resource that it is unable to sustain a consumer population.

Fig. 7.2b depicts the situation where the consumer nullcline is located at the right-hand side of the top of the parabolic resource nullcline, i.e., when \((K - h) / 2 < R^*\). The local vector field is identical to that of the Lotka Volterra model:

\[
J = \begin{pmatrix} -\alpha & -\beta \\ \gamma & 0 \end{pmatrix} \quad \text{with} \quad \text{tr} = -\alpha < 0 \quad \text{and} \quad \text{det} = \beta \gamma > 0. \tag{7.6}
\]

Thus, the non-trivial steady state will be stable whenever the consumer nullcline intersects the resource nullcline at the right-hand side of the maximum of the parabola. The trajectory starting with few consumers in a resource population at carrying capacity reveals that for the parameters that were used to make Fig. 7.2b, the steady state is a stable spiral point. In Fig. 7.2c the nullclines intersect at the left-hand side of the maximum of the parabola. Here the resource nullcline is unstable, and from the local vector field one now reads from the graphical Jacobian

\[
J = \begin{pmatrix} \alpha & -\beta \\ \gamma & 0 \end{pmatrix} \quad \text{that} \quad \text{tr} = \alpha > 0 \quad \text{and} \quad \text{det} = \beta \gamma > 0. \tag{7.7}
\]

The steady state is unstable because the local feedback of the resource on itself is positive: increasing the resource increases its growth rate. The reason for this positive feedback is the saturated functional response, as increasing the resource density will decrease the per capita killing rate, \( a / (h + R) \), of the resource. The behavior of the model in this situation is a stable limit cycle (see Fig. 7.2c and Fig. 7.3c). One can indeed check that in Fig. 7.2c none of the trivial steady states, i.e., \((\bar{R}, \bar{N}) = (0, 0)\) or \((K, 0)\), is an attractor of the system. Therefore, the consumer cannot go extinct, and the stable limit cycle has to be the global attractor of the system. Fig. 7.2d just confirms that this model becomes similar to the Lotka-Volterra model when \( h \geq K \).
Paradox of enrichment

Models with the “humped” resource nullcline of Fig. 7.2 have been used for the famous Paradox of enrichment (Rosenzweig, 1971). Rosenzweig studied eutrophication (enrichment) of lakes with algae and zooplankton, and showed that increasing the carrying capacity of the algae failed to increase the density of the algae. The enrichment with nutrients for the algae rather increased the zooplankton density, lead to destabilization of the non-trivial steady state, and ultimately to stable limit cycles with such a wide amplitude that so closely approach the axes of the phase plane that species may go extinct (Rosenzweig, 1971). This ultimate loss of species richness was coined the “paradox of enrichment”. Because the amplitude of limit-cycles of algae and zooplankton observed in the field tend to be much smaller than those in these models (Arditi & Ginzburg, 1989; Ginzburg & Akçakaya, 1992; McCauley et al., 1999; Murdoch et al., 2002; Scheffer & De Boer, 1995), it remains unclear whether or not the paradox of enrichment occurs in nature. Nevertheless, the bifurcation diagram in Fig. 7.3 reveals that increasing the carrying capacity, $K$, of this model:
1. first increases the density of the algae as long as there is no zooplankton,
2. subsequently leaves the density of the algae at $R^* = h/(R_0 - 1)$ and increases the zooplankton density,
3. and finally destabilizes the system by a Hopf-bifurcation (see Chapter 11), leading to oscillations with larger and larger amplitudes.

Thus, enrichment of an oligotrophic system is expected to first increases the diversity of the system, i.e., when $R^* > K$, but could ultimately decrease the diversity by too large amplitude limit cycles (see Fig. 7.3).

Limit cycle behavior

When the non-trivial steady state is unstable the model displays oscillatory behavior and approaches a stable limit cycle (Fig. 7.2c and Fig. 7.3c). On the limit cycle the consumer and resource densities oscillate in an “out of phase” manner because consumer densities increase only after the resource has increased. Oscillatory behavior is frequently observed in biological populations. A famous ecological example is the oscillatory behavior of lynx and hare populations in Canada, that were discovered in the records of the furs brought in by hunters in the last century. Surprisingly, the hare and lynx cycles are not always out of phase, and ecologists are performing experiments to understand the precise mechanism underlying this famous oscillation (Stenseth et al., 1999). Another ecological example of consumer resource oscillations are the cycles of algae and zooplankton in the spring (McCauley et al., 1999; Fussmann et al., 2000; Murdoch et al., 2002; Yoshida et al., 2003). Bacterial population oscillate over several orders of magnitude because of toxin production (Cornejo et al., 2009). Periodic behavior is easily obtained in mathematical models and is frequently observed in nature. Note that these oscillations are autonomous: there is no periodic forcing from outside driving this. The periodic behavior arose by the destabilization of the non-trivial steady state, i.e., at a Hopf bifurcation (see Fig. 7.3 and Chapter 11).

Formal derivation of the Monod response by a QSSA

The Monod functional response can be derived in the same way as the conventional Michaelis-Menten enzyme expression was obtained. To this end one splits the consumers, $N$, into a
subpopulation \( C \) that is actually handling the resource, and a free subpopulation, \( F \), that is trying to catch the resource, \( R \). By conservation one knows that \( N = F + C \). To describe the consumers catching and handling resource one could write

\[
\frac{dC}{dt} = kRF - hC \quad \text{or} \quad \frac{dC}{dt} = kR(N - C) - hC ,
\]

where \( k \) is a rate at which the free consumers catch resource, and \( 1/h \) is the time they require to handle the resource. Since the time scale of handling resource is much more rapid than the time scale at which the resource and consumers reproduce, one can make a quasi steady state assumption for the complex, \( dC/dt = 0 \), and obtain that

\[
C = \frac{kNR}{h + kR} = \frac{NR}{h' + R} ,
\]

where \( h' = h/k \) is the resource density at which half of the consumers are expected to be handling resource. To see how this ends up in the resource population one could add \( dR/dt = kRF - hC = 0 \) to an ODE for the resource, e.g., \( dR/dt = rR(1 - R/K) - kRF \), giving

\[
\frac{dR}{dt} = rR(1 - R/K) - hC = rR(1 - R/K) - \frac{hNR}{h' + R} ,
\]

which is a normal Holling type-II functional response. For the consumers one could argue that the birth rate should be proportional to the number of consumers that are handling and consuming resource, and write that

\[
\frac{dN}{dt} = cC - dN = \frac{cNR}{h' + R} - dN ,
\]

which again delivers the Monod saturated consumer resource model.

One can also use this analysis to learn how to write ODEs for a consumer consuming several different resource. Let \( k_i \) be the catch rate for resource \( i \), and assume for simplicity that all resource species require the same handling time. By the \( k_i \) parameter, the consumer can have different preferences for the different resource species. The conservation equation now becomes \( N = F + \sum_i C_i \), and for each complex one writes \( dC_i/dt = k_iR_iF - hC_i = 0 \). Summing all \( dC_i/dt \) equations yields

\[
\sum_i \frac{dC_i}{dt} = \sum_i k_iR_iF - h \sum_i C_i = \sum_i k_iR_i(N - \sum_j C_j) - h \sum_i C_i = 0 ,
\]

which can be rewritten into

\[
\sum_i C_i = \frac{N \sum_i k_iR_i}{h + \sum_j k_jR_j} \quad \text{and, hence,} \quad C_i = \frac{Nk_iR_i}{h + \sum_j k_jR_j} .
\]

For each resource, \( i \), one can again add \( dC_i/dt = k_iR_iF - hC_i = 0 \) to

\[
\frac{dR_i}{dt} = rR_i(1 - R_i/K_i) - k_iR_iF \quad \text{giving} \quad \frac{dR_i}{dt} = rR_i(1 - R_i/K_i) - \frac{hR_iN}{h + \sum_j k_jR_j} .
\]

For the consumers one would argue that their reproduction is proportional to all consumers in complex with resource, and write that

\[
\frac{dN}{dt} = c \sum_i C_i - dN = \frac{cN \sum_i k_iR_i}{h + \sum_j k_jR_j} - dN .
\]

Although this all works out quite nicely, this does not imply that saturated functional responses are truly due to the handling time derived here, or the one defined in Eq. (7.2). One could also argue that saturation is simply due to satiation of the consumers at high resource densities.
7.2 Sigmoid functional response

Tumor cells are quite resistant to the cytotoxic effect of killer cells in the immune system, and may require multiple contacts with such cytotoxic cells before they die. At low killer cell densities this involves cooperative effects where tumor cells are destroyed by interacting with multiple killer cells, and this gives rise to a sigmoid functional response (Gadhamsetty et al., 2017). Additionally, large herbivores hardly graze if the vegetation cover is very poor. Finally, at low prey densities individuals can hide efficiently in “refugia”, leading to low consumption rates at low densities. Although the latter two examples can be described with a “shifted” Monod saturated functional response, i.e., \( f(R) = \frac{R-k}{h+R-k} \), where \( k \) is the resource density where consumption starts, this is typically modeled with a sigmoid functional response.

Replacing the saturated functional response of the previous model with a sigmoid Hill function, we obtain

\[
\frac{dR}{dt} = rR(1 - R/K) - \frac{aR^2N}{h^2 + R^2} \quad \text{and} \quad \frac{dN}{dt} = \frac{caR^2N}{h^2 + R^2} - \delta N .
\] (7.17)
The $R_0$ of the consumer remains $R_0 = ca/\delta$, and the $dN/dt = 0$ nullcline remains a straight line that is now located at $R^* = h/\sqrt{R_0 - 1}$ (see Fig. 7.5). Sketching the nullcline of the resource is much more challenging. Setting $dR/dt = 0$ and canceling the $R = 0$ solution, we obtain

$$N = \frac{r(h^2 + R^2)}{aR} \left(1 - \frac{R}{K}\right),$$

(7.18)

which has a vertical asymptote at $R = 0$, and is zero when $R = K$. One can take the derivative of this function to find its minima and maxima (see Section 13.6 in the appendix), but because this all becomes rather complicated, one typically constructs the nullcline graphically (Noy-Meir, 1975). The procedure is to separate the ODE into its positive logistic growth term, $f(R) = rR(1 - R/K)$ and its negative sigmoid predation term, $g(R, N) = \frac{aR^2N}{h^2 + R^2}$. Both functions can be sketched as a function of the resource density $R$ (see Fig. 7.4a), and the points where they intersect correspond to points on the $dR/dt = 0$ nullcline. The logistic function, $f(R)$, is a parabola intersecting the horizontal axis at $R = 0$ and $R = K$. The consumption term, $g(R, N)$, is a sigmoid function with a maximum increasing with the consumer density, $N$. Sketching $g(R, N)$ for various values of $N$ we read in Fig. 7.4a at which $R$ values $g(R, N) = f(N)$, and copy these $R$ values with the corresponding value of $N$ as a point of the nullcline in Fig. 7.4b.

To know where in Fig. 7.4a the curves intersect it is crucial to know their slopes around the origin, which is determined by their local derivative, i.e.,

$$\partial_R f(R) = r - 2rR/K, \quad \text{which for } R = 0 \text{ equals } r,$$

(7.19)

showing that the local slope of the parabola in the origin is $r$,

$$\partial_R g(R, N) = \frac{2aRN}{h^2 + R^2} = \frac{2aR^3N}{(h^2 + R^2)^3}, \quad \text{which for } R = 0 \text{ yields } 0,$$

(7.20)

confirming that the sigmoid curves leave the origin with slope zero. The sigmoid curves therefore always start below the parabola, whatever the consumer density $N$. Because the maximum of the parabola is $rK/4$, and that of the predation term $aN$, the $g(R, N)$ functions will exceed the top of the parabola at sufficiently high values of $N$ (see Fig. 7.4a). Since $h < K$ this leads to a $dR/dt = 0$ nullcline with a minimum and a maximum in Fig. 7.4. When $h$ is too large the nullcline declines monotonically (see Fig. 7.5d). In Section 13.6 in the appendix we derive that the nullcline is non-monotonic when $h < \frac{K}{3\sqrt{3}} \approx \frac{K}{5}$, that the minimum of the nullcline is located below $R = h\sqrt{K}$, and the maximum remains located around $R = K/2$.

When $R^* < K$, the model has three steady states: the trivial $(0, 0)$ and $(K, 0)$ saddle points, and a non-trivial steady state that in Fig. 7.5(a) and (b) is very similar to the monod-saturated model. When $R^* > K/2$ the state is stable (Fig. 7.5a), and when the consumer nullcline is located in between the minimum and the maximum the steady state is unstable, such that the one and only attractor of the model is a stable limit cycle (Fig. 7.5b). There is a qualitatively new steady when the vertical consumer nullcline is located on the left-hand side of this minimum, and the graphical Jacobian of this new steady state is

$$J = \begin{pmatrix} -\alpha & -\beta \\ \gamma & 0 \end{pmatrix} \quad \text{with } \text{tr}J < 0 \text{ and } \det J > 0,$$

(7.21)

which therefore is a stable point (Fig. 7.5c). As the non-trivial steady state will have neutral stability when the consumer nullcline is located such that it intersects the minimum or the maximum of the resource nullcline, this model can undergo two Hopf bifurcations (see below in Fig. 7.6e). When the saturation constant, $h > \frac{K}{3\sqrt{3}}$, the consumer nullcline declines monotonically, giving rise to a Lotka-Volterra like phase plane, where the non-trivial steady state is always stable (Fig. 7.5d).
7.2 Sigmoid functional response

Figure 7.5: Qualitatively different phase spaces of the sigmoid saturated model of Eq. (7.17). The red line is the resource nullcline intersecting the horizontal axis at $R = K$. The blue vertical consumer nullcline is located at $R^* = \frac{h}{\sqrt{R_0} - 1}$. Black lines are trajectories starting just above the carrying capacity of the resource. In Panels (a-c) we set $h < \frac{K}{3\sqrt{3}}$ such that the resource nullcline has a minimum and a maximum (see Section 13.6). If $h \ll K$, Eq. (7.18) simplifies to $N = \frac{R}{a} (1 - \frac{R}{K})$, showing that the maximum of the resource nullcline is located around $R = K/2$. In Panel (a) we set $R^* > K/2$, making the non-trivial steady state stable. In Panel (b) we set $R^* < K/2$, making the non-trivial steady state unstable, and giving rise to a stable limit cycle. In Panel (d) we set $h > \frac{K}{3\sqrt{3}}$, which makes the $dR/dt = 0$ nullcline monotonically declining. This figure was made with the model sigmoid.R.

Bifurcation diagrams

Enrichment, i.e., increasing $K$, can also cause a Hopf bifurcation in this model, giving rise to stable limit cycles that grow in amplitude with the distance to the Hopf bifurcation (Fig. 7.6a, b and d). However, because the resource nullcline keeps its asymptote approaching the vertical axis, whatever the value of $K$ (Fig. 7.6c), the trajectory cannot approach this axis very closely, and resource and consumer densities do not become as small as in the Monod-saturated model. Thus, we do not expect the ultimate extinction of the Paradox of enrichment (Rosenzweig, 1971) in the sigmoid-saturated model, but we do see that enrichment increases the consumer rather the resource when both are present (Fig. 7.6a–c). Our expression for locations of the minimum and maximum of the resource nullcline, i.e., $R \simeq h \sqrt{K}$ and $R \simeq K/2$, respectively, confirm that the minimum hardly shifts when $K$ is increased, while the maximum is proportional to $K$. Hence a stable steady state with a consumer nullcline located at $K/2 < R^* < K$ readily destabilizes when $K$ is increased, but is not expected to become stable again because $R^*$ will remain larger than
Figure 7.6: Bifurcation diagrams and phase planes of the sigmoid-saturated model. In the bifurcation diagrams heavy red lines represent stable steady states, light blue lines unstable steady states, and black points minima and maxima of a stable limit cycle. Panels (a–d) illustrate the effect of increasing the carrying capacity, $K$, as bifurcation diagram (a) and (b), a phase plane with nullclines for various values of $K$ (c), and a phase plane with nullclines and trajectory for the largest values of $K$ (d). Panel (e) depicts the effect of changing $\delta$ on the consumer, where the black points indicate the minima and the maxima of the stable limit cycle that exists between the two Hopf bifurcations. Panel (g) is a bifurcation diagram made by showing the steady state of the resource taking the number of consumers as a “parameter”. This depicts the typical diagram with alternative steady states and hysteresis (see Chapter 11). This figure was made with the model `sigmoid.R`.

$R = \sqrt{K}$. For the algae-zooplankton systems the reduced amplitude of the limit cycles is quite important because the oscillations that are observed in nature are much “milder” than those of the Monod-saturated model for realistic parameter values (Arditi & Ginzburg, 1989; Ginzburg & Akçakaya, 1992; McCauley et al., 1999; Murdoch et al., 2002; Scheffer & De Boer, 1995; Arditi & Ginzburg, 2012). Measurements of the functional response of zooplankton grazing on algae strongly support a Holling type-II response, however.

To illustrate the two Hopf bifurcations that this model may undergo we move the position of the consumer nullcline located at $R = R^*$, e.g., by changing $\delta$ (see Fig. 7.6e). When $\delta$ is too large the consumer cannot be maintained (because $R^* > K$), and $(\bar{R}, \bar{N}) = (K, 0)$ is the one and only attractor (see Fig. 7.6e). Decreasing $\delta$ somewhat allows the consumer to invade, its steady state value increases with decreasing $\delta$, and for a very narrow range of $\delta$ the non-trivial steady state is stable. The value of $\bar{N}$ is maximal at the Hopf bifurcation (because the consumer nullcline is located at the maximum of the resource nullcline). Here a stable limit cycle is born, the non-trivial steady state is unstable, and $\bar{N}$ declines when $\delta$ is further decreased. The second Hopf bifurcation occurs when the consumer nullcline is located at the minimum of the resource
nullcline. The limit cycle dies, the steady state becomes stable again, and \( \bar{N} \) increases steeply upon decreasing \( \delta \) further. First, note that the shape of \( \bar{N} \) in Fig. 7.6e) resembles the shape of the \( \frac{dR}{dt} = 0 \) because we “travel” along that nullcline while changing \( \delta \). Second, the steady state at high resource densities is only stable for a narrow range of consumer death rates, \( \delta \), because the functional response looses its dependence of the resource at high resource densities, i.e., \( f(R) = \frac{R^2}{h+h} \approx 1 \) when \( R \gg h \), and, as a consequence the ODE of the consumers simplifies to \( \frac{dN}{dt} \approx (ca-\delta)N \), which hardly depends on \( R \). Generically, the consumer nullcline is therefore expected to be located in regions where \( R \approx h \), and because we have to choose \( h \ll K \) to have a non-monotonic resource nullcline, this will typically be below \( K/2 \), i.e., below the maximum, like in Fig. 7.5c).

Finally, this model is famous because it allows for multiple steady states of the resource at particular values of the consumer. For instance, treating the consumer density as a “parameter”, which could represent the fixed rate at which the resource is being harvested, e.g., by a fixed stock of grazing herbivores grazing vegetation, or a fixed fleet of fishermen, we only need to rotate the phase plane such that we plot the consumer nullcline as a function of the consumer density, \( N \) (see Fig. 7.6f). The nullcline provides \( \bar{R} \) as a function of \( N \) because \( \frac{dR}{dt} = 0 \) at this line. For intermediate values of \( N \) there are three alternative steady states \( \bar{R} \). The vector field taken from Fig. 7.5 demonstrates that the upper and lower states are stable, and that the middle one is unstable. At some high values of the consumers, \( N = N_2 \), the upper two states merge and disappear (this is a so-called saddle-node bifurcation), leaving the low \( \bar{R} \) state as the only attractor (corresponding to an over-exploited resource). At a much lower value of the consumers, \( N = N_1 \), the lower two states merge and disappear (another saddle-node bifurcation), leaving the upper \( \bar{R} \) state as the only attractor (corresponding to “healthy” harvested resource). If one were to start harvesting this resource, starting at \( N = 0 \), the resource would suddenly collapse at \( N = N_2 \). After the collapse it is difficult to restore the resource to “healthy” levels, because the harvesting rate has to be reduced to \( N = N_1 < N_2 \). This “memory” of the system is called hysteresis, and in one of the exercises we will study how such catastrophes can be predicted (Scheffer et al., 2009; Veraart et al., 2012; Scheffer et al., 2012).

7.3 2-dimensional functional response functions

The functional responses considered hitherto depend on the resource density only, and can hence be written as 1-dimensional functions \( f(R) \). If there is direct competition between consumers for catching resource one would have a situation where the per capita consumption efficiency declines with the consumer density, i.e., a 2-dimensional functional response \( f(R,N) \) for which \( \partial_N f() < 0 \). Predators that increase their feeding efficiency, e.g., by hunting in groups, also require a “predator-dependent functional response”, but with the property that \( \partial_N f() > 0 \). Arguing that predator are only expected to find prey located within their territory, Arditi and Ginzburg (1989; 1992) proposed a ratio-dependent functional response, \( f(R/N) \), that is analyzed in the exercises.

In ecology Beddington (1975) and DeAngelis et al. (1975) independently proposed a 2-dimensional functional response by adding a term by which the consumers increase the saturation constant, e.g.,

\[
f(R, N) = \frac{aR}{h + eN + R},
\]

which is intuitively appealing because increasing the consumer density just increases the resource density at which the consumption rate becomes half maximal, and because for \( e = 0 \) it simplifies
Figure 7.7: The two qualitatively different nullcline constructions of the Beddington consumer-resource model. In Panel (a) we have set $a/e < r$ and in (b) we consider $r < a/e$

into the Monod saturated functional response (Abrams, 1994). The parameter $e$ defines the strength of the competition between the consumers, and setting $e < 0$ would deliver a function where consumers help each other. For a large resource population Eq. (7.22) approaches

$$\lim_{R \rightarrow \infty} \frac{aR}{h + eN + R} = a,$$

showing that the interpretation of $a$ remains the maximum amount of resource a consumer can handle per unit of time.

Eq. (7.22) has also been used to describe the rate at which neutrophils kill bacteria (Malka et al., 2012), and can be derived mechanistically for various types of transient interactions between cells upon binding each other (De Boer & Perelson, 1995) using an extension of the Michaelis-Menten approach (Borghans et al., 1996). In the exercises we will show that replacing a mass-action interaction term, $aXY$, by this “double saturation” function, $\frac{a_{XY}}{1 + X/k_x + Y/k_y}$, conveniently limits the rate of this term when either $X$ or $Y$ becomes large. When either $X \ll k_x$ or $Y \ll k_y$ the term simplifies into a classical saturation function, when $X \ll k_x$ and $Y \ll k_y$, the term simplifies into the same mass-action process.

Because Eq. (7.22) appears to be quite general, we will study the nullclines of consumer-resource models having this “Beddington” functional response,

$$\frac{dR}{dt} = rR(1 - R/K) - \frac{aRN}{h + eN + R},$$

$$\frac{dN}{dt} = \frac{caRN}{h + eN + R} - dN.$$  \hspace{1cm} (7.24)

The consumer nullcline is obtained by setting $dN/dt = 0$ and finding the solutions

$$N = 0 \quad \text{and} \quad N = \frac{ca - d}{de} \left( R - \frac{h}{e} \right) = \frac{R_0 - 1}{e} R - \frac{h}{e}.$$  \hspace{1cm} (7.25)

The last expression defines a line with slope $(R_0 - 1)/e$ that intersects the horizontal axis at $R = h/(R_0 - 1)$. The consumer nullcline is therefore a slanted line with the same minimal resource density $R^* = h/(R_0 - 1)$ as the Monod saturated model (see Fig. 7.8).

Depending on the parameters, the resource nullcline can adopt two qualitatively different forms, which can be revealed by a similar graphical construction as we performed for the sigmoid
Figure 7.8: Three qualitatively different phase spaces of the Beddington consumer-resource model. The critical resource density for net consumer growth, \( R^* = \frac{a}{he-1} \). Panel (a) depicts a case where \( a/e < r \). The steady state is a stable node. In Panel (b) and (c) we set \( a/e > r \). The steady state is stable when the consumer nullclines intersects at the right-hand side of the maximum of the resource nullcline (Panel b). Otherwise it is unstable and the behavior is a stable limit cycle (Panel c). Figure was made with the model `beddington.R`.

functional response. The parabola in Fig. 7.7 is the logistic function \( L(R) = rR(1 - R/K) \), having slope \( r \) in the origin. Plotting the predation term \( F(R, N) = \frac{aRN}{h+eN+R} \) as a function of \( R \) defines a family of curves depending on the consumer density \( N \) (see Fig. 7.7). The slope of these functions in the origin is found by taking the derivative with respect to \( R \):

\[
\frac{\partial F(R, N)}{\partial R} = \frac{aN}{h+eN+R} - \frac{aRN}{(h+eN+R)^2}
\]

which for \( R = 0 \) yields

\[
\frac{aN}{h+eN}.
\]

The slope in the origin therefore increases with the consumer density. Next, for large numbers of consumers we observe that the predation term approaches

\[
\lim_{N \to \infty} \frac{aRN}{h+eN+R} = \frac{a}{e} R,
\]

showing that the predation term, \( F(R, N) \), approaches a slanted asymptote with slope \( a/e \), when it is plotted as a function of \( R \) (see Fig. 7.7).

We therefore have to consider two cases. If \( a/e \ll r \) the predation functions will intersect the logistic parabola only once. One therefore obtains a resource nullcline with a vertical asymptote (see Fig. 7.7 and Fig. 7.8). Actually, when \( a/e \approx r \), this vertical asymptote can disappear allowing the resource nullcline to intersect the vertical axis (not shown). If \( a/e \gg r \) there will be one intersection point at low consumer densities, two intersections at intermediate numbers, and no intersection points at high consumer numbers. This yields a truncated “parabola” similar to that of the Monod-saturated model. Because the consumer nullcline can intersect either on the left of the maximum, or on the right side, one obtains two qualitatively different phases spaces (see Fig. 7.8b & c). The non-trivial steady states of Fig. 7.8a and b are stable because the graphical Jacobian

\[
J = \begin{pmatrix} - & - \\ + & - \end{pmatrix},
\]

has a negative trace and positive determinant. In Fig. 7.8c the consumer nullcline intersects the resource nullcline in its unstable part, and the Jacobian,

\[
J = \begin{pmatrix} + & - \\ + & - \end{pmatrix},
\]
Figure 7.9: Bifurcation diagrams of the Beddington consumer-resource model. In Panel (a) we study the Paradox of enrichment by increasing the carrying capacity, $K$, of the resource starting with the stable steady state of Fig. 7.8b (where $a/e > r$), and observe that enrichment results in a Hopf bifurcation, where a stable limit cycle is born which ultimately has a very wide amplitude. Panel (b) illustrates that increasing the consumer interference parameter, $e$, can take the unstable steady state of Fig. 7.8c through a Hopf bifurcation, where the stable limit cycle dies. Panel (c) depicts the effect of changing $\delta$. Figure was made with the model beddington.R.

Bifurcations of the Beddington model

Note that the monotonically declining “Beddington saturated” resource nullcline in the phase plane of Fig. 7.8a, that is obtained when $a/e < r$, is not very different from the “Monod saturated” nullcline in Fig. 7.2d and the “sigmoid saturated” resource nullcline in Fig. 7.5d, which were both obtained by limiting the effect of the consumer by taking a high saturation constant $h$ (e.g., setting $h \approx K$). In the first phase plane of the Beddington model, Fig. 7.8a, the per capita killing rate of the consumer is “limited” because it either attacks slowly, i.e., low $a$, or has strong interference, i.e., high $e$. The stable non-trivial steady state of the Beddington model will not undergo a Hopf bifurcation when the carrying capacity, $K$, is increased simply because the $a/e < r$ is independent of $K$, and hence there is no Paradox of enrichment (Huisman & De Boer, 1997). In the opposite case, $a/e > r$, with more vigorous consumption, the non-trivial steady state can be stable (Fig. 7.8b) or unstable (Fig. 7.8c, and the bifurcation diagram in Fig. 7.9a reveals the classical “enrichment” picture with Hopf bifurcation and a stable limit cycle growing in amplitude when $K$ is increased. The effect of consumer interference, $e$, is shown in Fig. 7.9b, where starting in the unstable figuration of the Monod-saturated model, $e = 0$, we observe that the limit cycle shrinks and dies when $e$ is increased. Increasing $e$ decreases the steepness of the consumer nullcline, making it more likely to intersect in the stable part of the resource nullcline. Note that further increasing $e$ will ultimately violate the condition, $a/e > r$. Thus, at some value of $e$, the consumer nullcline will change from its non-monotonic shape to a monotonically declining nullcline (like in Fig. 7.8b). Since this does not change the properties of the steady state, i.e., this is not a bifurcation, this change is not reflected in the bifurcation diagram of Fig. 7.9b. Finally, we study the effect of the consumer death rate, $\delta$, in Fig. 7.9c, and observe the same Hopf bifurcation, and that we now have a reasonable range of death rates.
where the non-trivial steady state is stable.

The total quasi steady state assumption

The 2-dimensional functional response of Eq. (7.22) can be derived by an extension of the conventional Michaelis-Menten QSSA (Huisman & De Boer, 1997). Following the “total” QSSA of Borghans et al. (1996), we again split the consumers, \( N \), into a subpopulation \( C \) that is actually handling the resource, and a free subpopulation, \( F \), that is trying to catch the resource, \( R \). We know write conservation equations for both the consumer and the resource, \( N = F_N + C \) and \( R = F_R + C \), and to describe the consumers catching and handling resource we again write

\[
\frac{dC}{dt} = k_R F_N - hC \quad \text{or} \quad \frac{dC}{dt} = k(R - C)(N - C) - hC ,
\]

(7.30)

where \( k \) is a rate at which the free consumers catch resource, and \( 1/h \) is the time required to handle and kill the resource. By the QSSA \( dC/dt = 0 \) we have to solve \( C \) from the quadratic equation

\[
kC^2 - C(kR + kN + h) + kRN = C^2 - C(R + N + h') + RN = 0 ,
\]

(7.31)

where \( k' = k/h \), which for small \( C \) can be simplified into

\[
C = \frac{RN}{h' + R + N} ,
\]

(7.32)

which has a similar from as the consumption term in the Beddington model of Eq. (7.24).

7.4 Summary

There are several generic saturation functions to model that “consumers” (e.g., predators, killer cells, or infectious hosts), cannot handle an infinite number of “resource” (e.g., prey, tumor cells, or susceptible hosts) per unit of time. The most well-known Holling type-II and III saturation functions correspond to the Hill functions explained in Chapter 13. Resource-consumer models based upon a saturated functional response tend have a peaked resource nullcline, with a stable and unstable parts (which was not possible in Lotka-Volterra like models). Because such saturation effects allow for a positive feedback within the resource population, by decreasing the per capita killing rate when resource densities increase, resource-consumer models with a saturated functional response can have a Hopf bifurcation where a stable limit cycle is born. Periodic behavior is therefore a very natural outcome in such models. In the steady states where the consumer is present, resource densities tend to be determined (largely) by the parameters of the consumer (which mimics results obtained with Lotka-Volterra like models). Because saturation functions can be derived mechanistically by quasi steady state assumptions, we would know how to generalize them to high-dimensional situations with several resources and/or consumer species. An extension of the conventional Michaelis-Menten QSSA suggests a 2-dimensional functional response that depends on both resource and consumers. Finally, models based upon this “Beddington” functional response have a slanted consumer nullcline, and either a peaked or a monotonically declining resource nullcline.

7.5 Exercises
Question 7.1. Michaelis-Menten
The famous Michaelis-Menten term is the result of a QSSA in enzymatic reactions. Since we have used similar QSSAs in the derivation of our functional responses, we here refresh our memory on the classical Michaelis-Menten derivation. Consider the chemical reaction for the formation of some product $P$ from a substrate $S$, and let the enzyme $E$ catalyzes the reaction, i.e.,

$$E + S \xrightarrow{k_1} C \xrightarrow{k_2} E + P.$$ 

Because the enzyme is released when the complex dissociates one writes a conservation equation, $E + C = E_0$.

a. Write the differential equations for the product $P$ and the complex $C$. Use the conservation equation!

b. Assume that the formation of the complex is much faster than that of the product, i.e., make the QSSA $dC/dt = 0$.

c. Write the new model for the product. Simplify by defining new parameters.

d. Write an ODE for the substrate, and note that you can add $dC/dt$ to simplify $dS/dt$ because $dC/dt = 0$.

Question 7.2. Parameters
A simple resource consumer model based on a saturated functional response is:

$$\frac{dR}{dt} = a_1 R (1 - R/K) - b_1 R \frac{N}{c_1 + R}$$

$$\frac{dN}{dt} = -a_2 N + b_2 N \frac{R}{c_2 + R}$$

a. Give a biological interpretation and the dimension of all parameters.

b. Is it biologically reasonable to choose $b_1 = b_2$?

c. Give an interpretation for the following parameter choices $c_1 = c_2$, $c_1 > c_2$ and $c_1 < c_2$.

Question 7.3. Dampened oscillations (Grind)
Because simplification is so important when we make models for complex biological systems we also tend to use mass-action terms for most of the interactions between the various populations in a model. Although mass-action terms provide a natural starting point, they come with several drawbacks. First, mass-action terms tend to give rise to models resembling the Lotka-Volterra equations, in which one can often cancel each variable from its own ODE when computing steady states. This leads to the strange result that the length of the food chain determines which variables respond to a change of parameters (Arditi & Ginzburg, 1989; Abrams, 1994; Kaunzinger & Morin, 1998; De Boer, 2012). Second, mass-action terms can give rise to “wild” dynamics because they involve the multiplication of two population densities that may both be small and both be large. One area where this is causing problems is the standard model for HIV infection, with target cells, $T$, infected cells, $I$, and an immune response $E$, which typically only approaches its steady state after dampened oscillations that are not found in data. On the website we provide the document hiv.R containing two version of the same model,

$$\frac{dT}{dt} = s - d_T T - \beta T V,$$

$$\frac{dI}{dt} = \beta T V - d_I I - k_I E,$$

$$\frac{dE}{dt} = a E V - d_E E,$$

where we have made a QSSA such that $V = I$, and an “equivalent” model using “Beddington”
interaction terms,

\[
\begin{align*}
\frac{dT}{dt} &= s - d_T T - \frac{\beta TV}{1 + T/h_\beta + V/h_\beta}, \\
\frac{dI}{dt} &= \frac{\beta TV}{1 + T/h_\beta + V/h_\beta} - d_I I - \frac{kIE}{1 + I/h_k + E/h_k}, \\
\frac{dE}{dt} &= \frac{aEV}{1 + E/h_a + V/h_a} - d_E E,
\end{align*}
\]

where again \( V = I \), and which approaches the previous model when \( h_\beta, h_k, h_a \to \infty \).

a. Study the conventional dynamics of the standard model, and see check that the behavior of the Beddington version is similar when the saturation constants are set to high values.

b. Study if lowering the saturation constants dampens the oscillations.

c. Can you provide a biological argument why using these “Beddington” interaction terms does make some sense?

d. The same `hiv.R` file also provides the Beddington consumer-resource model in a notation allowing one to smoothly go from Lotka-Volterra equations to a Beddington saturated response. Note that we keep the location of the consumer nullcline the same when we change the saturation. Does this confirm the results of the HIV-model?

**Question 7.4. Curvature (Grind)**

It is widely recognized that the complicated resource nullcline of Fig. 7.5 requires a shifted or a sigmoid functional response. This is not generally true, however. There are functional responses that look very similar to the Monod saturated function, and nevertheless deliver a resource nullcline with a minimum and a maximum. These response functions can be constructed from the general definition of hyperbolic functions and can be written as

\[
f(R) = \frac{2R}{H + R + \sqrt{(H + R)^2 - 4\gamma HR}}.
\]  

(7.33)

When one sets the “curvature parameter” \( \gamma = 0 \), this becomes equal to the Holling type II function, \( f(R) = R/(H + R) \). Setting the curvature to \( \gamma = 1 \) delivers the discontinuous Holling type I function, \( f(R) = \min(1, R/H) \), which is not so easy to check analytically. Both functions have the same slope, \( \partial_R f = 1/H \) at \( R = 0 \), but at \( R = H \) the \( f(R) = 1/2 \) for \( \gamma = 0 \), while it is at its maximum, \( f(R) = 1 \), for \( \gamma = 1 \). To be able to change the curvature of this function without changing its value at the saturation constant, one solves \( R \) from \( f(R) = 1/2 \) in Eq. (7.33) to find that the half maximal values occur at \( R = H(1 - \gamma/2) \). Thus, defining \( h \) as the resource density where \( f(R) \) is half maximal, i.e., \( h = H(1 - \gamma/2) \), one can define \( H = h/(1 - \gamma/2) \) to obtain a function that is half-maximal at \( R = h \) for any value of \( \gamma \). A consumer-resource model using the scaled version of Eq. (7.33) as a functional response is available as the file `hyper.R`. Use this to study how the properties of our models depend on the curvature of the functional response.

a. Use the `curve()` function in R to plot Eq. (7.33) for different values of \( \gamma \) (with and without defining \( H = h/(1 - \gamma/2) \)). Examples for this are given in the file `hyper.R`.

b. Study the behavior of a consumer-resource model for various values of \( \gamma \).

c. Does the behavior of the model depend on the curvature of the functional response?

**Question 7.5. Ratio-dependent predation (Grind)**

Arditi & Ginzburg (1989) and Ginzburg & Akçakaya (1992) criticized the consumer-resource models discussed in this chapter (see also their book (Arditi & Ginzburg, 2012) with an excellent review of many relevant data sets). One criticism is that these models “predict” that feeding the resource fails to increase the resource density at steady state, another one is that when these models are used to describe algae-zooplankton systems, they tend to oscillate with a too
wide amplitude (Arditi & Ginzburg, 1989; Ginzburg & Akçakaya, 1992; McCauley et al., 1999; Murdoch et al., 2002; Scheffer & De Boer, 1995). Finally, they argue that a consumer will never interact with all individuals in the resource population, as it will typically only resources found in its own neighborhood (e.g., territory). They proposed a very simply “improvement” of consumer-resource models by making the consumption dependent of the amount of resource per consumer, $R/N$, and called this “ratio-dependent predation”. When a consumer can only interact with $\hat{R} = \frac{R}{N}$ resources, and we use a conventional functional response, one would write

$$ f(\hat{R}, N) = \frac{a\hat{R}}{h + \hat{R}} \quad \text{or} \quad f(R, N) = \frac{aR/N}{h + R/N} = \frac{aR}{hN + R}, $$

which then defines the ratio-dependent consumer resource model

$$ \frac{dR}{dt} = rR(1 - R/K) - \frac{aRN}{hN + R}, \quad \frac{dN}{dt} = \frac{caRN}{hN + R} - dN. $$

To study the dimensions of the parameters one can test the functional response for a large resource population:

$$ \lim_{\hat{R} \to \infty} \frac{a\hat{R}}{hN + \hat{R}} = \lim_{\hat{R} \to \infty} \frac{a}{hN/\hat{R} + 1} = a, $$

which demonstrates that the parameter $a$ has the simple interpretation of the maximum amount of resource consumed per consumer. One can therefore also define the fitness as $R_0 = ca/d$.

This model is available on the website as the file ratio.R.

a. Study the nullclines and trajectories. Hint: like in the Beddington model, there are two qualitatively different regimes.

b. Can one destabilize a steady state by eutrophication?

**Question 7.6. Eutrophication**

Consider an algae-zooplankton system based upon a sigmoid functional response (see Fig. 7.5). Since a perfectly vertical zooplankton nullcline need not be realistic (Arditi & Ginzburg, 1989; Ginzburg & Akçakaya, 1992), we allow for some direct competition between zooplankton at high densities, and evaluate the model by studying the effect of eutrophication.

a. Make a model of the system described above, and sketch the nullclines (by hand).

b. What parameter best defines with the nutrient availability in such an ecosystem, and how would you study the effect of eutrophication?

c. What are the possible effects of eutrophication, given either a strong or a weak intra-specific competition for the zooplankton? Draw the qualitatively different nullcline situations.

d. What do you learn from this about the usage of models to predict environmental effects?

**Question 7.7. Luckinbill**

Fig. 7.10 depicts the data of Luckinbill (1973). The horizontal axis gives the time in either hours (Panel A) or days (Panels B & C). The vertical axis is population density in numbers per ml. The solid line depicts the resource *Paramecium* and the dotted line the consumer *Didinium*. Panel A: *Paramecium* and *Didinium* in normal medium. Panel B: *Paramecium* and *Didinium* in a medium with methyl-cellulose, which increases the viscosity of the medium. At day 17 *Didinium* dies out. Panel C: as Panel B after halving the concentration of food for the resource *Paramecium*. In Panels B and C the fat line at the top gives the density of *Paramecium* in the same medium in the absence of the consumer.

a. Write a simple consumer resource model to explain these data.

b. Identify the differences between the experiments with differences in parameter values of the model.
Figure 7.10: The data from Luckinbill (1973). The horizontal axis gives the time in either hours or days, and the vertical axis the population density in numbers per ml. The solid line is the resource *Paramecium* and the dotted line the consumer *Didinium*. Panel A: *Paramecium* and *Didinium* in normal medium. Panel B: *Paramecium* and *Didinium* in a medium with methyl-cellulose, which increases the viscosity of the medium, which decreases the food intake of *Didinium*. Panel C: as Panel B but with half the amount of food for *Paramecium*. In Panels B and C the fat line at the top represents the population density of *Paramecium* in the absence of the consumer.

c. Draw for each of the three situations the nullclines of the model, and a trajectory corresponding to the data.

d. Does your model provide a good interpretation of the data?

e. What are the most important differences between the model and the data?

**Question 7.8. Filter feeders**

Copepods are filter feeders. The organ they use for filtering is also used for respiration, and filtering is continued even in the presence of large amounts of food. Excess food is killed and excreted. The phytoplankton on its own grows exponentially until it approaches its carrying capacity. Assume a mass action predation term.

a. Make a model describing the interaction between copepods and phytoplankton.

b. Analyze the model using nullclines.

c. How does the return time of this model differ from the return time of a standard model without saturation of the consumer consumption?

d. How does the behavior of this model differ from the model without saturation of the consumer consumption?
Functional response

e. Mussels are filter feeders that can separate respiration and food uptake. In the presence of large amounts of food, respiration continues whereas food uptake saturates. Analyse this new system using nullclines and draw a trajectory in phase space.

**Question 7.9. Exponential function response**

Consumer resource models with a saturated functional response are not always written with a Hill function. An equally simple saturation function is the exponential function:

\[
\frac{dR}{dt} = rR(1 - R/K) - aN(1 - e^{-\ln[2]R/h}) \quad \text{with} \quad \frac{dN}{dt} = caN(1 - e^{-\ln[2]R/h}) - dN.
\]

Solving \(1/2 = e^{-\ln[2]x/h}\) delivers \(x = h\), which means that the functional response remains half maximal at \(R = h\).

a. What is the meaning of the parameter \(a\)?

b. We have seen that replacing the simple Monod function with the hyperbolic function of Eq. (7.33) had a large impact on the phase space of this model. Check with Grind whether the same is true for the exponential functional response (see the file exp.R).

**Question 7.10. Wolves**

Wolves hunt in packs and help each other catch resource (this is also true for several other consumer species, e.g., spoonbills).

a. Devise a model for this situation using a functional response with \(\partial N f(R, N) > 0\).

b. Study the model by phase plane analysis (depending on the functional response you have devised, you may require Grind).

**Question 7.11. Saturation in consumers**

Sometimes there is a maximum rate at which resource can be killed by the consumers. An example is susceptible hosts that are infected by infected individuals. One would then write something like

\[
\frac{dR}{dt} = rR(1 - R/K) - aRf(N) \quad \text{where} \quad f(N) = \frac{N}{h + N},
\]

and where \(a\) is the maximum death rate of the resource \(R\) when there is an infinite consumer population.

a. Sketch the nullclines of this model.

b. Verify these with Grind.
Chapter 8

Modeling chains

The models considered hitherto were composed of maximally two ODEs, for a resource and its consumer, respectively. Here we begin by considering higher dimensional models by adding an ODE for the population controlling the “consumers”. This is the classical situation in ecological food webs that typically contain several “trophic” layers, where the consumers eating the first resource layer (e.g., algae, $R$) are the resource of another consumer (e.g., zooplankton, $N$), that may in turn be predated by a “top-predator” (e.g., fish, $M$). It is typically not clear how many tropic levels one should implement in such a model, e.g., we could also start with nutrients as the first layer, and/or add predatory fish eating the former top-predator. Similar chain models appear when modeling viral infections in a host, because the intermediate population of infected cells, $N$, is responsible for removing susceptible target cells, $R$, by novel infections, and may also invoke an immune response, $M$, removing the infected cells. It is well known that the steady states of such chains strongly depend on the length of the chain (Arditi & Ginzburg, 1989; Abrams, 1994; Kaunzinger & Morin, 1998; De Boer, 2012), which is an troublesome result because we often make quite arbitrary choices on the number of levels to include in our models. For instance, the immune response, $M$, could trigger a response of regulatory T cells. Or a lake with predatory fish controlling fish, that are controlling zooplankton, that are controlling algae, that are consuming nutrients, may (sometimes) be visited by birds catching the predatory fish. Adding yet another layer of control will radically change the properties of the state state. Actually, food chains with an even or odd number of layers have very different steady state properties (Arditi & Ginzburg, 1989; Abrams, 1994), and although this may seem strange, there is experimental data from 2-dimensional and 3-dimensional bacterial food chains confirming these “strange” predictions from the models (Kaunzinger & Morin, 1998). In this chapter we will first confirm this troublesome result, and then show it is a consequence of the mass action interaction terms of the models we typically write. Vitaly Ganusov (2016) argues that the most sensible approach in mathematical modeling is to always develop multiple alternative models, and in this chapter we learn that one should not only vary the underlying biological assumptions, but also the form of the mathematical terms.

8.1 A 3-dimensional chain

Extending the Lotka Volterra with an additional layer, $M$, is straightforward, e.g.,

\[
\frac{dR}{dt} = [r(1 - R/K) - bN]R, \quad \frac{dN}{dt} = [bR - d - cM]N \quad \text{and} \quad \frac{dM}{dt} = [cN - e]M, \quad (8.1a,b,c)
\]
where \( M \) could be fish eating zooplankton, \( N \), or an immune response of cells killing infected cells, \( R \). This simple model has several steady states, and we will study what happens when the carrying capacity, \( K \), of the resource, \( R \) (i.e., algae or target cells), is increased. In the ecological interpretation the carrying capacity reflects the amount of nutrients available for the algae in the ecosystem, and in the virological interpretation \( K \) is the number of target cells present in uninfected individuals, e.g., the size of the liver when we are considering a hepatitis virus. Assume for the moment that one can increase the size of the liver (e.g., by drinking too much alcohol). In the absence of the second population, the third one cannot be maintained, and when \( N = M = 0 \), one obtains the obvious \( \bar{R} = K \) from Eq. (8.1a), i.e., a resource at carrying capacity. Thus, increasing \( K \) also increases \( \bar{R} \). We have seen in the previous chapter that, in the absence of \( M \), the consumer can only invade and be maintained when its \( R_0 > 1 \), which here means that \( bK/d > 1 \). Thus, at low values of the carrying capacity there is not enough resource, \( \bar{R} = K \), in the system to maintain the consumer (i.e., as long as \( K < d/b \)). If, after increasing \( K \), the consumer has successfully invaded, the new steady state (still without \( M \)) is

\[
\bar{R} = \frac{d}{b} \quad \text{and} \quad \bar{N} = \frac{r}{b} \left(1 - \frac{d}{bK}\right) = \frac{r}{b} \left(1 - \frac{1}{R_0}\right) .
\]

Note that the previous state \((\bar{R}, \bar{N}, \bar{M}) = (K, 0, 0)\) still exists, but has become unstable because \( dN/dt > 0 \) in the neighborhood of that state (see Fig. 8.1a). The nature of the steady state of the resource has changed radically because it is now completely determined, or “controlled”, by the parameters of the second population, i.e., \( b \) and \( d \).

Similarly, the third population, \( M \), can only invade when its \( R'_0 = c\bar{N}/e > 1 \). Because \( \bar{N} \) increases as a function of \( K \) (see Eq. (8.2b)), and would approach a maximum \( \bar{N} = r/b \) when \( K \to \infty \), the fitness of the third population can be defined as \( R'_0 = \frac{c}{e} \). We see that the third population can only invade and be maintained when the carrying capacity, \( K \), is sufficiently large. Considering the case when \( M \) is present we solve the steady state of the resource and consumer,

\[
\bar{N} = \frac{e}{c} , \quad \bar{R} = K \left(1 - \frac{b e}{c r}\right) \quad \text{and} \quad \bar{M} = \frac{b\bar{R} - d}{c} ,
\]

where we re-observe the parameter condition \( R'_0 = \frac{c}{e} > 1 \). Since \( \bar{N} \) is solved from Eq. (8.1c), \( \bar{R} \) had to be solved from Eq. (8.1a), and the steady state \( \bar{M} \) was computed from Eq. (8.1b). The steady state of the resource is now again determined by its own parameters \( r, b \) and \( K \), in combination with the two parameters of the third population, \( c \) and \( e \).

If we were to add a fourth population, \( F \), controlling the \( M \) population, e.g., predatory fish or regulatory T cells, one would write

\[
\frac{dM}{dt} = [cN - e - fF]M \quad \text{and} \quad \frac{dF}{dt} = (fM - g)F ,
\]

and one would have solve \( \bar{M} = g/f \) from Eq. (8.4a), \( \bar{R} = \frac{d + c\bar{M}}{e} \) from Eq. (8.1b), \( \bar{N} \) from Eq. (8.1a), and finally \( \bar{F} = \frac{c\bar{N} - e}{f} \) from Eq. (8.4a). Summarizing, we observe that the biological parameters determining the steady state of each population in this chain of populations controlling each other, depends on the length of the chain, \( n \). When \( n = 1 \) the steady state resource density, \( \bar{R} = K \), when \( n = 2 \) or \( n = 4 \) \( \bar{R} \) is independent of \( K \), and if \( n = 3 \) \( \bar{R} \) is proportional to \( K \). Which biological parameters determine the steady state of \( R \) therefore depends on the parity of \( n \): for even length chains \( \bar{R} \) is determined by its controller \( N \), and for odd length chains \( \bar{R} \) depends at least partly on its own parameters. Since it is typically unclear how many (trophic) layers one should incorporate in a model, this is a rather disturbing result pinpointing a lack of robustness of steady state expressions of these chain models (De Boer, 2012).
8.2 Chains with saturating interacting terms

The results derived in the previous section have to do with the fact that most populations in these models are replicators, which means that their ODEs can be written as \( \frac{dx_i}{dt} = f_i(x) x_i \), where \( x \) is a vector representing the \( n \)-dimensional state of the system. Solving the non-trivial steady state therefore typically involves cancelling the \( x_i = 0 \) solution from its own equation, and subsequently solving \( f_i(x) = 0 \). Since the \( f_i(x) \) terms in Eq. (8.1) correspond to the terms within the square brackets, i.e.,

\[
f_R(R, N) = r(1 - R/K) - bN , \quad f_N(R, M) = bR - d - cM \quad \text{and} \quad f_M(N) = cN - e , \quad (8.5)
\]

we observe that only \( f_R \) depends on itself, i.e., \( R \). Because \( f_N \) and \( f_M \) are independent of \( N \) and \( M \), respectively, their steady states are necessarily solved from another equation, i.e., \( \bar{N} \) from \( f_M = 0 \) and \( \bar{N} \) from \( f_R = 0 \).
The fact that the steady state expression of $x_i$ can become independent from $x_i$ is a consequence of the simplicity of the interaction terms, which are all mass action terms here. For instance, if we replace all mass action terms with conventional saturation terms, i.e.,

$$\frac{dR}{dt} = \left[ r \left( 1 - \frac{R}{K} \right) - \frac{bN}{h_R + R} \right] R, \quad \frac{dN}{dt} = \left[ \frac{bR}{h_R + R} - d - \frac{cM}{h_N + N} \right] N,$$

and

$$\frac{dM}{dt} = \left[ \frac{cN}{h_N + N} - e \right] M,$$

(8.6a,b,c)

we observe that $f_N$ becomes dependent on $N$ when $M$ is present, but that $f_M$ remains independent of $M$. All steady state expressions remain dependent on their own variable when we choose for a Beddington functional response, e.g.,

$$\frac{dR}{dt} = \left[ r \left( 1 - \frac{R}{K} \right) - \frac{bN}{h_R + R + N} \right] R, \quad \frac{dN}{dt} = \left[ \frac{bR}{h_R + R + N} - d - \frac{cM}{h_N + N + M} \right] N,$$

and

$$\frac{dM}{dt} = \left[ \frac{cN}{h_N + N + M} - e \right] M,$$

(8.7a,b,c)

but unfortunately the steady state expressions of this model become so complex that they are no longer insightful. Thus, the disturbing results derived in the previous section depend on the simplicity of mass-action interaction terms. One would therefore have to establish the functional form of these interactions before one knows whether or not these results are an artifact, or a realistic feature of truly simple interaction terms.

Because solving the steady state of Eq. (8.7) is laborious, one can resort to studying the difference between these models numerically by bifurcation analysis. Fig. 8.1a-c depicts the steady states derived above for Eq. (8.1) that is based upon mass action interaction terms. The steady state of $R$ is independent of the carrying capacity, $K$, when the chain is 2-dimensional, and increases with $K$ when it is 1 or 3-dimensional. $N$ and $M$ can invade at transcritical bifurcations located at $K = K_N$ and $K = K_M$, respectively. The steady state of $N$ first increases as a function of $K$, but is independent of it when $M$ is present (see Fig. 8.1a-c). For large values of the saturation constants, $h_R$ and $h_N$, bifurcation diagrams of Eq. (8.7) will look very similar to Fig. 8.1a-c because the Beddington interaction terms approach a mass action term whenever $h_R \gg R + N$ and $h_N \gg N + M$. (One can write the functions in Eq. (8.7) as $b'N \frac{N}{1 + R/h_R + N/h_R}$ with $b' = b/h_R$ to see that one can make $h_R$ arbitrary large, and adjust $b'$ to arrive at the same mass action term). The bifurcation diagrams in Fig. 8.1d-f reveal that all steady states always increase with $K$, whatever the dimension, $n$, of the chain for reasonably small values of the saturation constants, i.e., $h_R = h_M < K$.

We conclude that the classical observation that steady states of “control” chains depend on a small subsets of the parameters only, and that this depends on the length of the chain (Arditi & Ginzburg, 1989; Abrams, 1994; Kaunzinger & Morin, 1998; De Boer, 2012), is a consequence of the simple interaction terms of these chains. For more complicated interaction terms, like the Beddington functional response, it will depend on the parameters how strongly the nature of the steady state values changes when new populations are added to the chain. For instance, in Fig. 8.1d the dependence of $\bar{R}$ of $K$ hardly changes when $N$ invades, but that of $\bar{N}$ strongly depends on the presence of the third population, $M$. Finally, note that we have here chosen the carrying capacity, $K$, as a bifurcation parameter, basically to repeat the famous Paradox of enrichment result of Rosenzweig (1971), and that very similar results would have been obtained if other bifurcation parameters were chosen (you can test this by modifying the chain.R code).
8.3 Other famous chain models

The chain models discussed above have a form where a subsequent population “controls” the previous one, i.e., they have interaction terms between all populations of adjacent levels, like in an ecosystem where the next trophic level feeds upon the previous one. Fortunately, not all chains in biology are of this form, and hence need not suffer from the strong dependence of the chain length. For instance, the famous 4-dimensional chain of susceptible, exposed, infected and recovered (SEIR) model in epidemiology (see Chapter 6), i.e.,

$$\frac{dS}{dt} = s - dS - \beta SI, \quad \frac{dE}{dt} = \beta SI - (d + \gamma)E, \quad \frac{dI}{dt} = \gamma E - (\delta + r)I, \quad \text{and} \quad \frac{dR}{dt} = rI - dR,$$

has only one interaction term between the levels, i.e., the $\beta SI$ term. The “resource” is here defined as susceptible hosts, $S$, that are infected at rate $\beta$ by infected hosts, $I$, which first become exposed un-infectious hosts, $E$, then infectious hosts, $I$, that suffer from a death rate, $\delta \geq d$, and may recover into immune hosts, $R$. In the absence of infections $\bar{S} = s/d$. For an epidemic at steady state, we work from right to left to see that

$$\bar{R} = \frac{r}{d} \bar{I}, \quad \bar{I} = \frac{\gamma}{\delta + r} \bar{E}, \quad \bar{S} = \frac{(d + \gamma)(\delta + r)}{\gamma \beta}, \quad (8.8)$$

and hence that $\bar{E} = \frac{s}{d + \gamma} - \frac{d(\delta + r)}{\gamma \beta}$ has to be solved from the first equation. This reveals that $\bar{R}$ and $\bar{I}$ are simply proportional to their previous level, and will always be present when $\bar{E} > 0$. The condition $\bar{E} > 0$ defines the one and only transcritical bifurcation in this 4-dimensional chain, corresponding to the parameter condition where the infection can get established (i.e., $R_0 = \frac{s \gamma \beta}{d(d + \gamma)(\delta + r)} > 1$; see Fig. 8.2b and Chapter 6).

Another common chain to consider is the expansion of a population by a cascade of cell divisions,

$$\frac{dN_0}{dt} = s - (p + d)N_0, \quad \frac{dN_i}{dt} = 2pN_{i-1} - (p + d)N_i \quad \text{and} \quad \frac{dN_n}{dt} = 2pN_{n-1} - dN_n, \quad (8.9)$$

with $\bar{N}_n = \frac{s}{d} - \frac{(p + d)N_n}{d}$. For $\bar{E} > 0$ and $\frac{d}{d + \gamma} > 0$, this chain gets established. The condition $\bar{E} > 0$ defines the one and only transcritical bifurcation in this 4-dimensional chain, corresponding to the parameter condition where the infection can get established (i.e., $R_0 = \frac{s \gamma \beta}{d(d + \gamma)(\delta + r)} > 1$; see Fig. 8.2b and Chapter 6).

**Figure 8.2:** The behavior of the SEIR model in Panels (a,b) and the Kinetic proof reading model in Panels (c). Panel (a) depicts the establishment of an epidemic in a population starting at steady state. Panel (b) shows that the infection in Panel (B) can invade at the transcritical bifurcation point where $R_0 = 1$. Panel (c) shows the contour lines where $C$ (red, $n = 0$ line) or $C_n$ (blue, $n = 10$ or $n = 100$ curved lines) exceeds a certain threshold, $\theta$, for the Michaelis Menten model of Eq. (8.14) and the Kinetic proof reading model of Eq. (8.15), respectively. The cells will get activate above the nullcline, i.e., when the off-rate is sufficiently low and/or the ligand concentration is sufficiently large. For $n = 10$ the nullcline approaches a vertical asymptote corresponding to the critical off-rate above which signaling never starts, whatever the ligand concentration, $L$. This figure was made with the files seir.R and proof.R.
where \( s \) cells per day are entering a division cascade of \( n \) divisions, and the index \( i \) denotes the number of completed divisions. Here the cells stop after \( n \) cell-divisions, and this chain has no interaction terms between its levels. The proliferation rate, \( p \), and the death rate, \( d \), are independent of the number of divisions completed. These populations are not controlling each other, and the steady can be derived by working from left to right, i.e.,

\[
\bar{N}_0 = \frac{s}{p + d}, \quad \bar{N}_i = \frac{2p}{p + d} \bar{N}_{i-1} \quad \text{and} \quad \bar{N}_n = \frac{2p}{d} \bar{N}_{n-1}, \tag{8.10}
\]

revealing that each level remains proportional to the previous one. Since the steady state of each sub-population, \( \bar{N}_i \), is always positive there should always be a steady state. Furthermore, in the exercises you will see that the Jacobi matrix, \( J \), of this system has a lower triangular form, i.e., all elements above the diagonal are zero. Since the eigenvalues of such matrices are solved from the characteristic equation

\[
(J_{00} - \lambda)(J_{11} - \lambda)(J_{22} - \lambda) \ldots (J_{nn} - \lambda) = 0 , \tag{8.11}
\]

you will discover that this steady is always stable, i.e., \( \lambda_{\text{max}} < 0 \). Intuitively, this is a natural result because in this chain each sub-population remains proportional to the previous one (see Eq. \( (8.10) \)), and the first sub-population approaches a steady state reflecting a balance between a source, \( s \), and its loss rate, \( p + d \). Eq. \( (8.10) \) can indeed be simplified into

\[
\bar{N}_0 = \frac{s}{p + d}, \quad \bar{N}_i = \frac{2^i p^i s}{(p + d)^{i+1}} \quad \text{and} \quad \bar{N}_n = \frac{s}{d} \left( \frac{2p}{p + d} \right)^n , \tag{8.12a,b,c}
\]

for \( i = 1, 2, \ldots, n - 1 \). Thus, the only effect of adding a level to this chain is that \( \bar{N}_n \) becomes \( \frac{2^n p^n}{p + d} \)-fold larger. Note that if we were to remove the factor two from these equations, this cascade would correspond to a chain of maturation steps, and that this would confirm that cells or individuals in such a chain would approach a stable "age" distribution. Finally, to model a population of quiescent cells, \( Q \), that occasionally are triggered to enter a cascade of cell divisions, one would replace the source parameter, \( s \), by the number of quiescent cells entering the cascade, e.g., \( s = aQ \), where \( a \) is a (potentially stochastic) activation rate, and add an ODE for the resting cells,

\[
\frac{dQ}{dt} = -aQ - dQ + d\sum f_i N_i , \quad \text{for} \quad i = 1, 2, \ldots, n , \tag{8.13}
\]

which allows a fraction, \( 0 \leq f_i \leq 1 \), of the cells that are lost from the cascade to revert to quiescence. Do you think this model with quiescent cells will also approach a steady state?

Finally, such an activation event of a cell may actually involve yet another chain of ODEs. A famous chain of equations (that actually is beyond the scope of this book because it involves phosphorylation of molecules rather than population dynamics) is the "Kinetic proofreading" chain, that was first proposed to improve the accuracy of transcription and translation (Hopfield, 1974; Ninio, 1975), and later to allow for the discrimination between ligands of low and high affinity during the activation of T cells (McKeithan, 1995). We here shortly address the latter by modeling the chain of phosphorylation events that receptors may undergo after binding their cognate ligand. Consider a population of \( R \) receptors on a cell with an on-rate, \( k_1 \), and an off-rate, \( k_{-1} \), for a particular ligand with a certain concentration \( L \), and assume that the cell will become activated when sufficient receptors are ligated into a receptor-ligand complex \( C \). The classical scheme for this is the Michaelis Menten reaction,

\[
F + L \xrightleftharpoons[k_{-1}]{k_1} C \quad \text{or} \quad \frac{dC}{dt} = k_1 FL - k_{-1} C , \quad \text{with} \quad F = R - C , \tag{8.14}
\]
where the density of free receptors, $F$, is given by the conservation equation $R = F + C$. After making the QSSA $dC/dt = 0$ one obtains the classical $C = \frac{RL}{K_m + L}$, where the Michaelis Menten constant, $K_m = k_{-1}/k_1$, is the inverse of the affinity. Since the number of complexes increases with the ligand concentration, $L$, until all receptors are ligated ($\bar{C} = R$), high concentrations of low-affinity ligands will ultimately activate the cell. Ligands can therefore not be discriminated on the basis of affinity, as a high concentration of a low-affinity ligand can provide the same signal as a low concentration of a high-affinity ligand (see the red straight line in Fig. 8.2c).

Kinetic proofreading does allow cells to discriminate between ligands, and the only requirement for that was the (realistic) extension of this scheme with a chain of modification steps of the complex, like phosphorylation events, that only occur when the receptor is binding the ligand. Upon dissociation of the ligand the receptor is assumed to de-phosphorylate rapidly (McKeithan, 1995). If the complex can become phosphorylated at a rate $k_2$, the scheme becomes

$$F + L \xrightleftharpoons[k_{-1}]{k_1} C_0, \quad C_{i-1} \xrightarrow{k_2} C_i \quad \text{and} \quad C_i \xrightarrow{k_{-1}} F,$$

where $F$ is again the concentration of free receptors. For receptors having $n$ different phosphorylation sites, this translates into the following chain

$$\frac{dC_0}{dt} = k_1FL - (k_{-1} + k_2)C_0, \quad \frac{dC_i}{dt} = k_2C_{i-1} - k_{i-1}C_i, \quad \text{and} \quad \frac{dC_n}{dt} = k_2C_{n-1} - k_{-1}C_n, \quad (8.15)$$

for $i = 1, 2, ..., n - 1$, and with the conservation equation $F = R - \sum_i^n C_i$. At steady state the concentration of the fully phosphorylated complex can be written as

$$\bar{C}_n = \frac{RL}{K_m + L} \left(\frac{k_2}{k_{-1} + k_2}\right)^n, \quad (8.16)$$

where the first term is the same Michaelis Menten function describing saturation at large ligand concentrations, and the second term resembling Eq. (8.12c) introduces a novel dependence on the off-rate, $k_{-1}$, which becomes steep for sufficiently large $k_{-1}$ and $n$ (McKeithan, 1995). High concentrations of low-affinity ligands (with a fast off-rate) will therefore no longer lead to high concentrations of $C_n$ on the cell surface (see Fig. 8.2c), allowing cells to discriminate between high and low-affinity ligands when their signaling is initiated after several phosphorylation steps only.

### 8.4 Summary

Biological models can often be written as chains where each level controls the previous layer. In chains of populations controlling one another the nature of the steady state can strongly depend on the length of the chain, but this depends on the type of interaction function used to model the control that the populations exert on one another. Other classical chains that do not involve multiple levels of control, have steady states that depend much less on the length of the chain, but increasing the chain length may increase the sensitivity of the steady state to particular parameters, which becomes a “feature rather than a bug” in the Kinetic proofreading model.

We have only discussed linear chains in this chapter because networks of populations controlling one another involve competition between populations, which is the subject of the next chapter.

### 8.5 Exercises
Question 8.1. Food chain
Consider a variant of Eq. (8.1) where the resource is not replicating:

\[ \frac{dR}{dt} = s - rR - bNR , \quad \frac{dN}{dt} = [bR - d - cM]N \quad \text{and} \quad \frac{dM}{dt} = [cN - e]M . \]

a. Find all steady states.
b. Do you find a similar dependence of the steady states on the length of the chain?

Question 8.2. Triangular Jacobian
Write the Jacobian of Eq. (8.9) to discover that the matrix has a triangular form. Keep the matrix simple by not substituting the steady state expressions for \( \bar{N}_i \). Observe that the discriminant of a matrix in triangular form is given by the product of its diagonal elements, and that solving the eigenvalues therefore corresponds to solving Eq. (8.11).

Question 8.3. Accumulating mutations (Grind)
Tumors like acute myeloid leukemia (AML) typically appear relatively late in life, and a recent paper by Abelson et al. (2018) demonstrates the onset of AML is typically preceded by the slow accumulation of somatic mutations in the hematopoietic progenitor cells undergoing clonal expansion throughout life (to maintain the various types of cells circulating in the blood). People not developing AML also accumulate mutations in their peripheral blood cells (albeit to a somewhat lower extent), and the basic idea is that mutations accumulate with every division these progenitor cells perform. Thus, leukemias are expected to arise after cells have completed a large number of divisions. Since not all cells having completed many divisions will have accumulated the mutations required for becoming leukemic, and we will argue that these cells become senescent and die, and write the following model,

\[ \frac{dN_0}{dt} = s - (p + d)N_0 , \quad \frac{dN_i}{dt} = 2pN_{i-1} - (p + d)N_i , \quad \text{for } i = 1, 2, \ldots, n , \]

\[ \frac{dS}{dt} = (1 - f)2pN_n - dS S \quad \text{and} \quad \frac{dL}{dt} = f2pN_n + rL(1 - L/K) , \]

where \( s \) is a source of progenitors from a stem cell compartment, \( p \) is a division rate, \( d \) is a death rate, \( S \) are senescent cells appearing after cells have completed \( n \) divisions, and \( L \) are leukemic cells that replicate autonomously at a rate \( r \), and ultimately approach a potentially large and life threatening carrying capacity, \( K \). Setting \( f \) to a small value would mean that most cells having completed \( n \) divisions do not become leukemic, and rather become senescent and die.

This model is provided as the file \texttt{leukemia.R}.

a. Do you think this is a reasonable model?
b. In the numerical model the division rate of the progenitor cells is set to \( p = 1/365 \text{ d}^{-1} \), to define a scenario where these cells on average divide once per year. Setting \( n = 50 \) (which would correspond to a Hayflick (1988) limit) and \( f \) to a small value, one would expect leukemias to develop late and rarely. Do you agree with this expectation?
c. Carefully read the model defined in the \texttt{leukemia.R} document to understand the notation by which the division cascade is implemented. Do you see leukemias develop late and rarely when you run this model?
d. What goes wrong and how would you repair that?
e. Would using the Smith-Martin (1973) model provide a solution?

Question 8.4. Chaos (Grind)
A simple system of a resource species \( R \) eaten by a consumer \( N \), eaten by a top-consumer \( M \) can have a chaotic attractor (Hogeweg & Hesper, 1978; Hastings & Powell, 1991); see Chapter
11. Consider the following system with two Holling type II functional response functions

\[
\frac{dR}{dt} = R(1 - R) - c_1 N f(R),
\]
\[
\frac{dN}{dt} = -a_N N + c_1 N f(R) - c_2 M g(N),
\]
\[
\frac{dM}{dt} = -a_M M + c_2 M g(N),
\]

where
\[
f(R) = \frac{R}{1 + b_1 R} \quad \text{and} \quad g(N) = \frac{N}{1 + b_2 N}.
\]

Hastings & Powell (1991) studied this system for the parameters \(2 \leq b_1 \leq 6.2, \ c_1 = 5, \ c_2 = 0.1, \ b_2 = 2, \ a_N = 0.4, \ \text{en} \ a_M = 0.01\). For biological reasons the time scale of the interaction between \(N\) and \(M\) was made slower than that between \(R\) and \(N\), i.e., \(a_N \gg a_M\). This model is available as the file \texttt{chaos.R}.

a. Sketch with pencil and paper the phase space of \(R\) and \(N\). Do you expect oscillations for their parameters in the absence of the top-consumer \(M\)?

b. Compute the expression of the \(\frac{dM}{dt} = 0\) nullcline, and sketch that line in the phase space of a. Do you expect \(M\) to invade?

c. Sketch the nullclines with Grind and see how they match those sketched with pencil and paper.

d. Vary the parameter \(b_1\) to observe how the model behavior changes (see the file \texttt{chaos.R}).

e. Do this with and without noise on one of the parameters.

**Question 8.5. Detritus**

In a closed ecosystem nutrients should cycle through the food chain and become available again when resource, consumers, and top-consumers die and decompose. One could write a conservation equation, \(K = F + R + N + M\), where \(K\) the total amount of nutrients in the system is the sum of the free nutrients, \(F\), and that contained in all organisms. Assuming that the growth of the \(R\)-population is proportional to the availability of free resources, one can extend Eq. (8.1) to study how in this system with recycling nutrients, the steady states and the nullclines, change when the total amount of nutrients, \(K\), is increased.
Chapter 9

Competition

Competition for resources like space, light, nutrients, food, growth factors, and/or susceptible hosts is ubiquitous in biology, and will occur whenever several populations are maintained by shared resources. Mathematical models for populations competing for resources can be derived mechanistically from the resource consumer models developed in the previous chapters by making a QSSA for the resource densities. Removing the resource changes the indirect interaction between the consumers into a direct one, which will deliver a functional form for the resource competition process. An important concept in resource competition is the principle of “competitive exclusion”, stating that populations that are maintained by consuming the same shared resource have to exclude each other at steady state. A famous data set confirming this is the competition between two species of Paramecium by Gause (1934). Competitive exclusion is actually the basis of Darwin’s “Survival of the fittest” concept. We will show that the consumer depleting the shared resource most will typically be the one and only survivor (Tilman, 1980, 1982), and that this need not be the species with the highest carrying capacity (or even $R_0$). Because the resource is depleted to a minimal density this is sometimes called the pessimization principle (Mylius & Diekmann, 1995). We will first confirm the competitive exclusion principle with a few simple models, and then turn to the much more complicated situation of a “network” in which several consumers are sharing several resources.

9.1 Competitive exclusion

To illustrate the concept in its most general form, first consider a closed compartment with a fixed amount of resource, $R$, that is taken up by $n$ consumer populations $N_i$ (for $i = 1, 2, \ldots, n$), and released when the organisms die. For $n = 2$ this could reflect the two Paramecium species in the medium of Gause (1934) competing for nutrients. Since the total amount of nutrients cannot change in this closed compartment, we write a conservation equation $K = F + \sum_i^n e_i N_i$, where $K$ is the total amount of nutrient in the compartment, $F$ represents the amount of free nutrients, and the $e_i$ parameters specify the amount of nutrient contained in a single individual of consumer $N_i$. A first model, based upon simple mass action terms would be

$$F = K - \sum_i^n e_i N_i,$$

$$\frac{dN_i}{dt} = N_i (b_i F - d_i), \text{ for } i = 1, 2, \ldots, n,$$  \textbf{(9.1)}

where we would define $R_{0i} = b_i K/d_i$ for the fitness of each consumer. Since the steady state of each $dN_i/dt = 0$ requires that $\bar{F} = d_i/b_i = K/R_{0i}$, each consumer generically require a unique
nutrient availability, and hence they cannot co-exist. Solving $dN_i/dt = 0$ in the absence of the other species gives the carrying capacities

$$K_i = \bar{N}_i = \frac{K - 1/R_0_i}{e_i} \quad \text{with} \quad \bar{F} = K - e_i\bar{N}_i = \frac{1}{R_0_i}.$$  \hspace{1cm} (9.2)

Let us order the consumers by their $R_0_i$, with $N_1$ being the fittest consumer, and $N_n$ having the lowest $R_0$. If the first species is present at its carrying capacity, corresponding to a nutrient density $\bar{F} = 1/R_0_1$, all other species cannot invade because their per capita growth rate,

$$b_i\bar{F} - d_i = b_i/R_0_i - d_i = 1/R_0_1 - 1/R_0_i < 0.$$  \hspace{1cm} (9.3)

We conclude that the species with the highest fitness, $R_0_i$, outcompetes all others, and that the resource is depleted to a level $F = 1/R_0_1$ (the latter result was also obtained in the earlier chapters).

Considering the two species of Paramecium in the medium of Gause (1934) one can obtain the same result by examining the nullclines of Eq. (9.1) for $n = 2$. These form two parallel lines

$$N_2 = \frac{K - 1/R_0_1}{e_1} - \frac{e_1}{e_2} N_1 \quad \text{and} \quad N_2 = \frac{K - 1/R_0_2}{e_2} - \frac{e_1}{e_2} N_1 ,$$  \hspace{1cm} (9.4)

for the first and second population, respectively, which have the same slope $-\frac{e_1}{e_2}N_1$ when $N_2$ is plotted on the vertical axis (see Fig. 9.1b). Since the species with the largest fitness, $R_0_1$, corresponds to the upper nullcline, we reconfirm that this species will outcompete the other from any initial condition (see Fig. 9.1b). Because the carrying capacity, $\bar{N}_i$, is inversely related to the nutrient content parameters, $e_i$, (which is a natural result), and the fitness, $R_0_i = b_iK/d_i$, is independent of the nutrient content parameter, the species winning the competition need not be the one with the high carrying capacity, i.e., one can parametrize the system such that $R_0_1 > R_0_2$ while $K_1 < K_2$, by choosing $e_1 > e_2$.

The competitive exclusion result does not change when we make the birth rate a saturation function of the free resource density, i.e.,

$$F = K - \sum_{i=1}^{n} e_i N_i \quad \text{with} \quad \frac{dN_i}{dt} = N_i \left( \frac{b_iF}{h_i + F} - d_i \right) , \quad \text{for} \ i = 1, 2, \ldots, n ,$$  \hspace{1cm} (9.5)

where we could define $R_0_i = b_i/d_i$ for the fitness of each consumer. Because these fitness values are only defined at infinite resource densities, one can now have a situation where the species with the largest fitness is outcompeted by the other species. The result that the species depleting the resource most will outcompete the other one remains valid, however. The carrying capacity of each population, i.e., the steady state of Eq. (9.5) with just one species, is now defined as

$$\bar{N}_i = \frac{K(R_0_i - 1) - h_1}{e_1(R_0_i - 1)} \quad \text{with} \quad \bar{F} = \frac{h_i}{R_0_i - 1}.$$  \hspace{1cm} (9.6)

Thus, the species with the lowest ratio of the saturation constant, $h_i$, over the “critical fitness”, $R_0_i - 1$, will deplete the resource to the lowest level. Since the minimum amount of resource required for the other species to survive is solved from

$$\frac{b_j\bar{F}}{h_j + F} > d_j \quad \text{or} \quad \bar{F} > \frac{h_j}{R_0_j - 1} ,$$  \hspace{1cm} (9.7)

we confirm that the species depleting the resource most outcompetes the other. Species with a lower saturation constant are therefore at an advantage. If one were to derive the nullclines
for a 2-dimensional version of this system, one would again find that these are two parallel lines with slope \(-\frac{c_i}{h_i}N_1\) when \(N_2\) is plotted on the vertical axis (not shown).

Since we learned in the previous chapter that the steady state of the resource is typically solved from the consumer equations, the results demonstrating competitive exclusion from the critical resource densities, are not expected to change when we “open” the system by replacing the free resource in Eq. (9.5) by a dynamic resource with its own kinetics. We have written resource equations with a source and loss term, or with a birth and death rate, and we have used mass action and saturated functional responses to describe the consumption. Restricting ourselves to saturated consumer birth rates we could therefore write

\[
\frac{dR}{dt} = s - dR - R \sum_{i=1}^{n} c_i N_i \quad \text{with} \quad \frac{dN_i}{dt} = N_i \left( \frac{b_i c_i R}{h_i + c_i R} - d_i \right) \quad \text{or} \quad (9.8)
\]

\[
\frac{dR}{dt} = s - dR - R \sum_{i=1}^{n} \frac{c_i N_i}{h_i + R} \quad \text{with} \quad \frac{dN_i}{dt} = N_i \left( \frac{b_i R}{h_i + R} - d_i \right) \quad \text{or} \quad (9.9)
\]

\[
\frac{dR}{dt} = rR \left( 1 - \frac{R}{K} \right) - R \sum_{i=1}^{n} c_i N_i \quad \text{with} \quad \frac{dN_i}{dt} = N_i \left( \frac{b_i c_i R}{h_i + c_i R} - d_i \right) \quad \text{or} \quad (9.10)
\]

\[
\frac{dR}{dt} = rR \left( 1 - \frac{R}{K} \right) - R \sum_{i=1}^{n} \frac{c_i N_i}{h_i + R} \quad \text{with} \quad \frac{dN_i}{dt} = N_i \left( \frac{b_i R}{h_i + R} - d_i \right) , \quad (9.11)
\]

for \(i = 1, 2, \ldots, n\) consumers, and where the first two and the latter two ODEs represent a non-replicating and replicating resource, respectively. Here \(c_i\) is the consumption rate of consumer \(i\), and in the two equations with mass action consumption (Eqs. 9.8 and 9.10), we let the birth rate be a saturation function of the amount of resources consumed. The saturation constant, \(h_i\), in Eqs. (9.8) and (9.10) also plays a role in the conversion from resource to consumers (one could even simplify these terms by dividing the numerator and denominator by \(c_i\), and defining a new saturation constant \(h'_i = \frac{b_i}{c_i}\)). For the other two equations with a saturated consumption term, one argue that the amount of resource consumed is proportional to the growth rate of the consumers, e.g., \(c_i = c h_i\), where \(c\) is the amount of resource (e.g., nutrient) contained in a single consumer, as is typically done for bacterial growth (Monod, 1949). Alternatively, one could argue for Eqs. (9.9) and (9.11) that the birth rate of the consumers is proportional to a saturated per capita consumption, i.e., \(b_i = c c_i\), where \(c\) is a conversion constant required for translating resource into consumers. (Remember that a saturated birth rate of a saturated consumption process would require different saturation constants in the resource and consumer equations; see Chapter 7). Finally, note that Eqs. (9.9) and (9.11) are not derived by the QSSA on the handling time we made in Chapter 7, because we here do not want assume that the consumers have equal saturation constants. A biological interpretation of the saturation functions in the resource ODEs of Eqs. (9.9) and (9.11) could be satiation of the consumers at high resource densities.

Because the critical resource density for each consumer in Eqs. (9.8–9.11) is defined as either

\[
R_i^* = \frac{h_i / c_i}{R_{0i} - 1} \quad \text{or} \quad R_i^* = \frac{h_i}{R_{0i} - 1} , \quad \text{where} \quad R_{0i} = \frac{b_i}{d_i} , \quad (9.12)
\]

all consumers require different resource densities at steady state, and cannot co-exist in equilibrium on a single resource unless they have identical parameters \(h_i, c_i, b_i\) and \(d_i\) (i.e., unless they occupy exactly the same niche). If we rank the species by their critical \(R_i^*\) values, we see that at steady state the first species with the lowest critical resource density will outcompete all others because when

\[
R = R_1^* \quad \text{one can see that} \quad \frac{dN_1}{dt} = 0 \quad \text{and} \quad \frac{dN_i}{dt} < 0 \quad \text{for} \quad i = 2, 3, \ldots n , \quad (9.13)
\]
where \( n \) is the number of consumers.

Note that if we had written mass action birth rates in Eqs. (9.8) and (9.10), i.e., \( \frac{dN_i}{dt} = (b_i R - d_i)N_i \), the critical resources densities would have been defined as \( R_i^* = \frac{d_i}{b_i} = \frac{1}{\rho_i} \), which again reveals that different consumers require different resource densities at steady state, and that the species with the highest fitness, \( R_0 \), depletes the resources most, and outcompetes all other consumers. Finally, note that the steady state of the most competitive consumer, i.e., the one with the lowest \( R_i^* \), need not be stable when the consumption is saturated (see Eqs. (9.9) and (9.11)). If this is the case one expects a stable limit cycle of \( R \) and this most competitive \( N \), and the question becomes whether or not other consumers can invade at this limit cycle. In the exercises we will demonstrate that this is possible, emphasizing that competitive exclusion is an equilibrium result only.

### 3-dimensional nullclines

Albeit unusual and redundant, one can obtain the same results by realizing that these \( R_i^* \) values define the locations of the consumer nullclines on the resource axis. For instance, Fig. 9.1c and (d) depict the 3-dimensional state space of Eqs. (9.8) and (9.10) for \( n = 2 \) consumer species. The 3-dimensional nullcline of the resource can be drawn by separately considering the \( N_1 \) versus \( R \) plane for \( N_2 = 0 \), and the \( N_2 \) versus \( R \) plane for \( N_1 = 0 \). For instance, the \( \frac{dR}{dt} = 0 \) nullcline of Eq. (9.8) has a carrying capacity \( \bar{R} = \frac{s}{d} \), which is the intersection point on the \( R \)-axis when both \( N_1 \) and \( N_2 \) are zero (see the circle on the \( R \)-axis). Considering the backward \( N_2 = 0 \) plane, one obtains from Eq. (9.8) that \( N_1 = \frac{s}{(c_1 R) - d/c_1} \), which has a vertical asymptote \( R = 0 \), and a horizontal asymptote \( N_1 = -d/c_1 \) that is approached for \( R \to \infty \). The \( \frac{dR}{dt} = 0 \) nullcline in the \( N_2 = 0 \) plane therefore has the hyperbolic shape depicted in Fig. 9.1c. Since the same arguments apply for the plane where \( N_1 = 0 \), one finds a similar hyperbolic nullcline in the bottom plane of the phase space in Fig. 9.1c. The resource nullcline of Eq. (9.10) can be obtained similarly, revealing conventional Lotka-Volterra like nullclines (Fig. 9.1d).

To test the stability of the steady states of a 3-dimensional phase space one has to resort to an invasion criterion and apply that to each of the steady states (that are marked by circles or bullets):

1. In Fig. 9.1d the origin is unstable because \( \frac{dR}{dt} > 0 \) in its neighborhood (note that the origin is not a steady state in Fig. 9.1c).
2. The carrying capacity of the resource in Fig. 9.1c and d is unstable because it is located above the consumer planes, i.e., both \( \frac{dN_1}{dt} > 0 \) and \( \frac{dN_2}{dt} > 0 \) when \( R = s/d \) or \( R = K \).
3. The circled intersection point of the \( N_2 \) and the \( R \)-nullcline in the bottom plane is unstable because it is located on the right side of the \( N_1 \)-nullcline, i.e., if \( N_1 \) were introduced in this state it would grow and invade.
4. The intersection point marked by a bullet in the \( N_2 = 0 \) plane at the back is stable because locally \( \frac{dN_2}{dt} < 0 \). Since the 2-dimensional equilibrium of \( R \) with \( N_1 \) is stable, we reconfirm that \( N_1 \) excludes \( N_2 \) because its nullcline is located at a lower prey density. Generally, we see that the steady state of the consumer depleting the resource most (see the black bullet) is located below the other consumer nullclines, implying that the other consumers cannot invade.
9.1 Competitive exclusion

Figure 9.1: Competitive exclusion in the simple model of Eq. (9.1) in Panels (a-b), and in 3-dimensional models of Eqs. (9.8) and (9.10) with a saturated functional response, for a non-replicating (c) and replicating (d) resource, respectively. This figure was made with the files comp.R and comp3d.R.

**Quasi steady state**

To study how resource competition would shape the interaction between the two competitors, one can make a QSSA for the resource in Eqs. (9.8–9.11), and substitute that into the corresponding consumer equations. This is feasible only for Eqs. (9.8) and (9.10) with mass action consumption terms. For the non-replication resource of Eq. (9.8) one obtains

$$\hat{R} = \frac{s}{d + \sum c_i N_i},$$  

(9.14)
and substitution of $\hat{R}$ into the corresponding consumer equation gives
\[
\frac{dN_i}{dt} = N_i \left( \frac{b_is}{s + (h_i/c_i)(d + \sum c_j N_j)} - d_i \right) = N_i \left( \frac{\beta_i}{1 + \sum N_j/k_j} - d_i \right),
\]
(9.15)
where $\beta_i$ and $k_j$ are complicated combinations of several parameters (i.e., $\beta_i = b_i c_i s / (c_i s + h_i d)$ and $k_i = c_i h_i / (c_i s + h_i d)$). The simplified form in Eq. (9.15) reveals that this is an extension of one of the density dependent birth models in Chapter 3, with an inverse Hill function $f(N) = 1/(1 + N/k)$ describing the effect of the population density on the per capita birth rate. The “carrying capacity”, $K_i$, of a consumer can be found by setting all other $N_j = 0$ (i.e., all $j \neq i$), and solving $dN_i/dt = 0$ from Eq. (9.15)
\[
K_i = \frac{s}{h_i} \left( R_0i - 1 \right) - \frac{d}{c_i} = \frac{s}{c_i R^*_i} - \frac{d}{c_i},
\]
(9.16)
i.e., the most competitive species having the lowest $R^*_i$ tends to have the highest carrying capacity (although this depends on $h_i$ and $c_i$). The 2-dimensional nullclines of this QSS model would again be two parallel lines (see Fig. 9.1c).

For the replicating resource of Eq. (9.10) one obtains
\[
\hat{R} = K \left( 1 - \frac{1}{r} \sum c_i N_i \right),
\]
(9.17)
revealing that a rapidly growing resource remains closer to its carrying capacity at steady state consumption. Substituting this into the consumer equation gives
\[
\frac{dN_i}{dt} = N_i \left( \frac{b_i (r - \sum c_i N_i)}{(h_i/c_i)(r/K) + r - \sum c_i N_i} - d_i \right),
\]
(9.18)
which is again not based upon the simple mass action interaction terms of classical Lotka-Volterra competition model (see Section 9.2). One may recognize the mass action terms of the Lotka-Volterra in the numerator, implying that this will resemble the Lotka-Volterra competition model when $(h_i/c_i)(r/K) + r \gg \sum c_i N_i$. The “carrying capacity”, $K_i$, of a consumer can again be found by setting all other $N_j = 0$ (for all $j \neq i$), and solving $dN_i/dt = 0$ from Eq. (9.18), i.e.,
\[
\bar{N}_i = \frac{r}{c_i} \left( 1 - \frac{R^*_i}{K} \right).
\]
The 2-dimensional nullclines of this QSS model would again be two parallel lines (visually project the consumer planes onto the resource plane in Fig. 9.1d).

Summarizing, we find competition equations with interaction terms that are more complicated than mass action terms. You may want to sketch the 2-dimensional nullclines of the QSS models of Eq. (9.15) and Eq. (9.18) to find that these are linear, and resemble those of the Lotka-Volterra competition model.

### 9.2 The Lotka-Volterra competition model

The $n$-dimensional Lotka-Volterra competition model is typically written as
\[
\frac{dN_i}{dt} = r_i N_i \left( 1 - \sum_{j=1}^{n} A_{ij} N_j \right),
\]
(9.19)
9.2 The Lotka-Volterra competition model

The Lotka-Volterra competition model given in Eq. (9.20) describes the dynamics of two species, $N_1$ and $N_2$, where the interaction matrix, $A_{ij}$, collects the competition coefficients between the species. The diagonal elements of this matrix define the carrying capacities, i.e., $K_i = 1/A_{ii}$, because in the absence of interspecific competition Eq. (9.19) simplifies to logistic growth equations, $\frac{dN_i}{dt} = r_iN_i(1 - A_{ii}N_i)$. Thus, the Lotka-Volterra competition model basically extends the logistic growth model phenomenologically with additional mass-action competition terms (a Grind model with an arbitrary number of species, $n$, all having the same carrying capacity, $K_i = 1$, having random off-diagonal $A_{ij}$ elements is provided as the file $\text{matrix.R}$). The competition models we derived “mechanistically” by a QSSA for the resource dynamics were quite different because of their non-mass-action interaction terms (see also (O’Dwyer, 2018)). Finally, the fact that the growth rates, $r_i$, can be cancelled when one considers the steady state of Eq. (9.19) is also due to its phenomenological nature. In the models we derived ourselves the birth and death rates play a decisive role in the competitive strength of a species.

Note that we have would obtained the mass action terms of the Lotka-Volterra model if we had written the consumer model of Eq. (9.10) with mass action terms, e.g., as $\frac{dN_i}{dt} = (b_iR - d_i)N_i$, and had substituted Eq. (9.17) for the resource. Thus, the Lotka-Volterra competition equations should be viewed as a simple phenomenological model, as they are only obtained when the consumer’s birth rate depends linearly on the amount of resources consumed. Moreover, a mass

Figure 9.2: The four qualitatively different nullcline configurations of the Lotka Volterra competition model given in Eq. (9.20). The red line and the blue lines depict the $dN_1/dt = 0$ and $dN_2/dt = 0$ nullclines, respectively, and the black lines are trajectories. $N_1$ has a faster growth rate than $N_2$, i.e., $r_1 = 2r_2$, which affects the trajectories but not the nullclines. This figure was made with the file $\text{lotkaComp.R}$.
action consumer model is not easily extendable into competition for several resources, as one would obtain several independent “birth rates”, e.g., \( \frac{dN_i}{dt} = (\sum_{j=1}^{n} b_{ij} R_j - d_i)N_i \) when there are \( n \) different resources. We therefore continue with saturated birth rates in the next section.

The Lotka-Volterra competition model remains useful however, because it is a simple phenomenological model (like logistic growth or the Lotka-Volterra predator-prey model). Further, one can simplify the model by scaling the carrying capacity of each species to one (by defining a non-dimensional population size \( n_i = N_i/K_i \)), which means that one can set all \( A_{ii} = 1 \), and recompute the other \( A_{ij} \) values by dividing them by \( K_j \) (see Section 13.5). The scaled version of the Lotka-Volterra competition model is useful for summarizing the four qualitatively different phase planes of two competing species. To sketch the nullclines of a 2-dimensional Lotka-Volterra competition model, we define the horizontal axis by \( N_1 \) and the vertical axis by \( N_2 \). The two simplified forms define the classical Lotka-Volterra nullclines running from \( N_i = 1 \) on their own axis to \( 1/A_{ij} \) on the opposite axis.

Choosing \( A_{ij} \) values that are either smaller or larger than one, one obtains classical four diagrams shown in Fig. 9.2. When one of the \( A_{ij} \) parameters is smaller than one and the other larger is than one, the nullclines fail to intersect (see Fig. 9.2a and b), and the species with the smallest \( A_{ij} \) parameter outcompetes the other. When both \( A_{ij} \) parameters are larger than one, the interspecific competition exceeds the intraspecific competition for both species and the nullclines intersect in an unstable equilibrium (Fig. 9.2c). This is called the “founder controlled” situation because the species that initially has the highest abundance has the highest chance to exclude the other, and ultimately approach its carrying capacity. The steady state is stable (see Fig. 9.2d) when both \( A_{ij} \) parameters are smaller than one, i.e., when the intraspecific competition exceeds the interspecific competition for both species, which is the typical situation for resource competition because the niche overlap between two species should be smaller than the niche overlap among members of the same species.

9.3 Several consumers on two resources

The previous sections demonstrated that two consumers on one resource are expected to exclude each other. Two consumers living from two different resources should be able to co-exist whenever they specialize to have sufficiently different requirements for both resources, as this would again make the intraspecific competition larger than the interspecific competition. The most extreme example would be that they specialize on using just one of the two resources, implying that they do not compete and each approach a carrying capacity defined by the availability of their unique resource, their consumption and \( R_0 \). In the general 2-dimensional phase space of Fig. 9.2, such a situation would correspond to perpendicular nullclines intersecting in stable node (with a Jacobian with zero off-diagonal elements).

Next, we will go beyond Lotka-Volterra and write more mechanistic models for the situation where several consumers use several resources while allowing for an overlap in their diet. Studying consumers using several resources mechanistically, one first has to decide whether or not these resources are “essential”, meaning that they cannot replace each other, or “substitutable”, meaning that they can be added up into a total intake (Tilman, 1980, 1982). First consider the
situation of several consumers sharing several substitutable resources, by defining birth rates depending on the summed resource intake, and generalize Eq. (9.8) into
\[
\frac{dN_i}{dt} = \left( \beta_i \frac{\sum_j c_{ij}R_j}{h_i + \sum_j c_{ij}R_j} - \delta_i \right) N_i , \quad \frac{dR_j}{dt} = s_j - d_jR_j - \sum_i c_{ij}N_iR_j , \tag{9.21}
\]
where the consumption rates, \(c_{ij}\), define the mass-action rates at which consumer \(i\) ingests resource \(j\). The saturation constants, \(h_i\), define the density of consumed resources at which the birth rate is half-maximal. Since at low consumption rates the saturation functions approach \(\sum_j c_{ij}R_j/h_i\), the saturation constants, \(h_i\), also play the role of a throphic conversion factor from the resource to the consumer level. For simplicity we let each resource contribute equally to the birth rate of each consumer (this can be repaired by multiplying the \(c_{ij}\) terms in Eq. (9.21a) with a weight \(w_{ij}\)).

Since the per capita birth and death rates of the consumers in Eq. (9.21) only depend on the resource densities one can draw several \(dN_i/dt = 0\) nullclines in a space defined by the resources. For two resources such a picture is called a Tilman diagram (Tilman, 1980, 1982); see Fig. 9.3a and Fig. 9.4a. Above, when we considered a single resource we defined \(R_i^*\) as the critical resource density of consumer \(i\). Now, for two resources the critical resource densities are defined by the consumer nullclines in the space spanned up by the resources, i.e., in Figs. 9.3a and 9.4a \(dN_i/dt > 0\) above its nullcline. If, and only if, two nullclines intersect, there is a combination of resource densities, \((R_1, R_2)\), at which \(dN_i/dt = dN_j/dt = 0\), suggesting that there could be a steady state at which both species co-exist. To sketch the consumer nullclines in a 2-dimensional Tilman diagram we solve \(dN_i/dt = 0\) in Eq. (9.21) for \(R_2\), to see that the nullclines all decline linearly as a function of \(R_1\):
\[
R_2 = \frac{h_i}{c_{i2}(R_{0i} - 1)} - \frac{c_{i1}}{c_{i2}} R_1 , \tag{9.22}
\]
where \(R_{0i} = \beta_i/\delta_i\). Since the resources contribute additively, we can define a critical resource density, \(R_{ij}^* = \frac{h_i}{c_{ij}(R_{0ij} - 1)}\), for each resource \(j\), and use this to simplify the nullcline of consumer \(i\) into \(R_2 = R_{2j}^* - \frac{c_{i1}}{c_{i2}} R_1\). Two of these simplified nullclines can only intersect when their slopes are unequal, i.e., when \(\frac{c_{i1}}{c_{i2}} \neq \frac{c_{j1}}{c_{j2}}\) and when their four intersects with the axes, i.e., \(R_2 = R_{21}^*, R_1 = R_{11}^*, R_2 = R_{12}^*, R_1 = R_{21}^*\), also allow the nullclines to cross (see Fig. 9.4a).

Note that when two species perfectly specialize on one resource, i.e., \(c_{21} = c_{12} = 0\), their Tilman diagram will have two intersecting perpendicular lines located at \(R_1 = R_{11}^*\) and \(R_2 = R_{22}^*\).

When two consumers \(i\) and \(j\) have the same diet, \(c_{i1} = c_{j1}\) and \(c_{i2} = c_{j2}\), the slopes of their nullclines will be parallel lines, and the species will exclude each other (see Fig. 9.3a) where we plot the nullclines of three consumers differing in their saturation constants only, i.e., \(h_3 > h_2 > h_1\). The fact that these lines are not intersecting means that there is no combination of resource densities, \((R_1, R_2)\), at which even two of the consumers can co-exist at steady state. Thus, the species with the lowest resource requirements, \(R_{ij}^*\), i.e., the one with the lowest nullcline in the Tilman diagram of Fig. 9.3a will outcompete the others. Requiring low amounts of consumed resources, i.e., having a low \(h_i\) parameter, consuming a lot, i.e., having high \(c_{ij}\) parameters, and having a high \(R_0\), all contribute to having low \(R_{ij}^*\)s, and becoming the superior competitor (see Fig. 9.3). Because there are only three consumers in the Tilman diagram of Fig. 9.3a, we can confirm this conclusion by making a QSSA for the two resources, and plotting “conventional” consumer nullclines in a 3-dimensional state space spanned up by the consumers (see Fig. 9.3b). Since the \(dN_1/dt = 0\) plane is located above the other two nullcline planes, this confirms that \(N_1\) will outcompete the other two consumers. Since a 2-dimensional Tilman diagram can contain any number of consumer nullclines, it is not limited to a maximum of three consumers, and can used to establish the superior competitor(s) in a large set consumers.
When the consumers have different diets their nullclines in the Tilman diagram may intersect, and in Fig. 9.4a we made a situation with three pairwise intersections by setting $N_1$ specialize on $R_1$ (by setting $c_{11} > c_{12}$), $N_2$ specialize on $R_2$ (by setting $c_{22} > c_{21}$), and making $N_3$ a generalist (by setting $c_{31} \simeq c_{32}$). Since the three nullclines do not intersect in one point, one can safely conclude that there is no combination of resource densities where all three $dN_i/dt = 0$, and hence that these three consumers cannot co-exist on just two resources (confirming the general competitive exclusion principle). Because the slopes of these nullclines depend on the ratio of the consumption rates, $c_{i1}/c_{i2}$, their heights on the saturation constant, $h_i$, and the fitness, $R_0$, of each consumer (see Eq. (9.22)), it is generically not expected to have an intersection point of more than two nullclines (see the exercises for a non-generic counterexample). However, depending on the parameters, any pair of consumer nullclines may intersect, and this intersection point would correspond to a steady state provided that for these resource densities there is also a steady state density of the two consumers such that $dR_1/dt = dR_2/dt = 0$. Thus, an intersection between two consumer nullclines need not be steady state of the full system (i.e., of Eq. (9.21)). Using newton() in Grind we have marked all steady states with two consumers with bullets (stable) and circles (unstable) in Fig. 9.4a. This illustrates that only two of the pairwise intersections correspond to a steady state. The intersection point in the middle, where $dN_1/dt = dN_2/dt = 0$, is a stable steady state because it is located below the $dN_3/dt = 0$ nullcline, implying that $N_3$ will decline at these resource densities. The left-most intersection point, where $dN_1/dt = dN_3/dt = 0$, is an unstable steady state because it is located above the $dN_2/dt = 0$ nullcline, implying that $N_2$ would successfully invade if introduced into this equilibrium of $N_1$ and $N_3$ with the two resources. For reasons that are not readily obvious from
Several consumers on two resources

Figure 9.4: Three consumers having different diets on two substitutable resources. In the Tilman diagram of Panel (a) each consumer nullcline obeys Eq. (9.22), and letting $N_1$ specialize on $R_1$ by setting $c_{11} > c_{12}$, $N_2$ specialize on $R_2$ by setting $c_{22} > c_{21}$, and making $N_3$ a generalist by setting $c_{31} \approx c_{32}$, $N_1$ has the steepest nullcline, $N_2$ the flattest, and $N_3$ has a slope close to $-1$. Because we have given the consumers similar total consumption rates, $c_1 + c_2$, and identical saturation constants, $h_i$, the nullclines tend to intersect in pairs. Only the middle intersection point where $dN_1/dt = dN_2/dt = 0$ can be a stable steady state because this is below the $dN_3/dt = 0$ nullcline, meaning that $N_3$ cannot invade at these low resource densities. The upper intersection point where $dN_1/dt = dN_3/dt = 0$ is a steady state (see Panel (c)), but because it is above the $dN_2/dt = 0$ nullcline it is unstable. The lower intersection point where $dN_2/dt = dN_3/dt = 0$ is not a steady state (see Panel (d)), and solving the system in the absence of $N_1$ leads to trajectories approaching $N_2 = K_2$. The bullet and the circle were obtained numerically by solving the system for all pairwise combinations of consumers. Panels (b–c) depict the consumer nullclines for all pairwise combinations of consumers, after making a QSSA for the resources. This confirms that there are only two steady states having two consumers present, and that the middle intersection point in Panel (a) is the one and only attractor for these parameters. This figure was made with the model additive.R.

the Tilman diagram in Fig. 9.4a, the right-most intersection point, where $dN_2/dt = dN_3/dt = 0$, is not a steady state. These results can again be confirmed by making a QSSA for the resources: and depicting all pairwise consumer phase spaces (Fig. 9.4b–d). Importantly, such a Tilman
diagram can be made for any set of consumers, and this analysis tells us (1) that the consumers
depleting the resources the most are expected to be the superior competitors, and (2) at steady
state no more than two consumers are expected to be expected to be maintained by two resources.

Because one cannot easily tell from a Tilman diagram whether or not an intersection point
 corresponds to a steady state, these diagrams are most informative for establishing which in-
tersections are absent, which truly indicate the absence of a steady state (see Fig. 9.3), and
to establish which pairwise intersection point is located at the lowest resource densities, which
predicts which pair of consumers forms the superior competitors. Above we have used an inva-
sion criterion to establish whether or not a steady state is stable, and concluded that the steady
state located at the lowest combination of resource densities tends to be stable, because the other
consumers decline at the lowest resource densities. However, this conclusion would be incorrect
as the lowest steady state could also be a saddle-point (see Fig. 9.2c), meaning that only one
consumer would survive, and that it depends on the initial densities who survives. The QSSA
nullclines in Fig. 9.4b–d do not intersect in a founder-controlled situation, however, and this is
somewhat intuitive because we here consider resource competition for substitutable resources.
The niche overlap of a consumer with itself is therefore always larger than that with any other
consumer, and hence the QSSA nullclines of any pair of consumers should correspond to that of
Fig. 9.2d. One see this by considering the non-intersecting nullclines in Fig. 9.4d, and decrease
the niche overlap between the species until the nullclines intersect. This will turn the dNj/dt = 0
nullcline more vertical and the dNk/dt = 0 nullcline more horizontal. The latter will create a
bifurcation point when the green dNk/dt = 0 nullcline intersects the carrying capacity, Kk, of
the superior species, Nk. Decreasing the niche overlap further results in a situation where the
nullclines intersect in the stable configuration of Fig. 9.3b. Note that setting the niche overlap
to zero would correspond to the necessarily stable situation of a perfectly horizontal and vertical
pair of nullclines. Thus, two consumers on two substitutable resources can always coexist if
their niche overlap is sufficiently small, as their non-trivial steady state is always expected to be
stable. This will change when we consider essential resources.

9.4 Essential Resources

To mechanistically model “essential” resources one would change Eq. (9.21) into
\[
\frac{dN_i}{dt} = \left( \beta_i \prod_j \frac{c_{ij} R_j}{h_{ij} + c_{ij} R_j} - \delta_i \right) N_i , \quad \frac{dR_j}{dt} = s_j - d_j R_j - \sum_i c_{ij} N_i R_j ,
\]
(9.23a,b)

where by the multiplication of saturation functions we require that all resources should be
consumed in sufficient amounts. Note again that this can be simplified by dividing the numerator
and denominator in each saturation function by \( c_{ij} \), and define \( h'_{ij} = h_{ij}/c_{ij} \). Since the nullclines
of Eq. (9.23a) only depend on the resource densities, one can again plot many dNj/dt = 0 in a
single Tilman diagram spanned up by two resources. For two consumers on two resources Eq.
(9.23a) into
\[
\frac{dN_1}{dt} = \left( \beta_1 \frac{c_{11} R_1}{h_{11} + c_{11} R_1} \frac{c_{12} R_2}{h_{12} + c_{12} R_2} - \delta_1 \right) N_1 , \quad \frac{dN_2}{dt} = \left( \beta_2 \frac{c_{21} R_1}{h_{21} + c_{21} R_1} \frac{c_{22} R_2}{h_{22} + c_{22} R_2} - \delta_2 \right) N_2 ,
\]
(9.24)
(9.25)

and Fig. 9.5(a) and (b) depicts two Tilman diagrams for this model. The consumer nullclines
in a phase spanned up by the two resources are hyperbolic functions with asymptotes defining
the minimal resource densities these consumers require. These asymptotes can be found by setting \( \frac{dN_i}{dt} = 0 \) for \( R_1 \to \infty \) or \( R_2 \to \infty \), i.e., \( R_1 = R^*_i \) and \( R_2 = R^*_i \) for \( i = 1, 2, \ldots, n \), respectively (see Fig. 9.5a and b). Whether or not the nullclines will intersect therefore depends on the \( R^*_i \)'s, and the species with the lowest requirements, \( h_{ij} \), the highest consumption rates, \( c_{ij} \), and highest \( R_0 \) will have the lowest nullcline, and be the winner whenever the nullclines fail to intersect.

In all panels of Fig. 9.5 we have set \( c_{11} > c_{12}, \ c_{22} > c_{21} \) and \( c_{31} \approx c_{32}, \) i.e., consumer one specializes on resource one, consumer two on resource two, and consumer three is a generalist, and in Fig. 9.5(c) and (d) we have used non-replicating resources defined by Eq. (9.23b). In the stable situation of Fig. 9.5c and c we accordingly set \( h_{11} > h_{12}, \ h_{22} > h_{21} \) and \( h_{31} = h_{32}, \) to let each species eat most of the resource it requires most (which would be “optimal” in an evolutionary sense (see the chapter by Tilman in (McLean & May, 2007))). We have made the
Competition

unstable situation of Fig. 9.5(b) and (d) by setting \( h_{11} = h_{12} = h_{21} = h_{22} \), which means that the first consumer competes more strongly with the second consumer that with itself because the second consumer eats more of resource two than consumer one. Apparently, the latter leads to an unstable steady state between them, and a situation where only one of the consumers survives. The initial condition will determine who persists, and hence this is called a “founder controlled” situation. Since the Tilman diagrams in Fig. 9.5(a) and (b) are much simpler than the QSSA nullclines in Panels (c) and (d), it would be much more efficient if one can read the stability of the steady state from the relative location of the consumer nullclines in the Tilman diagram. The next section shows how that can be done (albeit by a complicated procedure).

9.5  4-dimensional Jacobian

To formally study the stability of the steady state of these models one should study the Jacobian of the 4-dimensional system. Fortunately, this is feasible because this Jacobi matrix contains many zero elements. For instance, the Jacobian of a 2 \( \times \) 2 model with substitutable resources, i.e., Eq. (9.21) for two consumers and two resources, can be written as

\[
J = \begin{pmatrix}
\partial_R_i R'_1 & \ldots & \partial_N_i R'_1 \\
\cdots & \ddots & \cdots \\
\partial_R_i N'_2 & \ldots & \partial_N_i N'_2
\end{pmatrix} = \begin{pmatrix}
-d_1 - c_{11} \bar{N}_1 - c_{21} \bar{N}_2 & 0 & -c_{11} \bar{R}_1 & -c_{21} \bar{R}_1 \\
0 & -d_2 - c_{12} \bar{N}_1 - c_{22} \bar{N}_2 & -c_{12} \bar{R}_2 & -c_{22} \bar{R}_2 \\
\Phi_{1c11} & \Phi_{1c12} & 0 & 0 \\
\Phi_{2c21} & \Phi_{2c22} & 0 & 0
\end{pmatrix}
\]

(9.26)

where

\[
\Phi_1 = \frac{\beta_1 h_1 \bar{N}_1}{(h_1 + c_{11} R_1 + c_{12} R_2)^2} \quad \text{and} \quad \Phi_2 = \frac{\beta_2 h_2 \bar{N}_2}{(h_2 + c_{21} R_1 + c_{22} R_2)^2}
\]

Note that the two \( \partial_{N_i} N'_i \) elements are zero because \( \partial_{N_i} N'_i \) is the per capita growth rate, which is zero at steady state. The two \( \partial_{N_j} N'_i \) elements are zero because the consumer equations do not contain the other consumer, and the two \( \partial_{R_i} R'_i \) elements are zero because the resource equations do not contain the other resource. This Jacobian can be simplified into a matrix with the same structure of signs and zeros,

\[
J = \begin{pmatrix}
-\rho_1 & 0 & -\gamma_{11} & -\gamma_{21} \\
0 & -\rho_2 & -\gamma_{12} & -\gamma_{22} \\
\phi_{11} & \phi_{12} & 0 & 0 \\
\phi_{21} & \phi_{22} & 0 & 0
\end{pmatrix}
\],

(9.27)

where \( \rho_i \) elements define the feedback of the resources onto themselves, the \( \gamma_{ij} \) elements define the per capita amounts of resources consumed, and the \( \phi_{ij} \) terms define the contribution of resources to the growth of the consumer populations at steady state (Tilman, 1980). The characteristic equation of this Jacobi matrix can be obtained with Mathematica, and is defined as

\[
\lambda^4 + a_3 \lambda^3 + a_2 \lambda^2 + a_1 \lambda + a_0 = 0
\]

(9.28)

where

\[
a_3 = \rho_1 + \rho_2, \quad a_2 = \phi_{11} \gamma_{11} + \phi_{21} \gamma_{12} + \phi_{12} \gamma_{21} + \phi_{22} \gamma_{22} + \rho_1 \rho_2, \\
a_1 = \phi_{12} \rho_1 \gamma_{21} + \phi_{22} \rho_1 \gamma_{22} + \phi_{11} \gamma_{11} \rho_2 + \phi_{21} \gamma_{12} \rho_2 \quad \text{and} \quad a_0 = (\gamma_{11} \gamma_{22} - \gamma_{12} \gamma_{21})(\phi_{11} \phi_{22} - \phi_{12} \phi_{21})
\]

The steady state will be stable when all four solutions of the eigenvalues in Eq. (9.28) are negative. Fortunately, there is a general method to test this without having to solve this fourth-order polynomial. This is so-called Routh-Horwitz stability criterion on the \( n \) coefficients, \( a_i \),
of an \( n \)th order polynomial (May, 1974; Tilman, 1980). One of the Routh-Horwitz criteria is that all parameters, \( a_i \), in Eq. (9.28) should be positive (or all negative as one can multiply the equation with \(-1\)). Thanks to the many zeros in the Jacobi matrix we here have a simple situation where \( a_3 > 0, a_2 > 0, a_1 > 0 \), and only \( a_0 \) can be negative. Hence testing \( a_0 > 0 \) may reveal a biological insight into the criteria for co-existence of two consumers of two resources.

For substitutable resources, we know that the steady state can only exist if the two consumers have a different diet (see Fig. 9.3a). Therefore consider a case where consumer one specializes on resource one, and consumer two on resource two, i.e., \( c_{11} > c_{12} \) and \( c_{22} > c_{21} \) (see Fig. 9.4). Spelling out the first term of the \( a_0 \) equation, we see that in this case

\[
(\gamma_{11}\gamma_{22} - \gamma_{12}\gamma_{21}) = (c_{11}R_1c_{22}R_2 - c_{12}R_3c_{21}R_1) > 0 ,
\]

because \( c_{11}c_{22} > c_{12}c_{21} \). For the second term of the \( a_0 \) equation we observe in Eq. (9.26) that \( \phi_{11} > \phi_{12} \) when \( c_{11} > c_{12} \) and that \( \phi_{22} > \phi_{21} \) when \( c_{22} > c_{21} \). As a consequence

\[
\phi_{11}\phi_{22} - \phi_{12}\phi_{21} > 0 \quad \text{and, hence} \quad a_0 > 0 ,
\]

which fulfills this Routh-Horwitz criterion, allowing the steady state to be stable. We conclude that two consumers using two substitutable resources can co-exist, i.e., when their quasi steady state nullclines intersect, this steady state is expected to be stable (see Fig. 9.4b).

Although we here considered the case where the resources are maintained by a source, little changes when define replicating resources by replacing Eq. (9.21b) by

\[
\frac{dR_j}{dt} = r_jR_j(1 - R_j/K_j) - \sum_i c_{ij}N_iR_j , \tag{9.29}
\]

and continue to use Eq. (9.21a) for the consumers. The Tilman diagram remains the same because the ODEs for the consumer did not change. In the Jacobian of Eq. (9.26) only the upper two diagonal elements change into

\[
\rho_1 = r_1 - \frac{2r_1}{K_1}R_1 - c_{11}N_1 - c_{21}N_2 \quad \text{and} \quad \rho_2 = r_2 - \frac{2r_2}{K_2}R_2 - c_{11}N_1 - c_{21}N_2 ,
\]

both of which should remain negative. Hence, the Routh-Horwitz criteria remain the same and we again find that the steady state should be stable.

**Essential resources.** Can the Routh-Horwitz criteria also tell the difference between the stable and unstable situation in Fig. 9.5? Using a \( 2 \times 2 \) version of Eq. (9.23) for two consumers using two “essential” resources, we obtain an Jacobian that is quite similar to that of models with substitutable resources, as only the four \( \partial R_i N'_j \) elements change:

\[
\begin{pmatrix}
\partial R_1 N'_1 \\
\partial R_1 N'_2 \\
\partial R_2 N'_1 \\
\partial R_2 N'_2
\end{pmatrix} =
\begin{pmatrix}
\Phi_1 R_1 \\
\Phi_2 R_1 \\
\Phi_1 R_2 \\
\Phi_2 R_2
\end{pmatrix}
\begin{pmatrix}
\frac{R_1}{1 + R_1/H_{11}} \\
\frac{R_1}{1 + R_1/H_{12}} \\
\frac{R_2}{1 + R_2/H_{21}} \\
\frac{R_2}{1 + R_2/H_{22}}
\end{pmatrix}
\begin{pmatrix}
\phi_{11} \\
\phi_{21} \\
\phi_{12} \\
\phi_{22}
\end{pmatrix} \tag{9.30}
\]

where \( H_{ij} = h_{ij}/c_{ij} \) and

\[
\Phi_1 = \frac{\beta_1 N_1}{(H_{11} + R_1)(H_{12} + R_2)} \quad \text{and} \quad \Phi_2 = \frac{\beta_2 N_2}{(H_{21} + R_1)(H_{22} + R_2)} .
\]

The full Jacobian therefore has the same signs and zeros as the matrix in Eq. (9.26), which means that the same \( a_0 > 0 \) criterion remains a condition for stability.
Again consider a case where consumer one specializes on resource one, and consumer two on resource two, i.e., $c_{11} > c_{12}$ and $c_{22} > c_{21}$. Like above the first term of the $a_0 > 0$ criterion, $\gamma_{11}\gamma_{22} > \gamma_{12}\gamma_{21}$, remains satisfied. However, the second term, $\phi_{11}\phi_{22} > \phi_{12}\phi_{21}$, need not be satisfied because the relative values of $\phi_{ij}$ elements are no longer determined by the corresponding consumption rates, $c_{ij}$. For instance, if species one, which consumes most of resource one, would require more of resource two, i.e., if $h_{11} < h_{12}$ (see Fig. 9.5b), the positive contribution of the first resource may become smaller than that of the second, and one can obtain that $\phi_{11} < \phi_{12}$.

Setting the same “non-optimal” requirements for the second consumer one would also obtain that $\phi_{22} < \phi_{21}$ (see Fig. 9.5b). Whenever $(\phi_{11}\phi_{22} - \phi_{12}\phi_{21}) < 0$ and $(\gamma_{11}\gamma_{22} - \gamma_{12}\gamma_{21}) > 0$, the Routh-Horwitz criterion $a_0 > 0$ fails, and the steady state is expected to be unstable (see Fig. 9.5d).

Interestingly, we see that both consumers need to be restricted most by the resource they eat most, and that the condition $a_0 > 0$ has the biological interpretation that the species can co-exist when they evolve consumption rates reflecting their resource requirements, i.e., when the $\phi_{ij}$ terms concur with the $\gamma_{ij}$ terms (Tilman, 1980; McLean & May, 2007). Intuitively, one can understand that it is destabilizing when a consumer hardly consumes the resource it is mostly limited by (as an increase in the resource density would hardly increase is birth rate).

Finally, similar to deriving a graphical Jacobian from a local vector field, one can also estimate the relative sizes of the $\phi_{ij}$ terms from a Tilman diagram. In Fig. 9.5a we can see that $\partial R_1/N_1' = \phi_{11} > \partial R_2/N_1' = \phi_{12}$ because a small step to the right lands at a larger distance from the $dN_1/dt = 0$ nullcline that a small step to the top. Similarly, one can see that $\partial R_1/N_2 = \phi_{21} < \partial R_2/N_2' = \phi_{22}$, which tells us the Routh-Horwitz criterion, and the steady state should be stable (see Panel (c)). In Panel (b) the nullclines are reversed and these partial derivatives are just the other way around, which makes this un unstable steady state (see Panel (d)). This will become more clear in the exercises, where we simplify this model using a minimum function (Tilman, 1980, 1982). If we were to study this model with self-renewing resources, we would again obtain a very similar Jacobian and similar results (not shown).

Summarizing when consumers strongly require a resource that is more strongly depleted by another consumer than by themselves, they suffer more competition from the other consumer than from themselves. This destabilizes the steady state and leads to the “founder controlled” phase space of Fig. 9.5(d), where the initial condition determines which of the consumers survives.

9.6 Summary

The competitive exclusion principle stating that at steady $n$ resources can maximally maintain $n$ different consumers is a very general theoretical result that nevertheless seems to be contradicted by various biological systems maintaining a diverse community of consumers on a very limited variety of resources. Mechanistic models for resource competition require a distinction between essential and substitutable resources. One can study systems with many consumers using two (or three) resources in Tilman diagrams, and this reveals that the species depleting the resources most, because they can survive on the lowest resource densities, tend to be the superior competitors. The lowest resource density, $R^*$, required by a consumer to expand is therefore the most informative measure defining the most superior competitors, and species will only co-exist at equilibrium when their niches are sufficiently different. Replicating and non-replicating resources yield similar results for the outcome of the competition. The classical Lotka Volterra competition equations turn out to be bold simplifications generalizing over any number
of essential and substitutable resources, and are not readily obtained from QSS assumptions in more mechanistic consumer-resource models. The Lotka Volterra competition equations do allow us to summarize the four qualitatively different phase diagrams that one may expect for two competing populations.

9.7 Exercises

**Question 9.1. Migration**
Extend the scaled Lotka Volterra competition model of Eq. (9.19) with a small constant immigration of individuals.

**a.** Write the new differential equations for a 2-dimensional system.

**b.** Analyze the model using nullclines. Hint: first sketch the well-known qualitatively different phase spaces without this migration term, and then reason how the nullclines change if you add a *small* immigration parameter.

**c.** Define the stability of all the steady states.

**d.** Discuss competitive exclusion in this model.

**Question 9.2. Co-existence by trade-offs?**
Posfai *et al.* (2017) study the “Paradox of the plankton” by modeling resource competition between a large number of consumers. Their major idea is that consumers are expected to specialize on a subset of the resources, and therefore they introduce trade-offs among the consumption rates when parametrizing their model. Surprisingly, they find that an unlimited number of species can coexist, and that their model reproduces several features of natural ecosystems, including key-stone species and population dynamics characteristic of neutral theory. The consumer equation of their model takes the following form:

\[
\frac{dN_i}{dt} = \left( \sum_j \beta_{ij} c_{ij} R_j \right) - \left( h_{ij} + c_{ij} R_j - \delta_i \right) N_i,
\]

where each additional resource increases the maximum birth rate, \( \beta_i = \sum_j \beta_{ij} \), that is approached when all resources are available at large densities, i.e., when \( R_j \gg h_{ij} \) for all \( j \) (which would be the natural situation when all consumer densities are low).

**a.** This is different from Eq. (9.21a): is this a proper model for substitutable resources?

**b.** This is also different from Eq. (9.23a): is this a proper model for essential resources?

**c.** Use Grind to study the idea of a trade-off in our own models for competition between substitutable or essential resources. Do we find similar results, and —if so— what is actually required to repeat these results?

**d.** What do you think of this paper: is this indeed resolving the Paradox of the plankton?

**Question 9.3. Non-equilibrium co-existence (Grind)**
We have seen in this chapter that two species competing for the same resource cannot co-exist in a steady state. A fine example of non-equilibrium co-existence of two consumers using the same resource was devised by Yodzis (1989). By making a smart choice of the functional response functions, one can make a system where one consumer grows faster than the other at low prey densities, while the other does better at high consumer densities. If the consumer population oscillates between densities where the two consumers differ in performance, they need not exclude each other. Note that the two consumer nullclines remain parallel planes in the phase space, precluding the existence of a 3-dimensional steady state, and hence this remains in agreement with the equilibrium analyses in this chapter. To find parameters corresponding to this behavior
one should design an oscillatory predator prey system like we did in Chapter 7, and use invasion criteria allowing each of the predators to invade at the average prey density in the attractor set by the other predators. An example of a model allowing for the non-equilibrium co-existence is

\[
\begin{align*}
\frac{dR}{dt} & = rR(1 - R/K) - a_1RN_1 - \frac{a_2RN_2}{h + R}, \\
\frac{dN_1}{dt} & = a_1RN_1 - d_1N_1, \\
\frac{dN_2}{dt} & = \frac{a_2RN_2}{h + R} - d_2N_2, \\
\end{align*}
\]

where one predator has a linear functional response and the other a saturated Holling type II response.

a. Use pencil and paper to find parameters delivering functional responses that intersect each other.

b. Use this to find parameter values for which the consumers co-exist. Check the invasion of each of the predators in the attractor of the other.

c. Can one obtain the same result when both predators have a saturated functional response?

**Question 9.4. Larvae and adults**

a. Write a simple model for an insect population with an early larval stage, and a late adult stage. Assume that larvae only compete among themselves, and make sure that the insect population as a whole has a carrying capacity.

b. Let there be two “predators”, one feeding on the larvae and the other on the adults, e.g., a wasp laying eggs in the larvae and birds eating the adults. Since these predators are foraging on the same species they seem to occupy the same niche. Can these two predators nevertheless co-exist?

**Question 9.5. Gradients**

Consider two vegetations in an environmental gradient. In the first gradient only one of the two dominant plant species (A or B) is present in each sample, whereas in the second gradient a gradual change in the abundance of the two species (C and D) is observed. A series of 9 samples taken from one end of the gradient to the other end was recorded as in Table 9.1. Assume that these samples reflect equilibrium situations.

a. Provide an intuitive explanation for the above data.

b. Interpret these data in terms of nullclines of the Lotka-Volterra competition model.

c. What do you think of your intuitive explanation now?

d. What variation in the data is not reflected in the models?

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<th>Species B</th>
<th>Gradient 2: Species C</th>
<th>Species D</th>
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<td>9</td>
<td>0</td>
<td>70</td>
<td>0</td>
<td>70</td>
</tr>
</tbody>
</table>

Table 9.1: The data for the Gradients question.
Question 9.6. Density dependent birth rate
In this chapter we used mass-action consumption terms, but made the birth rate of the consumer a saturation function of the amount of resources consumed. Since this seems realistic we will investigate what kind of density dependence this delivers for the consumers. To keep things simple start with a scaled resource equation for a replicating resource,

\[
\frac{dR}{dt} = R(1 - R) - aRN \quad \text{and} \quad \frac{dN}{dt} = \left[ b - \frac{aR}{h + aR} - d \right] N,
\]

where \( N \) is the consumer with a maximum birth rate \( b \). We proceed as normal: make a QSS assumption for the resource and substitute this into the consumer equations.

a. What is the \( R_0 \) of the consumer?

b. Write the complete ODE for a single consumer and combine parameters to have it in its simplest form.

c. What is now the \( R_0 \) of the consumer?

d. Sketch the \textit{per capita} birth rate of the consumer as a function of the consumer density.

e. Which of the growth models of Chapter 3 describes this best?

f. We considered a replicating resource in this question. If you have time you can also sketch the \textit{per capita} birth rate of the consumer for a non-replicating resource, e.g., \( \frac{dR}{dt} = 1 - R - aRN \), where source and death have been scaled.

Question 9.7. Tilman’s competition model
To simplify the model for two consumers using two essential resources Tilman (Tilman, 1980, 1982; McLean & May, 2007) used minimum functions rather than saturation functions, by assuming that for any combination of resource densities, there should be a single limiting resource, e.g.,

\[
\frac{dN_1}{dt} = b_1 \min \left( \frac{c_{11}R_1}{h_{11}}, \frac{c_{12}R_2}{h_{12}} \right) - d_1 N_1 \quad \text{and} \quad \frac{dN_2}{dt} = b_2 \min \left( \frac{c_{21}R_1}{h_{21}}, \frac{c_{22}R_2}{h_{22}} \right) - d_2 N_2,
\]

where \( c_{ij} \) is the consumption rate of consumer \( i \) on resource \( j \), and \( h_{ij} \) determines how much the consumer needs to eat from each resource. The minimum function makes the resources both “essential”, i.e., both have to be consumed in sufficient amount, and the birth rate is limited by the resource that is most needed (i.e., high \( h_{ij} \)) and/or consumed less (i.e., low \( c_{ij}R_j \)).

a. Sketch Tilman diagrams of this model. Explain that this indeed corresponds to two essential resources.

b. One can simplify the model with two non-replicating resources by scaling the resource densities and time by setting \( s = d = 1 \), and write the quasi steady state resource densities as

\[
R_1 = \frac{1}{1 + c_{11}N_1 + c_{21}N_2} \quad \text{and} \quad R_2 = \frac{1}{1 + c_{12}N_1 + c_{22}N_2}.
\]

Use the model \texttt{tilman.R} to study the phase space of the two consumers. It is helpful to first consider two consumer with very different diets, i.e., give each species a unique preference in \( c_{ij} \) and \( h_{ij} \), and see if you can get co-existence.

c. Change parameters to obtain both a stable and an unstable equilibrium in this model. Can you use the Routh-Horwitz criterion to read the stability directly from the Tilman diagram? Note, you can also use the \texttt{newton()} function in Grind to check the Jacobian.

Question 9.8. Fitness (challenging)
In this book we typically used the fitness \( R_0 = b/d \) to clean up the equations, and in Eq. (9.12) we have seen that the critical resource requirement, \( R^*_i = h_i / [c_i (R_{0i} - 1)] \), where \( R_{0i} = b_i / d_i \) defines which species is the best competitor. This \( R_0 \) is based upon an infinite resource density, however. We could also have used the carrying capacity of the resource to define the \( R_0 \), and
would then have arrived at a complicated expression for the fitness, i.e.,

$$\hat{R}^{0}_i = \frac{b_i}{d_i} \frac{c_i R}{R_i + c_i R},$$

where $\hat{R} = s/d$. Since this contains all parameters defining $R_i^*$, and one could think that the species having the highest fitness, $\hat{R}^{0}_i$, should be the best competitor, i.e., have the lowest $R_i^*$. Due to the fact that the birth rates are saturation functions of the amount of resources consumed, one can already see that this need not always be true, as a consumer that is best at high resource densities, need not be the best one at low resource densities, i.e., around $R^*$.

**a.** Can you formalize this and show that the species with the lowest fitness, $\hat{R}^{0}_i$, can be the best competitor?

**b.** A related challenge is to make a phase plane where a typical $r$-selected species, with rapid birth and death rates and a low carrying capacity, outcompetes a typical $K$-selected species.
Chapter 10

Co-existence in large communities

The scaled Lotka Volterra competition model of Eq. (9.19) has been used in many different theoretical studies of competition in ecosystems. Thanks to its simplicity it has few parameters, and this has allowed theoretical ecologists to define “understandable” models composed of many competing species. We here discuss a few examples. The first considers competition along a resource axis, and has the restriction discussed in Chapter 9 that all $\gamma_{ij}$ parameters are smaller than one. In the second example the author did allow for the “founder controlled” situations shown in Fig. 9.5d and Fig. 9.2c. The third example generalizes even beyond the Lotka-Volterra model and considers the Jacobian of a large (and undefined) dynamical system, and studies that matrix by filling it randomly.

10.1 Niche space models

There is an interesting modeling formalism for resource competition that is based on a resource axis along which species are distributed (see Fig. 10.1) (MacArthur, 1972; May, 1974; Scheffer & Van Nes, 2006). Think of several species of Darwin finches that each have a preferred seed size because they evolved different beak sizes. The preference of each species can be modeled with a simple Gaussian function of the seed size $x$, i.e., $f_i(x) = \exp[-(x - x_i)^2/(2\sigma^2)]$ that is centered around the preferred seed size $x_i$ of species $i$ (see Fig. 10.1). One can interpret this function as the probability of using a seed of size $x$, i.e., seeds of the preferred size are consumed with probability one. For simplicity one assumes that the species are evenly distributed over the niche space. This boils the whole problem of niche overlap down to two parameters, i.e., $\sigma$ for the standard deviation of the Gaussian functions, and $d$ for the difference between the preferred seed sizes of neighboring species. The niche overlap between species is completely determined by the region where their respective Gaussian functions overlap. One can define the niche overlap as the probability of both species eating seeds of the same size, i.e., as the product of the Gaussian preference functions, which implies that the niche overlap is highest at the point where two neighboring species both use a resource most. To properly scale this one can normalize with the overlap that a species has with itself:

$$\alpha = \frac{\int_{-\infty}^{\infty} e^{-\frac{x^2}{2\sigma^2}} \times e^{-\frac{(x-d)^2}{2\sigma^2}} \, dx}{\int_{-\infty}^{\infty} e^{-\frac{x^2}{2\sigma^2}} \times e^{-\frac{x^2}{2\sigma^2}} \, dx} = e^{-\left(\frac{d}{2\sigma}\right)^2}.$$  \hspace{1cm} (10.1)
Figure 10.1: Resource usage of three “finch species” consuming seeds of different sizes. The distance between the preferred seed size of neighboring species is $d$, and $\sigma$ is the standard deviation of the Gaussian seed size preferences. The niche overlap between neighboring species at distance $d$ is $\alpha$, and hence the overlap between species at distance $2d$ is $\alpha^4$ (see Eq. (10.1)).

This confirms that the niche overlap $\alpha$ only depends on the distance $d$ weighted by the standard deviation $\sigma$. With $\alpha = e^{-\left(\frac{d^2}{2\sigma^2}\right)}$, the overlap of a species with itself is indeed defined by a distance $d = 0$ because $\alpha = e^0 = 1$. The overlap between the first and the last species in Fig. 10.1 is determined substituting by their distance $2d$ into Eq. (10.1), i.e.,

$$e^{-\left(\frac{(2d)^2}{2\sigma^2}\right)} = e^{-4\left(\frac{d^2}{2\sigma^2}\right)} = \alpha^4.$$ (10.2)

Likewise, one can see that the niche overlap between species at distance $3d$ will be $\alpha^9$.

An ecosystem of $n$ competing species that are equally distributed at distances $d$ on a resource axis can therefore be described with the Lotka-Volterra competition model of Eq. (9.19),

$$\frac{dN_i}{dt} = rN_i \left(1 - \sum_{j=1}^{n} A_{ij}N_j\right),$$ (10.3)

where we now know all the elements of the interaction matrix,

$$A = \begin{pmatrix}
1 & \alpha & \alpha^4 & \alpha^9 & \alpha^{16} & \cdots \\
\alpha & 1 & \alpha & \alpha^4 & \alpha^9 & \cdots \\
\alpha^4 & \alpha & 1 & \alpha & \alpha^4 & \cdots \\
\alpha^9 & \alpha^4 & \alpha & 1 & \alpha & \cdots \\
\alpha^{16} & \alpha^9 & \alpha^4 & \alpha & 1 & \cdots \\
\cdots & \cdots & \cdots & \cdots & \cdots & \cdots 
\end{pmatrix}$$ (10.4)

and where we have given all species have the same natural rate of increase, $r$ (because the different $r_i$ in Eq. (9.19) play no role in the competitive strength of the species at steady state).

One can analyse this model by increasing its diversity $n$ one by one. A system of two species obeys

$$\frac{dN_1}{dt} = rN_1(1 - N_1 - \alpha N_2) \quad \text{and} \quad \frac{dN_2}{dt} = rN_2(1 - N_2 - \alpha N_1).$$ (10.5)
We have learned in Fig. 9.2d that this 2-dimensional ecosystem will have a stable non-trivial steady state whenever \( \alpha < 1 \). By our definition of the maximal niche overlap of \( \alpha = 1 \) one concludes that two species can be located infinitely close on the resource axis and co-exist, i.e., we obtain for the critical niche overlap of a 2-dimensional system that \( \alpha = 1 \) and \( d/\sigma \to 0 \). Note that this is an “artifact” of using the scaled version of the competition model, i.e., Eq. (9.19). If two species have different birth rates, consumption rates, death rates, and carrying capacities, they will not co-exist if the niche overlap is very small.

Next consider three species. What would be the maximal niche overlap, or the minimal distance \( d \), required for co-existence of all three species? This can be analyzed by considering Fig. 10.1 and numbering the species from left to right as \( N_1 \), \( N_2 \), and \( N_3 \). This is a symmetric system, i.e., the ODEs of \( N_1 \) and \( N_3 \) should have the same structure, and \( dN_2/dt \) should have the strongest competition because it has two direct neighbors, i.e.,

\[
\frac{dN_1}{dt} = rN_1(1 - N_1 - \alpha N_2 - \alpha^4 N_3),
\]
\[
\frac{dN_2}{dt} = rN_2(1 - N_2 - \alpha(N_1 + N_3)),
\]
\[
\frac{dN_3}{dt} = rN_3(1 - N_3 - \alpha N_2 - \alpha^4 N_1).
\] (10.6)

The existence and stability of the 3-dimensional steady state can be investigated by testing the invasion of the species in the middle, \( N_2 \), in the steady state of those at the ends. For this invasion criterion one first sets \( N_2 = 0 \) to compute the steady state of the 2-dimensional system. Employing the symmetry of the system one sets \( N_1 = N_3 \), and obtains their steady state by solving \( \bar{N} = 1/(1 + \alpha^4) \) from \( 1 - \bar{N} - \alpha^4 \bar{N} = 0 \). When \( N_2 \to 0 \) the invasion of \( N_2 \) is described by \( dN_2/dt \approx rN_2(1 - \alpha 2\bar{N}) \). This means that co-existence is guaranteed whenever

\[
1 - \frac{2\alpha}{1 + \alpha^4} > 0 \quad \text{or} \quad 1 + \alpha^4 - 2\alpha > 0.
\] (10.7)

This fourth order equation can be solved numerically as \( \alpha < 0.54 \) (or \( d/\sigma > 1.54 \)), which means that the maximal niche overlap of a 3-dimensional system is \( \alpha \approx 0.54 \).

For four species one can test when one of the two species in the middle can invade in an (asymmetric) system of three species, and for five species one can again test the middle species in a steady state of four established species, and so on. The results of such a sequence are summarized in Fig. 10.2a which depicts the maximal niche overlap as a function of the diversity \( n \) of the ecosystem. The figure reveals a fast convergence to \( \alpha \approx 0.63 \) (or \( d/\sigma \approx 1.3 \)). This convergence is due to the fact that the impact of the species at the very ends of the resource axis decreases when the diversity increases. The limit that is ultimately approached, i.e., \( d/\sigma \approx 1.3 \), is called the “limiting similarity”. This simply means that species cannot be too similar; otherwise they exclude each other. Because the maximum niche overlap converges to \( \alpha \approx 0.63 \) when the diversity increases, one speaks of “diffuse competition”: several species together determine the intensity of the competition on each species.

### Infinite resource axis

The original analysis of this model by May (1974) addressed the relationship between the niche overlap and the diversity of the system by considering an infinite resource axis along which infinitely many species were distributed at distance \( d \). An infinite system has the mathematical
advantage that the effects of the edges disappear, which means that all equations become identical. Thanks to this simplification May (1974) was able to compute the Jacobian of the infinite system, and could compute the dominant eigenvalue of the Jacobian as a function of the niche overlap $\alpha$. Because all equations were identical by the assumption of an infinite system, no single species could ever go extinct, and the dominant eigenvalues were simply approaching zero when the niche overlap $\alpha$ was approaching our limiting similarity of $\alpha \approx 0.63$. In our analysis we were breaking the symmetry of the system by distinguishing the species in the middle from those at the borders, and were obtaining (transcritical) bifurcation points by increasing $\alpha$, where the species in the middle disappeared. Because the symmetry could not break in the original infinite system, and the eigenvalues were approaching zero when the niche overlap was increased, May (1974) had to define variation in the abiotic circumstances that required the value of the dominant eigenvalue to remain below some critical negative level. Doing so he obtained a limiting similarity that is very similar to the one derived numerically in Fig. 10.2. The mathematical analysis of May (1974) is addressed further in the last (challenging) exercise.

Lizard man

Pianka (1974) measured the niche overlaps between several species of lizards in various desert habitats from all over the world. He distinguished three niche dimensions: (1) food, as determined from the contents of their stomachs, (2) habitat, and (3) the time of the day at which they were active. These observations were translated into a single measure of the niche overlap considering both additive and multiplicative measures for defining the total niche overlap. Pianka observed that the niche overlap decreased when the diversity of the ecosystem increased (see Fig. 10.2b). Thus, at low species numbers there was no evidence for a limiting niche overlap in the data (compare Fig. 10.2a with b). Because the diversity ranged from four to forty species, and the theoretical niche overlap of Fig. 10.2a converged already to 0.63 before a diversity of ten species, Pianka (1974) concluded that the data contradicted the theory.

A simple solution for this contradiction was proposed by Rappoldt & Hogeweg (1980) who argued that the niche space considered by Pianka (1974) was in fact not 1-dimensional. In a 2-dimensional niche space the Gaussian curves become circular and can be tiled in a hexagonal

---

Figure 10.2: The limiting overlap computed numerically for the model of Eq. (10.3) (a) with the file `niche.R`, and the results of Pianka (1974) (b).
lattice. In such a 2-dimensional lattice there are many more species at the borders of the niche space, and it takes a much higher diversity for the effects of the borders to peter out. The lizard data of Fig. 10.2b therefore confirm the theory, rather than contradict it, because Pianka indeed had more than one niche dimension in his data (Rappoldt & Hogeweg, 1980). Finally, Pianka (1974) observed that deserts with the highest amount of rain per year had the highest diversity, which is not surprising because the total production (and hence the length of the resource axis) is probably limited by the precipitation in deserts. Because the niche overlap decreased when the diversity increased (Fig. 10.2b), we can understand from this model that the amount of precipitation was correlated negatively with the average niche overlap (see Pianka (1974)).

10.2 Monopolization

For our second example we turn to Yodzis (1978) who was interested in the relation between the diversity of a community and the strength of its competitive interactions. It is indeed quite difficult to have a good intuition about this relation. One could argue that if there is more competition that there will be more competitive exclusion, and hence less diversity. Studies by Gardner & Ashby (1970) and May (1972) have also suggested that the more interactions there are in ecosystems, and the stronger the interaction strengths, the lower the probability that a diverse ecosystem will be stable (see below).

Yodzis (1978) created diverse in silico ecosystems in computer simulations changing the intensity of the competitive interactions and the initial diversity of the simulation. Running the model on a computer, several of the species in the initial pool went extinct until the simulation approached a diversity that remained at a reasonably stable level over long periods of time. The model ecosystem had a large number of habitats in which all species could be present, and there was a diffusive flux of individuals from habitat to habitat. The abiotic circumstances were considered to be identical in each of the habitats, i.e., the same competition coefficients were used everywhere.

Yodzis (1978) considered an initial pool of \( n \) different species that were randomly distributed over \( m \) habitats, and defined \( N_{ai} \) as the population size of species \( i \) in habitat \( a \). The flux of individuals of species \( i \) between habitats \( a \) and \( b \) was described by a symmetric “dispersal” matrix \( D \), where \( D_{ab} \) depends inversely on the distance from habitat \( a \) to \( b \), and defines the rate at which individuals move from \( a \) to \( b \). Since \( D_{ab} \) is a per capita flux, the total flux of individuals from species \( i \) at habitat \( a \) to \( b \) has to be multiplied with the local population density \( N_{ai} \). The net flux of individuals between two habitats is then given by

\[
\frac{dN_{ai}}{dt} = D_{ab}N_{bi} - D_{ba}N_{ai} = D_{ab}(N_{bi} - N_{ai}) ,
\]

(10.8)

given that \( D_{ab} = D_{ba} \) because the distance from \( a \) to \( b \) is the same as that from \( b \) to \( a \). Like in a diffusion equation, we observe that the net flux is proportional to the difference in the concentrations, i.e., the difference between population sizes in the two habitats.

Combining an \( n \)-dimensional form of Eq. (9.19) with Eq. (10.8) one ends up with a model ecosystem of \( n \times m \) ODEs

\[
\frac{dN_{ai}}{dt} = N_{ai}\left(1 - \sum_{j=1}^{n} A_{ij}N_{aj}\right) + \sum_{b=1}^{m} D_{ab}(N_{bi} - N_{ai}) ,
\]

(10.9)
Co-existence in large communities

Figure 10.3: Figure 5.5 in Yodzis (1989) page 144: the steady state diversity as a function of the initial number of species, for various intensities of the competition $C$.

for $a = 1, \ldots, m$ and $i = 1, \ldots, n$. Here $A_{ij}$ is the interaction matrix containing all competition coefficients. The growth rates were removed mathematically by giving all species the same growth rate, and scaling time by this fixed growth rate. All species were given the same intraspecific competition by setting $A_{ii} = 1, \forall i$. The other competition coefficients and the dispersal rates were drawn randomly.

From Eq. (9.19) and Fig. 9.2 we have learned that the outcome of competition between any two species depends crucially on the ratio of the interspecific competition parameters $\gamma$ and the intraspecific competition strength (that was scaled to one). If both $\gamma$-s happen to be smaller than one, the nullclines intersect in a stable steady state, and if both are larger than one the non-trivial steady state is a saddle point leading to founder controlled competition (see Fig. 9.2). Yodzis (1978) varied the randomly chosen interaction strengths and defined a “global” competition strength parameter, $C$, for the probability that a randomly chosen matrix element was larger than one, i.e., $C = P(A_{ij} > 1)$. The values of the interaction matrix, $A_{ij}$, were drawn from a normal (or uniform) distribution. Knowing $C$, stable coexistence between any pair of species is expected with probability $(1 - C)^2$, and the unstable founder controlled phase space is expected with probability $C^2$. Competitive exclusion is expected when $A_{ij} < 1$ and $A_{ji} > 1$, or $A_{ij} > 1$ and $A_{ji} < 1$, which will occur with probability $2C(1 - C)$. We can do a sanity check and see that the sum $(1 - C)^2 + C^2 + 2C(1 - C) = 1$. Yodzis (1978) considered systems in which stable coexistence should be rare, i.e., he was working with distributions yielding high values of $C$. Choosing $C \geq 0.9$ the probability of any species pair having a stable coexistence was small, i.e., maximally $(1 - C)^2 \leq 0.01$. The probability of finding the founder controlled situation is much higher, i.e., $C^2 \geq 0.81$. Having set all parameters, i.e., all matrix elements, the species were distributed randomly but scarcely over the patches, i.e., initially most species were only present in a few patches, and would only then start to disperse to all other patches.

Running the simulations until a steady state was approached, a fraction of the species in the initial species pool would typically go extinct, and the ecosystem approached the diversity depicted in Fig. 10.3. The figure shows that increasing the diversity of the initial species pool, and/or increasing the competition strengths, increased the final diversity of the ecosystem. This suggests that the more complex the ecosystem the higher its diversity, which is a controversial result (Gardner & Ashby, 1970; May, 1972, 1974; Grime, 1997; Hanksi, 1997; McCann et al., 1998). The reason why the diversity increases with competition strength in these simulations is its spatial embedding, i.e., in each habitat one initially finds only a small selection of the species. Having many founder controlled situations the species that settle initially in a habitat can approach their carrying capacity before other species invade and approach sufficiently large numbers to have a chance to win the competition. Basically the model is a “resident always wins” system, and the final diversity is largely determined by the number of species that are
10.3 Stability and Persistence

The relationship between the complexity of a biological system and its stability has been debated over decades. Based on fairly romantic considerations ecologists have liked to think that the more diverse and complex an ecosystem, the higher its degree of stability. However, one could also turn this around by arguing that stable ecosystems have had more time to become diverse. Importantly, it remains unclear what one means with the stability of an ecosystem. This could vary from the local neighborhood stability that we have considered in this course, i.e., robustness against perturbations of the population sizes around the steady state (which was measured by the return time), to a mere persistence over time. It is rather obvious that most ecosystems are not persisting in stable steady states, because they are all driven by seasonal fluctuations and other disturbances. Robustness to invasion by new species can also be considered to be a form of stability. Unfortunately, we have no well-defined modeling approach to study what properties of an ecosystem would make it resilient to disturbances like the removal or introduction of a species.

Classical studies of the properties of random Jacobian matrices representing the local neighborhood stability of steady states of complex systems have changed the thinking about the relationship between stability and complexity (Gardner & Ashby, 1970; May, 1972, 1974). Consider an arbitrary steady state of an arbitrary (eco)system, and address the question whether this steady state is expected to be stable. To do so, one can write a random Jacobian $J$, of a system with $n$ species. To keep the analysis manageable one poses the following requirements:

1. Let every population have a carrying capacity and the same return time to this carrying capacity. For the Jacobian matrix this means that all elements on its diagonal have the value $-1$ (i.e., $\forall J_{ii} = -1$).
2. The off-diagonal elements of the matrix are set with a probability $P$. Thus, $P$ determines the likelihood that two species are involved in an interaction. $P$ determines the connectivity of the system, i.e., each species is expected to have $P(n-1)$ interactions with other species.
3. The interaction elements that are set are drawn from a normal distribution with mean $\mu = 0$ and standard deviation $\sigma$.

Summarizing, one draws a random matrix with dimension $n \times n$ of the following form

$$J = \begin{pmatrix}
-1 & 0 & 0 & a & 0 & 0 & -b & 0 & \ldots \\
0 & -1 & 0 & 0 & 0 & c & \ldots \\
0 & 0 & -1 & 0 & \ldots \\
-\ldots & \ldots & \ldots & \ldots & \ldots \ldots
\end{pmatrix}, \quad (10.10)$$

and this matrix is interpreted as the Jacobian of a steady state of an (eco)system, where $a, b, \ldots, d$ are randomly chosen values from a standard normal distribution.

Having drawn such a random Jacobian matrix, the question is how its stability depends on the parameters $n$, $P$, and $\sigma$. One can use the theory on the dominant eigenvalue of large random matrices to prove that the probability that the largest eigenvalue is negative, i.e., $\lambda_{\text{max}} < 0$, strongly depends on the condition

$$\sigma \sqrt{nP} < 1. \quad (10.11)$$
The biological interpretation of this rather abstract analysis is that increasing the number of interactions per species, \( nP \), and/or increasing the absolute interactions strengths, \( \sigma \), decreases the chance that the steady state is stable. This suggests that complex systems cannot a priori expected to be stable (Gardner & Ashby, 1970; May, 1972, 1974).

This result seems to contradict the co-existence of the many species in the niche space model (MacArthur, 1972; May, 1974). However, note that in the niche space model the average interaction strength decreases when the diversity increases (see Eq. (10.4)). Increasing the diversity \( n \) therefore implicitly decreases the interaction strength \( \sigma \). This may also be true for natural systems: when the number of species \( n \) increases, the number of connections per species, \( nP \), need not increase, and their average connection strength, \( \sigma \), may decrease.

A simple criticism on the analysis is that it only considers one steady state of the system, and that complex systems could have very many steady states, of which only one a few need to be stable to guarantee its persistence as a high-dimensional system. Thus, the ecosystem could be stable and still complex, after a few of its species have gone extinct. Despite these easy criticisms this work has changed the consensus view of “diversity entails stability” into the question “how come that complex systems persist over long periods of time?”.

## Persistence

The relationship between system complexity and diversity has also been studied in non-equilibrium conditions (Law & Blackford, 1992; Yodzis, 1989; Pimm, 1980; Post & Pimm, 1983). The basic approach is to make ecosystems with a predefined food chain structure and create many species by giving them randomly selected parameter values. Sometimes one finds that such randomly created ecosystems remain diverse in the absence of a stable steady state, i.e., they persist on a periodic or chaotic attractor (Law & Blackford, 1992). In other studies only a fraction of the randomly created ecosystems persists with all species present in an \( n \)-dimensional steady state (Roberts, 1974), and one could argue that these correspond to the type of systems one finds in nature. The last analysis confirms the classical random Jacobian analysis because the fraction of systems with an \( n \)-dimensional steady state decreases when the complexity increases (Roberts, 1974; Tilman et al., 1997).

## 10.4 Summary

The simplicity of the scaled Lotka-Volterra competition model has allowed us to formulate interesting and understandable models for large communities. When a sufficient number of species is packed along a (long) resource axis their degree of competition approaches a fixed niche overlap called “diffuse competition”. The species diversity at which this happens depends on the number of resource axes taken into consideration. Ecosystem diversity may also come about by a spatial distribution of species that is largely determined historically by the initial seeding of the system. The relationship between the diversity or complexity of an ecosystem and its degree of stability is not well established. Most ecosystems are not persisting in the neighborhood of stable steady states anyway. Non-equilibrium persistence, and robustness to invasion by novel species, are better measures of the long-term stability of ecosystems.
10.5 Exercises

Question 10.1. Invasion criterion
Consider a species immigrating into an area in which two other species are present that do not compete with each other. Each of these two species therefore has a density equal to the carrying capacity, and let the new species compete equally with the other two species. Assume that the carrying capacities are the same for all three species.

a. Assume that competition takes place in a one dimensional resource space like the one depicted in Fig. 10.1. Redraw the figure for this system where the established species do not compete, and where the new species competes with both.

b. Make an ODE model of three equations.

c. Determine the parameter conditions for successful invasion of the third species in the steady state of the other two.

d. Give a biological interpretation in terms of competition strengths.

e. Sketch the 3-dimensional phase space of this system for the invasion criterion. What do you expect to happen if the new species invades successfully?

Question 10.2. Control by parasites
Consider a population of songbirds with a birth rate that declines linearly with the population size, and have a death rate that is independent of the population density. Let the individuals be susceptible to an infection with a parasite that increases the death rate somewhat, but hardly affects the birth rate. Assume that transmission of parasites occurs upon contacts between infected and susceptible individuals, and obeys mass action kinetics. Let there be no vertical transmission, i.e., the parasite is not transmitted to eggs.

a. Write a natural model.

b. What is the $R_0$ and the carrying capacity of the population in the absence of the parasite?

c. What is the $R_0$ of the infection?

d. What is the population density of the susceptibles when the parasite is endemic?

e. Suppose this songbird competes with related bird species that occupies the same niche, but has a somewhat shorter life span, and is not susceptible to the parasite. Write a natural model for the 3-dimensional system.

f. Do you expect the resistant bird species to be present?

g. What would you expect for a large community of bird species, all sharing the same resource, but each being susceptible to a host specific parasite species?

Question 10.3. Monopolization
In the scaled Lotka Volterra model of Eq. (9.19) we have seen that the natural rate of increase of a species, $r_i$, has no effect on the competitive ability of a species. We know this is a consequence of the scaling because we also know that it is the species with the lowest resource requirements, $R_i^*$, that is the best competitor, and that $R_i^*$ depends on several parameters, including the birth and death rates, and hence the natural rate of increase $r_i = b_i - d_i$. In the model of Yodzis (1989) the natural rates of increase were also removed, see Eq. (10.9).

a. Do you expect that if species were to have different growth rates, that those with fast growth rates would be expected to survive better in the simulations?

b. Would this make a difference for the general conclusion that the diversity increases with the intensity of the competition?

Question 10.4. Symbiosis
This book has a strong emphasis on the resource competition between species that comes about whenever they are feeding on shared resources, and on direct interference competition. This
seems a rather negative view on ecology because many species are also involved in symbiotic interactions. These come in two basic forms: obligatory symbionts cannot grow in the absence of each other, and facultative symbionts help each other but do not strictly require each other.

**a.** Write a model for two symbionts that strictly require each other, and study your model by phase plane analysis (a model is available as the file `symbiosis.R`).

**b.** Change the previous model in an asymmetric symbiotic interaction. Let the first species be dependent on the second, and let the second be ignorant of the first. An example would be saprophytes.

**c.** Write a model for a facultative symbiosis.

**d.** Can you change the latter model into a model of obligatory symbionts by just changing the parameters?

**Question 10.5. Infinite niche space (Challenging)**

In an infinite implementation of Eq. (10.3) all species obey the same ODE

\[ \frac{dN_i}{dt} = N_i(1 - \sum_j A_{ij} N_j) , \]

which implies that they all have the same steady state

\[ \bar{N} = 1/\sum A_{ij} = 1/(1 + 2\alpha + 2\alpha^4 + 2\alpha^9 + \ldots) \simeq 1/(1 + 2\alpha) . \]

**a.** What is the Jacobian of this steady state? Hint: do not substitute the expression for the equilibrium density, but write \( \bar{N} \), and observe that the elements on the diagonal can be written as \( 1 - \bar{N} - \sum A_{ij} \bar{N} \).

**b.** Can one obtain the stability of the system directly from the interaction matrix \( A \), or should one first compute the Jacobian?

**Question 10.6. Random Jacobian**

On the website we provide an R-script `gardner.R` that fills a random fraction, \( P \), of the off-diagonal elements of a matrix with random numbers drawn from a normal distribution with an average \( \mu \) = 0 and a standard deviation \( \sigma \). All diagonal elements are set to \(-1\), and the dominant eigenvalue, \( \lambda \), is calculated. Interpreting this random matrix as the Jacobian of some dynamical system you can use this script to numerically repeat the analysis of Gardner & Ashby (1970) and May (1972, 1974).

**a.** What is the dominant eigenvalue when the connectivity, \( P \), is very low?

**b.** Can you confirm their result that \( \lambda < 0 \) when Eq. (10.11) holds?

**c.** There will be pairwise interactions in this matrix where (at the steady considered by this random Jacobian) where the populations seem to have a mutualistic interaction, i.e., \( J_{ij} > 0 \) and \( J_{ji} > 0 \). Do the results change if you don’t allow for such interactions?

**d.** The consumers in the models we have discussed typically do not have \( J_{ii} = -1 \) diagonal elements when we derive the Jacobian of their steady states. How would the results change when not all diagonal elements are set to \(-1\)?.
Chapter 11

Bifurcation analysis

In several chapters of this course we have encountered examples where the properties of a steady state changes at some critical parameter value. A good example is the steady state of the Monod saturated predator prey model which changes stability precisely when the vertical predator nullcline intersects the top of the parabolic prey nullcline. We have seen that at this “Hopf bifurcation point” the stability of the steady state is carried over to a stable limit cycle. In the same model there was another bifurcation point when the predator nullcline crosses the carrying capacity of the prey. This is a so-called “transcritical bifurcation” at which the presence of the predator is determined. In ODE models there are only four different types of bifurcations that can happen if one changes a single parameter. This chapter will illustrate all four of them and explain each of them in simple phase plane pictures.

Bifurcation diagrams depict what occurs when one changes a parameter, and therefore provide a powerful graphical representation of the different behaviors a model may exhibit for different values of its parameters. Bifurcation diagrams are typically made with special purpose software tools (like MatCont or XPPAUT); Grind has a fairly primitive algorithm for continuing steady states. In the exercises you will be challenged to sketch a few bifurcation diagrams with pencil and paper.

Several other bifurcations may occur if one changes two parameters at the same time. These can be summarized in 2-dimensional bifurcation diagrams, which can provide an even better overview of the possible behaviors of a model. Such 2-dimensional bifurcations will not be discussed here, and we refer you to books or courses on bifurcation analysis.

11.1 Hopf bifurcation

At a Hopf bifurcation a limit cycle is born from a spiral point switching stability. This was already discussed at length in Chapter 7 for models with a saturated functional response. Fig. 11.1 depicts the nullclines of a predator prey model with a sigmoid functional response for several different values of the death rate, \(d\), of the predator \(N\). In Chapter 7 we already calculated for the model

\[
\frac{dR}{dt} = rR(1 - R/K) - \frac{bR^2N}{h^2 + R^2} \quad \text{and} \quad \frac{dN}{dt} = \frac{cbRN^2}{h^2 + R^2} - dN ,
\]

(11.1)
that the non-trivial predator nullcline is a vertical line located at the prey density $R = \sqrt{\frac{h^2}{cb/d-1}} = h/\sqrt{R_0-1}$. Thus by changing the predator death rate $d$ one moves the predator nullcline, and because the predator death rate is not part of the ODE of the prey, the prey nullcline remains identical.

First consider values of the death rate $d$ in Fig. 11.1 for which the predator nullcline is located at the right side of the top of the humped prey nullcline. The graphical Jacobian is

$$A = \begin{pmatrix} -a & -b \\ c & 0 \end{pmatrix}$$

such that $\text{tr} = -a < 0$ and $\text{det} = bc > 0$. (11.2)

Close to the top of the prey nullcline the discriminant of this matrix, $D = a^2 - 4bc$, will become negative, and the steady state is a stable spiral point with eigenvalues $\lambda_{\pm} = -a \pm ib$. (Below we will see that the same steady state will be a stable node when the nullcline intersects in the neighborhood of the carrying capacity.) Decreasing the parameter $d$ the predator nullcline is shifted to the left, and will cross through the top of the prey nullcline. When located left of this top the graphical Jacobian is

$$A = \begin{pmatrix} a & -b \\ c & 0 \end{pmatrix}$$

such that $\text{tr} = a > 0$ and $\text{det} = bc > 0$. (11.3)
11.1 Hopf bifurcation

Figure 11.2: A bifurcation diagram with the two Hopf bifurcations of Fig. 11.1. The circles in panel (b) depict the stable limit cycle that exist between the two Hopf bifurcations for many different values of the parameter $d$.

Close to the top the discriminant, $D = a^2 - 4bc = tr^2 - 4 \det$, will remain to be negative, and the steady state is an unstable spiral point.

For the critical value of $d$ where the nullcline is located at the top, i.e., at $(K - h)/2$ (see Chapter 7) the graphical Jacobian is

$$A = \begin{pmatrix} 0 & -b \\ c & 0 \end{pmatrix}$$

such that $tr = 0$ and $det = bc > 0$.

The imaginary eigenvalues $\lambda_{\pm} = \pm ivbc$ have no real part and correspond to the structurally unstable equilibrium point of the Lotka Volterra model lacking a carrying capacity of the prey (see Eq. (5.19)). Summarizing, at a Hopf bifurcation a complex pair of eigenvalues moves through the imaginary axis. At the bifurcation point the steady state has a neutral stability, and a limit cycle is born.

Fig. 11.1 has little diagrams displaying the nature of the eigenvalues in so-called “Argand diagrams”. These diagrams simply depict the real part of an eigenvalue on the horizontal axis, and the imaginary part on the vertical axis (see Fig. 13.8). In these diagrams a complex pair of eigenvalues is located at one specific $x$-value with two opposite imaginary parts, and a real eigenvalue will be a point on the horizontal axis. The Hopf bifurcation can neatly be summarized as a complex pair moving horizontally through the vertical imaginary axis (see Fig. 11.1).

This is summarized in the bifurcation diagram of Fig. 11.2 which depicts the steady state value of the predator as a function of its death rate $d$. Stable steady states are drawn as heavy lines, and unstable steady states as light lines. We have chosen to have the predator on the vertical axis to facilitate the comparison with the phase portrait of Fig. 11.1, which also has the predator on the vertical axis (note that if we had chosen the prey on the vertical axis the steady state would be a line at $R = h/\sqrt{R_0 - 1}$). Sometimes one depicts the “norm”, i.e., $N^2 + R^2$, on the vertical axis, but this all remains rather arbitrary because it is not so important what is
Bifurcation analysis

Figure 11.3: The phase space for three values of $d$ around a transcritical bifurcation (a), and the bifurcation diagram (b) of a transcritical bifurcation with $d$ as the bifurcation parameter on the horizontal axis.

exactly plotted on the vertical axis as long as it provides a measure of the location of the steady state. The bifurcation diagram displays another Hopf bifurcation that occurs when the predator nullcline goes through the minimum of the prey nullcline. Between these critical values of $d$ there exits a stable limit cycle, of which we depict the amplitude by the bullets in Fig. 11.2b. Decreasing $d$ the limit cycle is born at the top and dies at the bottom of the prey nullcline, increasing $d$ this would just be the other way around. Fig. 11.2 does provide a good summary of the behavior of the model as a function of the death rate $d$.

In Fig. 11.2b the amplitude of limit cycle is depicted by the bullets reflecting predator densities at some predefined prey density. Conventionally closed circles are used to depict stable limit cycles, and open circles are used for unstable limit cycles (that we have not discussed explicitly in this book; but there is one in on the front page. To depict and study limit cycles one typically plots the predator value when the limit cycles crosses through a particular prey value. Such a prey value is called a Poincaré section, and on this Poincaré plane one can define the limit cycle as a map, mapping one point on the section to the next crossing by the limit cycle. The stability of the limit cycle is then determined from the “Floquet multipliers” of this map. This will not be explained any further in this book.

11.2 Transcritical bifurcation

If one increases the death rate $d$ in the same model, the predator nullcline moves to the right. As long as this nullcline remains left of the carrying capacity the non-trivial steady state will remain stable. However, at one specific value of $d$ it will change from a stable spiral into a stable node. In the Argand diagram this means that the complex pair collapses into a single point on the horizontal axis, after which the eigenvalues drift apart on the horizontal (real) axis (see Fig. 11.3). When the predator nullcline is about to hit the carrying capacity, one can be sure the
11.3 Saddle node bifurcation

The saddle-node bifurcations that occur in the sigmoid predator prey model of Eq. (11.1) are famous because of their interpretation of catastrophic switches between rich and poor steady states that may occur in arid habitats like the Sahel zone (Noy-Meir, 1975; May, 1977; Rietkerk & Van de Koppel, 1997; Scheffer et al., 2001; Scheffer, 2009; Hirota et al., 2011; Veraart et al., 2012). To illustrate this bifurcation one can treat the predator density as a parameter, representing the number of cattle (herbivores) that people let graze in a certain habitat. This reduces the model of Eq. (11.1) to the \( dR/dt \) equation. The steady states of this 1-dimensional model are depicted in Fig. 11.4a with the number of herbivores, \( N \), as a bifurcation parameter plotted on the horizontal axis. Because this parameter is identical to the predator variable plotted on the vertical axis of the phase spaces considered before, these steady states simply correspond to the \( dR/dt = 0 \) nullcline. The bifurcation diagram shows two saddle-node bifurcations (see Fig. 11.4a). At some critical value of the herbivore density on the upper branch, corresponding to a rich vegetation, disappears. At intermediate herbivore densities the vegetation can be in one of two alternative steady states, that are separated by an unstable branch (see Fig. 11.4a). This bifurcation diagram has the famous hysteresis where, after a catastrophic collapse of the vegetation, one has to sell a lot of cattle before the vegetation recovers (Noy-Meir, 1975; May, 1977; Rietkerk & Van de Koppel, 1997; Scheffer et al., 2001; Scheffer, 2009).
To show a more complicated bifurcation diagram with a Hopf bifurcation, and two different saddle-node bifurcations in the same predator prey model, we extend Eq. (11.1) with direct interference competition between the predators, i.e.,

$$\frac{dN}{dt} = \frac{cbNR^2}{h^2 + R^2} - dN - eN^2. \quad (11.5)$$

To illustrate the saddle node bifurcations we will study the model as a function of the competition parameter $e$, and will sketch a bifurcation diagram with $e$ on the horizontal axis (see Fig. 11.4).

First, choose a value of the death rate, $d$, such that the predator nullcline intersects at the left of the valley in the prey nullcline (see Fig. 11.4a). For $e = 0$ there is a single stable steady state. Increasing $e$ the predator nullcline will bend because the predator nullcline can be written as the sigmoid function

$$N = \frac{(cb/e)R^2}{h^2 + R^2} - d/e, \quad (11.6)$$

intersecting the horizontal axis at the now familiar $R^* = h/\sqrt{R_0 - 1}$. The prey nullcline remains the same because it does not depend on the $e$ parameter. By increasing the curvature with $e$, this low steady state first undergoes a Hopf bifurcation in the valley of the prey nullcline (see Fig. 11.4b & c). Then the predator nullcline will hit the prey nullcline close its top (see the arrow), which creates two new steady states at a completely different location in phase space. Increasing $e$ a little further leads to the formation of two steady states around this first intersection point (see the other arrow). One is a saddle point and the other a unstable node (see Fig. 11.4c). A “saddle node” bifurcation is a catastrophic bifurcation because it creates (or annihilates) a completely new configuration of steady states located just somewhere in phase space.

### 11.4 Pitchfork bifurcation

Thus far we have discussed three bifurcations, i.e., the Hopf, transcritical, and saddle node bifurcation, and we could all let them occur in a conventional predator prey model. The fourth, and final, bifurcation is called the pitchfork bifurcation, and can be demonstrated from the scaled competition model of Eq. (9.19) extended with a small immigration term:

$$\frac{dN_1}{dt} = i + rN_1(1 - N_1 - cN_2) \quad \text{and} \quad \frac{dN_2}{dt} = i + rN_2(1 - N_2 - cN_1). \quad (11.7)$$
Whenever the competition parameter $c$ is smaller than one, the species are hampered more by intraspecific competition than by interspecific competition, and they will co-exist in a stable node (see Fig. 11.5a), and there will be one stable steady state. Increasing $c$ above one will change this node into the saddle point corresponding to the unstable founder controlled competition (see Fig. 11.5b). In between these two cases there is a bifurcation point of $c$, where one real eigenvalue goes through zero (see Fig. 11.5c). Because of the hyperbolic nature of the nullclines, one can see that when the non-trivial steady state becomes a saddle, the nullclines form new steady states around the two carrying capacities. These new states are stable nodes (see Fig. 11.5b & c). In the bifurcation diagram this is depicted as two branches, one for the stable node becoming a saddle point, and one for the stable nodes born at the bifurcation point. Because of the shape of the solutions in this bifurcation diagram this is called a pitchfork bifurcation.

Both the pitch fork bifurcation and the Hopf bifurcation have mirror images. At a so-called subcritical Hopf bifurcation point an unstable limit cycle is born from an unstable spiral point becoming stable. In a subcritical pitchfork bifurcation, an unstable branch of two outward steady states encloses a stable branch in the middle. Both will not further be discussed here.

11.5 Period doubling cascade leading to chaos

Having covered all possible bifurcations of steady states in ODE models we will illustrate one bifurcation that limit cycles may undergo when one parameter is changed, i.e., the period doubling bifurcation. This bifurcation will again be explained by means of a simple example, because it occurs in a large variety of models. The bifurcation is interesting because a cascade of period doubling bifurcations is a route to chaotic behavior. In ODE models we have discussed two types of attractors: stable steady states and stable limit cycles. A chaotic attractor, or strange attractor, is a third type of attractor that frequently occurs in ODE models (with at least three variables).

The example is taken from Yodzis (1989) and is a model with two prey species that are eaten...
Figure 11.7: Period doubling cascade of the limit cycle of Eq. (11.8). In Panel (a) the model behavior is a simple limit cycle, in Panel (b) the limit cycle makes two loops before returning to the same point, in Panel (c) we see a chaotic attractor. This Figure was made with the file rrn.R.

by a single predator

\[
\begin{align*}
\frac{dR_1}{dt} &= R_1(1 - R_1 - \alpha_{12}R_2) - a_1R_1N, \\
\frac{dR_2}{dt} &= R_2(1 - R_2 - \alpha_{21}R_1) - a_2R_2N, \\
\frac{dN}{dt} &= N(ca_1R_1 + ca_2R_2 - 1),
\end{align*}
\]

(11.8)
11.5 Period doubling cascade leading to chaos

Figure 11.8: Period doubling cascade of the limit cycle of Eq. (11.8) illustrated by plotting 200 values of $R_1$ obtained for many different values of $a_1$. The values of $R_1$ are recorded when the trajectory crosses a Poincaré plane located around $R_2 = 0.8$. Note how similar this is to the famous bifurcation diagram of the Logistic map.

with simple mass-action predation terms. Time is scaled with respect to the death rate of the predator, and both carrying capacities have been scaled to one. Setting the parameters $\alpha_{12} = 1$ and $\alpha_{21} = 1.5$ the prey species exclude each other in the absence of the predator (see Fig. 11.6). The behavior of the model is studied by varying the predation pressure, $a_1$, on the winning species. By setting $a_2 = 1$ and $c = 0.5$, i.e., $ca_2 = 0.5$, the model is designed such that the predator cannot survive on $R_2$ alone. For $3.4 \leq a_1 \leq 5.5$ one obtains a stable steady state where all three species co-exist. Around $a_1 = 5.5$ this steady state undergoes a Hopf bifurcation, and a stable limit cycle is born. (Note that at $a_1 = 3.4$ a transcritical bifurcation allows the second prey to invade (because the first one suffers sufficiently from the predation), and that at $a_1 = 2$ a second transcritical bifurcation occurs when the predator can invade.)

Fig. 11.7 shows what happens if $a_1$ is increased further. For $a_1 = 6$ there is a simple stable limit cycle that was born at the Hopf bifurcation (see Fig. 11.7a). At $a_1 = 8$ this limit cycle makes two rounds before returning to its starting point: the period has approximately doubled at a period doubling bifurcation somewhere between $6 < a_1 < 8$. This repeats itself several times, and at $a_1 = 10$ the system is already chaotic (see Fig. 11.8).

Chaotic behavior is defined by two important properties:
1. An extreme sensitivity for the initial conditions. An arbitrary small deviation from a chaotic trajectory will after sufficient time expand into a macroscopic distance. This is the famous “butterfly” effect where the disturbance in the air flow caused by a butterfly in Africa flying to the next flower causes a rainstorm in Europe after a week.
2. A fractal structure: a strange attractor has a layered structure that will appear layered again when one zooms in (e.g., see Fig. 11.8).

The first property is obviously important for the predictability of ecological models. It could very well be that one will never be able to predict the precise future behavior of several ecosystems (like we will never be able to predict the weather on June 17 in the next year). This sensitivity comes about from the “folding” and “stretching” regions in strange attractors where many trajectories collapse and are torn apart again.
11.6 Summary

Varying a single parameter of an ODE model its steady states may undergo four different bifurcations. Some are catastrophic because they involve a large jump in phase space. Bifurcation diagrams provide an excellent summary of the possible behaviors of a model. We have discussed chaotic behavior to demonstrate that it is one of the common and expected behaviors of simple ecological models. Despite being strange it is a normal behavior.

11.7 Exercises

Question 11.1. Biomanipulation
Lakes often look green because of eutrophication. Such lakes have a high density of algae and fish, and little zoo-plankton. Experiments show that catching sufficient fish can make the water clear again. Scheffer (1991) proposed the following model:

\[
\frac{dA}{dt} = A(1 - A/k) - pZ \frac{A}{1 + A},
\]

\[
\frac{dZ}{dt} = -mZ + pZ \frac{A}{1 + A} - F \frac{Z^2}{h^2 + Z^2},
\]

where \(A\) represents algae and \(Z\) zoo-plankton. Basically, this is the same Holling type II model as considered above, extended with predation by a fixed density of the fish, \(F\), having a sigmoid functional response. Study the model for the parameters: \(h = 1, m = 0.4, p = 0.5, 5 \leq k \leq 15,\) and \(0 \leq F \leq 1;\) see the model fish.R.

a. Choose different values for the parameters indicated by the ranges, and draw nullclines.
b. Is it possible to have a permanent effect by temporarily (e.g., once) removing a large fraction of the fish?
c. Sketch the bifurcation diagram of the model with the carrying capacity \(K\) on the horizontal axis.
d. Identify all the bifurcations.
Chapter 12

Numerical exercises

12.1 Grind

Most phase portraits in this book were made with a computer program called Grind, for Great integrator differential equations. The current version of Grind is an R-script called grind.R (previous versions were coded in C or Fortran: Grind has a very long history that started in 1983!). Grind is based upon the R-packages deSolve, FME, and rootSolve developed by Karline Soetaert and colleagues (Soetaert & Herman, 2009; Soetaert et al., 2010; Soetaert, 2009; Soetaert & Petzoldt, 2010), and uses a function in R for plotting contour lines to make phase planes. Grind simplifies the interface to these libraries by defining five easy-to-use functions:

- **run()** integrates a model numerically and provides a time plot or a trajectory in the phase plane,
- **plane()** draws nullclines and can provide a vector field or phase portrait,
- **newton()** finds steady states (using the Newton-Raphson method) and can provide the Jacobian with its eigenvalues and eigenvectors,
- **continue()** performs parameter continuation of a steady state, providing a bifurcation diagram,
- **fit()** fits a model to data by estimating its parameters, and depicts the result in a timeplot.

The best way to get started is to download the manual, [http://tbb.bio.uu.nl/rdb/grindR/tutorial.pdf](http://tbb.bio.uu.nl/rdb/grindR/tutorial.pdf), and run a few of the tutorials. We will work in the RStudio environment, which has a window for the code, a console window, a window defining the environment, and a window for asking help or viewing graphics. Download the **grind.R** and the **lotka.R** files from the [http://tbb.bio.uu.nl/rdb/grindR/](http://tbb.bio.uu.nl/rdb/grindR/) webpage, store them in a local directory, and open both of them via the **File** menu. Both will be tabs in the code window. Set the working directory to the folder where your R-codes are stored (Set working directory in the **Session** menu of RStudio). Files with then be opened and saved in that directory.

First “source” the **grind.R** file (button in right hand top corner) to define the five functions. (In case you get an error message like “Error in library(deSolve): there is no package called deSolve”, the three Soetaert libraries have to be installed by using Install Packages in the **Tools** menu of RStudio). When **grind.R** is successfully “sourced”, it is time to “run” the model with its parameter and state definitions from the **lotka.R** script. In the R-console below the **lotka.R** panel, one can then type the function calls given in the example session below. Once you have a picture that you like, you may copy the lines creating that figure into the **lotka.R**
window for later usage. (Use “Run” or “Control Enter” to execute lines from the `lotka.R` panel into the console).

Start with tutorial 1 on phase plane analysis and parameter continuation. Read tutorials 2, 3, and 4 on events, delay equations, and vectors, and finish off with tutorial 5 on parameter estimation. Next embark on the following numerical exercises.

### 12.2 Numerical exercises

#### Question 12.1. Paradox of Enrichment
Repeat the Rosenzweig (1971) analysis with the Holling type II consumer resource model:

\[
\frac{dR}{dt} = bR(1 - R/k) - d_1R - \frac{eNR}{h + R} \quad \text{and} \quad \frac{dN}{dt} = -d_2N + \frac{ceNR}{h + R},
\]

which is provided on the website as `rosenzweig.R`.

- **a.** Think about simple and reasonable parameter values. Use pencil and paper during your computer exercises: make sure that populations can grow, i.e., have an $R_0 > 1$.
- **b.** Draw nullclines, check the various possibilities, and run trajectories for each case.
- **c.** Study the effect of eutrophication by increasing the carrying capacity.
- **d.** Continue the non-trivial steady state as a function of $k$ (with the `continue()` command).
- **e.** Do the same for a model having a functional response with “predator interference”.
- **f.** Replace the $f = R/(h + R)$ functional response by one with a refugium with a size of $r$ prey individuals, i.e., $\hat{R} = \max[0, R - r]$ and $f = \hat{R}/(h + \hat{R})$; see Page 59 and the R-file `refugium.R` where the `pmax()` function is called.

#### Question 12.2. Fishing herring
In Chapter 3 you made an exercise on fishing a population of herring. We had the following model:

\[
\frac{dH}{dt} = rH(1 - H/k) - Q
\]

where $Q$ is the quorum that was allowed to be caught per unit of time. Although the maximum yield was $rk/4$ we showed that one cannot set the quorum to $Q = rk/4$.

- **a.** Confirm your earlier analysis by setting $Q = rk/4$ and study a population of herring with a carrying capacity that fluctuates somewhat due to weather conditions (you may use the file `herring.R` for this).
- **b.** Now replace the fixed quorum by a fraction $f$ that one can maximally catch, i.e., study $dH/dt = rH(1 - H/k) - fH$, again allowing for a noisy carrying capacity.
- **c.** What is economically speaking the optimal value of $f$? Hint: compute the steady state, $\bar{H}$, and the expected harvest, $f\bar{H}$, and compute its maximum by taking the derivative $\partial f$.
- **d.** Study the model for this optimal $f$ for a noisy carrying capacity. What happens if you allow for “human error”, i.e., if you allow for noise on $f$?
- **e.** What is the expected harvest at this optimal $f$? Is that lower than $Q = rk/4$?

#### Question 12.3. Fitting the Gause data from 1934
The classical experiments of Gause (1934) demonstrated that two species cannot coexist on a single resource. In his experiments he was growing several species Paramecium either in isolation, or in combination. In the figure on the left you see that the growth curve of P. aurelia and P. caudatum on their own can very reasonably be described by a logistic growth equation, and in Gause’s own handwriting one can read the parameter values he estimated for the logistic function. To describe the competition the logistic equation was extended into a Lotka Volterra competition model (see Eq. (9.19)), but the two competition coefficients cannot be read from the figure. Let’s go and fit this data to verify the parameters provided in the Figure, and establish the two unknown competition parameters. Read Section 13.8 in the Appendix for some background on parameter fitting.

a. The data is available in the directory data on the website, in the files aurelia1 and caudatum1 for the solitary experiments, and in the files aurelia2 and caudatum2 for the combined experiment. The file GauseLV.R allows you to read the files and fit the data. Note that the model contains a “dummy” parameter on which is 0 or 1 to switch between solitary and combined experiments. Take Gause’s estimates as an initial guess, and fit both solitary data sets to estimate the rate of increase and carrying capacity of both species. Do you obtain a good fit and do your estimates agree with Gause’s estimates?

b. Next save the new estimates in the parameter vector p, and estimate the two competition parameters α and β. Which species suffers most from its competitor? Would you have expected that? Hint: sketch the nullclines for the estimated parameters.

c. Since one of the competition parameters is larger than one, it seems that that particular species suffers more from its competitors than from its conspecifics. Can this be explained by resource competition?

d. Fitting the data in two separate steps need not deliver the best possible combination of parameter estimates. Therefore, also fit the four data sets simultaneously to for all parameters (except for the initial conditions). Note that you have to fix the dummy parameter on to allow for competition only in the last two data sets. Do you find very different results?

e. Finally, one can do the same fitting while bootstrapping the data to obtain confidence intervals on the estimates. Do these confidence intervals suggest that all parameters are identifiable? Are the two competition parameters α and β sufficiently different to indeed conclude that α > β?

f. On the website we also provide a more mechanistic model in which the two species consume a resource (see the file GauseMonod.R). With this model you can test whether or not these results could just be due to resource competition. Do check the identifiability of the parameters.

**Question 12.4. Cryptic oscillations**
The now classical experiments of Bohannan & Lenski (1997) demonstrated that when *E. coli* is cultured with its bacteriophage T4, the system can initially display predator-prey like oscillations, and later develop so-called “cryptic” oscillations where the phage densities continue to oscillate, but the *E. coli* densities become stable. The solid line in the Figure depicts the total population size of *E. coli* and the dotted lines that of the T4 phage. They study this in more detail in a later paper (Bohannan & Lenski, 1999), and this data is also discussed in Figure 4.6 of the excellent book of Weitz (2015), See Yoshida et al. (2007) for a paper on cryptic oscillations in algae-zooplankton communities.

**Question 12.5. Lymphocyte migration**

Naive T cells in the immune system circulate via the blood between various lymphoid organs, such as the spleen and many different lymph nodes. The residence time in the blood is short, and under normal conditions only a small percentage of the naive T cells reside in the blood. In the spleen the residence time is about 6 hours and a typical residence time for a peripheral lymph node is about 13.5 hours (Textor et al., 2014). A simple model considering the number, *N*, of naive T cells specific for a particular antigen (e.g., a peptide derived from a virus) would be

\[
B = N - S - L, \quad \frac{dS}{dt} = iS_B - e_SS \quad \text{and} \quad \frac{dL}{dt} = niLB - e_LL, \quad (12.1)
\]

where *B* is the number of cognate naive T cells in the blood, *S* is the number of cells in the spleen, *L* is the total number of cells in all *n* lymph nodes, and the *i* and *e* parameters are influx rates and efflux rates into the lymphoid organs. Textor et al. (2014) estimate that *i_S* = 1h\(^{-1}\) and that *ni_L* = 1.5h\(^{-1}\), i.e., most cells leave the blood by entering a lymph node, but the spleen is the organ receiving the vast majority of naive T cells from the blood. Estimating *n* is difficult because lymph nodes have different volumes, and there are many small “nodes” like Peyers patches in the gut. Textor et al. (2014) estimate that in a mouse there are about *n* = 39 major lymph nodes.

When an organism is challenged by a pathogen in one of its tissues, proteins from the pathogen are transported to the lymph node(s) draining this tissue, and this triggers an immune response by the cognate naive T cells that are present in this lymph node(s). Since there are so many lymph nodes, only a small fraction, i.e., about 1/*n*, of the naive T cells is expected be present in the draining lymph node. However, various experiments have demonstrated that during a localized infection almost all cognate naive T cells are recruited into the immune response on a time scale of a few days. Since cognate naive T cells are trapped in the draining lymph node when they find their antigen there, one would predict that they will slowly accumulate there. This accumulation is expected to be too slow because naive T cells exiting from another lymph node have only a 1/*n* probability to arrive in the draining lymph node, and therefore probably end up in another node, where they are expected to spend another 13.5 hours (Textor et al., 2014). In one of the questions below you will study how long this would take. The real solution for recruiting most naive T cells is to enlarge the influx into the draining lymph node, and it is quite spectacular how inflamed lymph nodes can increase their blood supply by angiogenesis.
To study this we extend the model by assigning one of the lymph nodes as the draining lymph node, and provide this one lymph node with parameters $f_i$ and $f_e$ to modify its influx and efflux upon infection,

$$\frac{dS}{dt} = iSB - eSS, \quad \frac{dL}{dt} = (n - 1)iLB - eLL, \quad \frac{dD}{dt} = fiL - feLD, \quad (12.2)$$

where $B = N - S - L - D$ and $f_i = f_e = 1$ when there is no infection. This model is available as the file circulation.R.

a. Why can this model be written without a differential equation the number of cells in the blood? What would $dB/dt$ be if one were to write it? Would that be an identical model?

b. Find the steady state of Eq. (12.2) by running the model in the absence of an infection. How many cognate naive T cells are there in any particular lymph node?

c. The steady state of Eq. (12.1) is

$$\bar{S} = \frac{eLisN}{eLis + eLis + esnlL} \quad \text{and} \quad \bar{L} = \frac{esnlN}{eLis + eLis + esnlL},$$

(see the Mathematica notebook circulation.nb). How many cells do you expect to be present in the blood at steady state? Do you understand why the number of cells in the spleen, $\bar{S}$, increases with the efflux, $eL$, of cells from the lymph nodes?

d. If cognate naive T cells fail to egress from the draining lymph node containing their antigen, how long would it take to accumulate 50% of the cells? Hint: run the model.

e. Textor et al. (2014) cite papers showing that the rate of influx in a draining lymph node can increase 9-fold within a few days. How long would it take to accumulate 50% of the cells in the draining lymph node if the influx is increased 9-fold from the start? Hint: do this numerically with Grind.

f. How would you modify Eq. (12.2) to increase the influx into the draining lymph node more gradually?

Question 12.6. Improving HIV therapy?

HIV infection can nowadays successfully be treated by combination therapies with several antiretroviral compounds (cART). Different medications suppress different stages of the viral life cycle, such as the reverse transcription of viral RNA into DNA, the integration of that DNA into the host cell genome, and the protease splitting the HIV-polyprotein into the mature function proteins forming the novel virions. We will test some of these combinations in a generally accepted model of the HIV-1 life cycle, which is composed of CD4$^+$ target cells, $T$, recently infected cells, $I_1$, productively infected cells, $I_2$, and virus particles, $V$. The $I_1$ cells correspond to the pre-integration phase, and therefore do not produce novel virions (this is called the "eclipse" phase). Since we are considering a steady state corresponding to a chronic infection (that we will perturb by treatment), we start with ignoring the dynamics of the immune response, and just assume that both type of infected cells are killed by a steady state immune response at a rates $k_1$ and $k_2$, respectively. Leaving out the immune response, we write 4 ODEs,

$$\frac{dT}{dt} = s - dTT - \beta(1 - \epsilon_\beta)TV,$$

$$\frac{dI_1}{dt} = \beta(1 - \epsilon_\beta)TV - (d_1 + \gamma(1 - \epsilon_\gamma) + k_1)I_1,$$

$$\frac{dI_2}{dt} = \gamma(1 - \epsilon_\gamma)I_1 - (d_2 + k_2)I_2,$$

$$\frac{dV}{dt} = pI_2 - cV,$$
where $0 \leq \epsilon_\beta < 1$ is the efficacy of a treatment blocking reverse transcriptase, and $0 \leq \epsilon_\gamma < 1$ is the efficacy of a treatment blocking integration of viral DNA into the host genome. Note that this model resembles the SEIR model of Eq. (6.9). This model is present on the website as the file `integrase.R`, with parameter values taken from Gadhamsetty et al. (2016). The effect of adding a treatment with such an integrase inhibitor is described in Cardozo et al. (2017).

In the absence of infection the target cells approach $\bar{T} = s/dT$, which we scale to one by setting $s = dT$. We also scale the density of virions to that of the productively infected cells by setting $p = c$, i.e., at steady state $\bar{V} = I_2$. (Because the kinetics of the virions is much faster than that of the cells, $V$ will also be similar to $I_2$ when the system is not at steady state, i.e., $dV/dt = 0$ would have been a realistic QSSA). The infection rate $\beta$ in the model is “corrected” for this scaling of $V$. The eclipse phase of HIV-1 is about a day, i.e., $\gamma = 1$, and it is not known whether the cellular immune response primarily affects $I_1$ cells or $I_2$ cells. We will therefore consider both cases, which are called “early” and “late” killing in Gadhamsetty et al. (2016). It is well known that during effective treatments blocking new infections, e.g., $\epsilon_\beta \to 1$, the viral load comes down at a rate of about one per day (Ho et al., 1995; Markowitz et al., 2003). This slope is typically called $\delta$. Gadhamsetty et al. (2016) reset the unknown $d_1$ and $d_2$ parameters in the early and late killing regime to guarantee that their model delivers the correct $\delta \approx 1 \, d^{-1}$ downslope in both scenarios.

a. The infection rate estimated by Gadhamsetty et al. (2016) was based upon the observation that the initial replication rate of the virus is about $1.5 \, d^{-1}$ (using the formula $\beta = (d_1 + \gamma + 1.5)/(d_2 + 1.5)/\gamma$. This is before the cellular immune response starts killing infected cells (i.e., when $k_1 = k_2 = 0$). Can you check the growth rate of the virus load by simulating the initial expansion of the virus? Hint: also ask Grind for the eigenvalues of the uninfected steady state; what is dominant eigenvalue?

b. At what value of $\beta$ would the $R_0$ of the infection be less than one? Hint: perform a parameter continuation of $\beta$ to see when the uninfected steady state becomes stable. How efficacious should the treatment be to eradicate the virus in this model?

c. What is the effect of an efficacious therapy blocking $\beta$? Do you observe a slope close to $\delta = 1 \, d^{-1}$? Does that depend on which cells are killed by the immune response?

d. What is the effect of adding on an efficacious therapy blocking $\gamma$? Does that depend on which cells are killed by the immune response? How can it be that adding a treatment can slow down the eradication of the virus? Would you take this drug?

e. If you are enjoying this exercise you may consider implementing the immune response used by Gadhamsetty et al. (2016):

$$\frac{dE}{dt} = \frac{pE}{h + V + E} \bar{V} - dE E,$$

and replace the $k_1$ and $k_2$ parameters by $k_1E$ and $k_2E$ terms. Study how the immune response affects the acute phase of the infection, and check if it affects the slopes observed during treatment. Studying the Gadhamsetty et al. (2016) and Cardozo et al. (2017) paper in combination would be an interesting project.

**Question 12.7. Stem cell renewal**

Many tissues and populations of cells are maintained by a subpopulation of stem cells. A classical example is the formation of several populations of circulating cells in the blood by a relatively small population of haematopoietic stem cells (HSCs) in the bone marrow, or the stem cells located deep in the crypts of the epithelial layer lining the gut. Stem cells are self-renewing cells that (at least sometimes) divide into two different daughter cells, which is called an asymmetric division. When a sufficient fraction of their daughter cells remains as a stem cell, the stem cell

*Numerical exercises*
population can maintain itself, and provide progeny to the populations of differentiated cells that depend on it. It is unclear how stem cells regulate the fraction of asymmetric divisions, as at least half of their cell divisions should deliver a daughter with stem cell properties. Otherwise the stem cell population declines. The first question of this exercise is to write a model for the simplest situation where on average half of the daughter cells remains a stem cell while the other half differentiates. You will see that this fraction should be more than one half to compensate for the death of stem cells, and hence that it is unclear how the fraction of asymmetric divisions is regulated.

Lander et al. (2009) developed an interesting model for this problem by arguing that the fraction of renewal divisions delivering a daughter with stem cell properties should depend on the density of the population. This could either be the total density, i.e., stem cells plus differentiated cells, the density of differentiated cells, or the density of stem cells. This is interesting because this entails the population with at least two density dependent mechanisms, one regulating the fraction of self-renewal divisions, and another regulating the rate of cell division. They develop a chain of equations where at every level cells may divide asymmetrically, and Lander et al. (2009) show that the parameters of that system determine which population in the chain will function as stem cells for the entire chain. Here we simplify their model by considering just two populations: stem cells, $S$, and differentiated cells, $D$. In the questions below we ask you to devise a model where both the fraction of asymmetric divisions, $0 < f(D) \leq 1$, and the division rate of the stem cells, $g(D)$ for growth, depends on the density of differentiated cells. Following Lander et al. (2009) suggestions it would be natural to allow for a larger fraction of asymmetric divisions, and a higher division rate, when the population is small and the tissue should be regenerated. Such a model can be studied numerically by taking the file lander.R as a template.

**a.** Write a simple model for a population of stem cells, $S$, and differentiated cells, $D$, with a fixed division rate of the stem cells, and where on average half of the stem cell divisions are asymmetric.

**b.** Expand your model to account for the situation where the fraction of asymmetric divisions, $0 < f(D) \leq 1$, is regulated by the density of differentiated cells.

**c.** Expand the previous model to allow for a density dependent division rate of the stem cells.

**d.** Differentiated cells may also divide, and this rate could also depend on the density. How would that change the model, and do you expect qualitatively different dynamical regimes?

**e.** Finally, think of a more spatial model where the stem cells are localized on a substrate allowing a maximum of $K$ cells to bind. One could imagine that only daughter cells finding a free spot on this substrate remain as stem cells. Can you write an ODE model for such a situation?

**Question 12.8. Early warning signals**

The notion that we might be able to observe “early warning” signals in time series data of systems that are about to collapse is receiving a lot of attention recently (Scheffer et al., 2009; Veraart et al., 2012; Scheffer et al., 2012). This theory is based upon the simple fact that when a system approaches a catastrophic bifurcation (like a saddle-node bifurcation) the dominant eigenvalue is approaching zero, implying that the return time of the system to its steady state is becoming very long. Thus, an increasing return time of a system under slowly changing environmental conditions could provide a warning signal for an upcoming catastrophe. It would be extremely important if one could indeed detect such early warning signals in the time series of any particular system, because one could change the environmental conditions to prevent a future disaster. Long return times should be associated with more variation in the data, and to a better correlation between subsequent data points. The review paper by Scheffer et al. (2009) provides interesting examples of early warning signals in biological data, and clearly
explains the underlying theory in several boxes. Read this paper before you embark on this exercise. On the website we provide a Grind model (\texttt{warning.R}) based upon the ODE, $dX/dt = X(1 - X/K) - \frac{cX^2}{1+X^2}$, used in the legend of their first figure, where they set $K = 10$ and vary the consumption rate $c$.

a. Plot the steady state of $X$ as a function of the consumption parameter $c$ (using the \texttt{continue()} function).

b. Add noise to the system by adding and removing individuals using the option \texttt{after} in your call to \texttt{run()}. It is wise to prevent negative values of $x$ by calling \texttt{abs()} within \texttt{after} (see the file \texttt{warning.R}). Check for different values of $c$ how the system responds to the noise. Plot $X_{t+1}$ as a function of $X_t$ and compute the (auto)correlation between the two. Note that you plot autocorrelations by saving the data delivered by model simulations, e.g., \texttt{data <- run(1000,...,table=TRUE)}, and then plot the value of $X$ as a function of a previous value of $X$, e.g., \texttt{plot(data$X[1:999],data$X[2:1000],pch="."}). Finally note that you can calculate correlations with the R-function \texttt{cor()}.

c. Study the behavior of the model by very slowly changing $c$, while performing a simulation (with or without noise). Add $dc/dt = \epsilon$ to the model, and make epsilon a very slow parameter, and then perform a long \texttt{run()}.

d. Another form of stochasticity is to allow for noise on a parameter, i.e., on $K$. Test how the system responds to noise on one of its parameters.

e. Do you think you would be able to predict a catastrophic bifurcation, and what would be the best approach to detect this?

You have seen that early warning signals are not always, and one of the reasons for this is discussed in a paper by Boerlijst \textit{et al.} (2013). Boettiger and Hastings also discuss the predictability of critical transitions (Boettiger & Hastings, 2012, 2013; Boettiger \textit{et al.}, 2016).

**Question 12.9. Linear models**

Study the linear system

$$\frac{dx}{dt} = ax + by \quad \text{and} \quad \frac{dy}{dt} = cx + dy .$$

What is the steady state of this system? Derive the Jacobi matrix for this system and use your knowledge of the eigenvalues of this matrix to choose values of $a, b, c,$ and $d$ such that you obtain a stable node, a spiral, and a saddle point. The model is provided as the file \texttt{linear.R}.

**Question 12.10. Noise and $r$ and $K$-selected species**

Study the logistically growing population

$$\frac{dN}{dt} = rN(1 - N/K) ,$$

by adding noise to one of its parameters, and by adding noise to the population density (use the file \texttt{rknoise.R} for this). Use the concept of $r$ and $K$-selected species and study species with different growth rates $r$ (the population size can always be scaled to $K = 1$).

**Question 12.11. Sexual reproduction**

All population models considered thus far fail to distinguish between the two sexes. Basically these models only consider the females in a population, and ignore the males. Extend the Lotka Volterra competition model with sexual reproduction, using a simple Hill function for the probability that a female finds a male, and see how this effects its possible phase spaces, and their biological interpretation. A Grind model is provided in the file \texttt{sexual.R}.
Chapter 13

Appendix: mathematical prerequisites

13.1 Phase plane analysis

Most mathematical models in biology have non-linearities and can therefore not be solved explicitly. One can nevertheless obtain insight into the behavior of the model by numerical (computer) analysis, and/or by sketching nullclines and solving for steady states. One determines the stability of the steady states from the vector field, and by linearization around the steady states.

The long-term behavior of a model typically approaches a stable steady state, a stable limit cycle, or a chaotic attractor. Phase plane analysis is a graphical method to analyze a model to investigate these behavioral properties of a model. Consider a model of two variables $x$ and $y$,

$$\frac{dx}{dt} = f(x,y) \quad \text{and} \quad \frac{dy}{dt} = g(x,y). \ (13.1)$$

One can define a “phase space” with $x$ on the horizontal axis and $y$ on the vertical axis, where each point in this space is one particular “state” of the model. To obtain further insight in the model one sketches the “nullclines” $f(x,y) = 0$ and $g(x,y) = 0$. This is useful because at the former nullcline $dx/dt$ switches sign, and at the latter $dy/dt$ switches sign. Two simple nullclines therefore typically define regions with qualitatively different signs of the two differential equations. Nullclines enable one to localize all steady states of the model because these correspond to the intersections of the nullclines (i.e., $f(x,y) = g(x,y) = 0$). This is very useful because models may have multiple steady states.

For each steady state one has to determine whether it is an attractor, i.e., a stable steady state, or a repellor, i.e., an unstable equilibrium. The local vector field around a steady state in a phase space with nullclines often provides sufficient information to see whether the steady state is stable or unstable. In 2-dimensional phase spaces there are three classes of steady states: nodes, saddles, and spirals. Nodes and spirals are either stable or unstable, and a saddle point is always unstable because it has a stable and an unstable direction. The two nullclines intersecting at the equilibrium point define four local regions of phase space, each with its unique local vector field. The four local vector fields define the nature of the steady state.

A simple example is a “stable node”, for which all four vector fields point towards the steady state...
Appendix: mathematical prerequisites

(see Fig. 13.1a). A stable node is therefore approached by trajectories from all four directions (Fig. 13.1b). When the vector fields point outward in all four regions the equilibrium is an “unstable node” (Fig. 13.1c), and trajectories are repelled in all four directions (Fig. 13.1d). The local vector fields in Fig. 13.1e define a “saddle point”, which has a stable and an unstable direction (Fig. 13.1f). The stable direction of a saddle point defines a “separatrix” because all trajectories starting at either side of this line end up in another attractor (i.e., a separatrix defines different basins of attractions).

The local vector field can also suggest rotation (see Fig. 13.2). Rotating vector fields are typical for spiral points. The local vector field fails to provide sufficient information to determine with absolute certainty whether a spiral point is stable or unstable. However, one can get some good suggestion for the stability from the vector field. In Fig. 13.2c, for instance, and one can see that increasing $y$ from its steady state value makes $dy/dt > 0$. Locally, there must be some positive feedback allowing $y$ to increase further when $y$ increases. This is definitely destabilizing, and the trajectory in Fig. 13.2d confirms that this is an “unstable spiral” point. Conversely, the spiral point in Fig. 13.2a is stable, and locally has negative feedback for both $x$ and $y$ (i.e., increasing $x$ makes $dx/dt < 0$ and increasing $y$ makes $dy/dt < 0$), which has a stabilizing influence. Because the stability of spiral points also depends on the local difference in time scales of the horizontal ($x$) and vertical ($y$) variables, the local vector field is not always sufficient to determine the stability of the steady state. Even the suggestion of rotation in a local vector field is not sufficient to determine with certainty that the steady state is a spiral. Fig. 13.2e & f show that the same vector field defining a stable spiral point in Fig. 13.2a can actually also correspond to a stable node.

Example: Lotka Volterra model

Using the famous Lotka Volterra model as an example we review a few methods for analyzing systems of non-linear differential equations. The Lotka-Volterra predator prey model can be written as:

$$
\begin{align*}
\frac{dR}{dt} &= aR - bR^2 - cRN \\
\frac{dN}{dt} &= dRN - eN,
\end{align*}
$$

(13.2)

where $a, b, c, d,$ and $e$ are positive constant parameters, and $R$ and $N$ are the prey and predator densities. The derivatives $dR/dt$ and $dN/dt$ define the rate at which the prey and predator densities change in time.

A first step is to sketch nullclines (0-isoclines) in phase space. A nullcline is the set of points $(R, N)$ for which the corresponding population remains constant. Thus, the $R$-nullcline is the set of points at which $dR/dt = 0$. Setting $dR/dt = 0$ and $dN/dt = 0$ in Eq. (13.2) one finds

$$
\begin{align*}
R &= 0, \quad N = \frac{a - bR}{c} \quad \text{and} \quad N = 0, \quad R = \frac{e}{d},
\end{align*}
$$

(13.3)

for the prey nullclines and the predator nullclines, respectively. These four lines are depicted in Fig. 13.3. For biological reasons we only consider the positive quadrant.

A second step is to determine the vector field. Not knowing the parameter values, one considers extreme points in phase space. In the neighborhood of the point $(R, N) = (0, 0)$, for example, one can neglect the quadratic $bR^2$, $cRN$, and $dRN$ terms, such that

$$
\begin{align*}
\frac{dR}{dt} &\approx aR, \quad \frac{dN}{dt} \approx -eN.
\end{align*}
$$

(13.4)
13.1 Phase plane analysis

Figure 13.1: Qualitatively different steady states determined by the local vector field in the four regions defined by the nullclines. Stable node (a,b): the vector field points inwards in all four sections. Unstable node (c,d): the vector field points outwards in all four sections. Saddle point (e,f): the vector field points inwards in two sections, and outwards in the other two regions. A saddle point is an unstable steady state with a stable and an unstable direction.

Since the former is strictly positive, and the latter strictly negative, we assign (−+) to the local direction of the vector field (see Fig. 13.3). This means that $dR/dt > 0$ below the $R$-nullcline, i.e., we sketch arrows to the right, and that at the left hand side of the $N$-nullclines $dN/dt < 0$, i.e., we sketch arrows pointing to the bottom. At the $R$ and $N$-nullclines the arrows are vertical and horizontal, respectively. The derivatives switch sign, and the arrows switch their direction, when one passes a nullcline. Nullclines therefore separate the phase space into regions where the derivatives have the same sign.

An important step is to determine the steady states of the system. A steady state, or equilibrium, is defined as $dR/dt = dN/dt = 0$. Graphically steady states are the intersects of the nullclines.
Figure 13.2: Qualitatively different steady states determined by the local vector field in the four regions defined by the nullclines. Spiral points (a-d): the vector field suggests rotation. The spiral point in (a,b) is stable, which can be guessed because increasing $x$ at the steady states makes $dx/dt < 0$, and increasing $y$ at the steady states makes $dy/dt < 0$ (which is stabilizing). The spiral in (c,d) is unstable, which can be guessed because increasing $y$ at the steady states makes $dy/dt > 0$ (which is destabilizing). Panels (e & f) illustrate that nodes can also have a rotating vector field, i.e., that one cannot tell with certainty from the local field whether or not a steady state is a spiral point.

Analytically, one finds

$$(R, N) = (0, 0), \quad (R, N) = (a/b, 0) \quad \text{and} \quad (R, N) = \left( e^d \frac{da - eb}{dc} \right)$$

as the three steady states of this system. Note that the non-trivial steady state only exists when $\frac{da - eb}{dc} > 0$. We will further analyze the model for the parameter condition that all three steady states exist, i.e., we consider $da > eb$.

Finally, one has to determine the nature of the steady states. For the steady states $(0, 0)$ and $(a/b, 0)$ one can read from the vector field that they are saddle points. Around $(a/b, 0)$ the
vertical component is the unstable direction, and around \((0, 0)\) the horizontal component is the unstable direction. This is not so simple for the non-trivial point. Because there is no stable and unstable direction in the vector field the non-trivial steady state cannot be a saddle point, and it has to be a node or a spiral point. To determine its stability one can check for local feedback. Increasing \(R\) in the steady state makes \(dR/dt < 0\), and increasing \(N\) in the steady state keeps \(dN/dt = 0\) because one lands exactly on the \(dN/dt = 0\) nullcline (see Fig. 13.3). Because locally there is no positive feedback we suggest that the non-trivial steady state is stable. One can derive the full Jacobian of this model and confirm that this non-trivial steady state is stable.

### 13.2 Graphical Jacobian

Very often it is sufficient to determine the signs of the Jacobi matrix from the local vector field around the steady state (see the accompanying Ebook (Panfilov et al., 2016)). Consider the vector field around the steady state of some system \(dx/dt = f(x, y)\) and \(dy/dt = g(x, y)\). Around the steady state \((\bar{x}, \bar{y})\) in the phase space \((x, y)\) the sign of \(dx/dt\) is given by the horizontal arrows, i.e., the horizontal component of the vector field. The sign of \(\partial_x f\) can therefore be determined by making a small step to the right, i.e., in the \(x\) direction, and reading the sign of \(dx/dt\) from the vector field. Similarly, a small step upwards gives the effect of \(y\) on \(dx/dt\), i.e., gives \(\partial_y f\), and the sign can be read from the vertical arrow of the vector field. Repeating this for \(\partial_x g\) and \(\partial_y g\), while replacing \(x, y\) with \(R, N\), one finds around the steady state \((0, 0)\) in Fig. 13.3:

\[
J = \begin{pmatrix}
\partial_x f & \partial_y f \\
\partial_x g & \partial_y g
\end{pmatrix} = \begin{pmatrix}
\alpha & 0 \\
0 & -\beta
\end{pmatrix},
\]

(13.6)

where \(\alpha\) and \(\beta\) are positive constants. Because \(\det(J) = -\alpha\beta < 0\) the steady state is a saddle point (see Fig. 13.8). For the steady state without predators one finds

\[
J = \begin{pmatrix}
-\alpha & -\beta \\
0 & \gamma
\end{pmatrix},
\]

(13.7)

Because \(\det(J) = -\alpha\gamma < 0\) the equilibrium is a saddle point. For the non-trivial steady state one finds

\[
J = \begin{pmatrix}
-\alpha & -\beta \\
\gamma & 0
\end{pmatrix},
\]

(13.8)
Figure 13.4: Linearization of a non-linear function: \( f(x) \approx f(\bar{x}) + \partial_x f(\bar{x})(x - \bar{x}) = f(\bar{x}) + f' h \). The heavy line is the local tangent \( f' = \partial_x f(\bar{x}) \) at \( x = \bar{x} \).

and because \( \text{tr}(J) = -\alpha < 0 \) and \( \det(J) = \beta\gamma > 0 \) the equilibrium is stable. This method is also explained in the book of Hastings (1997).

### 13.3 Linearization

Complicated non-linear functions, \( f(x) \), can be approximated by a local linearization around any particular value of \( x \) (see the accompanying Ebook (Panfilov et al., 2016)). Fig. 13.4 shows that the local tangent at some point linearizes the function so that nearby function values can be estimated. This derivative can be used to approximate the curved \( f(x) \) around a particular value \( \bar{x} \), and from Fig. 13.4 we can read that

\[
f(x) \approx f(\bar{x}) + \partial_x f(\bar{x})(x - \bar{x}) ,
\]

where \( h = x - \bar{x} \) is a small step in the \( x \)-direction that we multiply with the local slope, \( \partial_x f(\bar{x}) \), to approximate the required change in the vertical direction. Basically, one estimates the vertical displacement by multiplying the local slope with the horizontal displacement. A simple example would be the function \( f(x) = 3 \sqrt{x} \) (with derivative \( f' = 3/[2\sqrt{x}] \)). The true function values for \( x = 4 \) and \( x = 5 \) are \( f(4) = 6 \) and \( f(5) = 6.71 \), respectively. We can approximate the latter by writing

\[
f(5) \approx f(4) + \frac{3}{2\sqrt{4}} \times 1 = 6 + 3/4 = 6.75 , \tag{13.9}
\]

which is indeed close to \( f(5) = 6.71 \). The same can be done for 2-dimensional functions, i.e.,

\[
f(x, y) \approx f(\bar{x}, \bar{y}) + \partial_x f(\bar{x}, \bar{y})(x - \bar{x}) + \partial_y f(\bar{x}, \bar{y})(y - \bar{y}) . \tag{13.10}
\]
13.4 Convenient functions

Once we have a sketch of how some process should depend on a variable of the model, we need to translate this graph into a mathematical function. We here let you become familiar with a few families of convenient functions, i.e., Hill-functions and exponential functions. These will be used to formulate positive and negative effects of populations onto each other. Because these functions are dimensionless and remain bounded between zero and one, i.e., $0 \leq f(x) \leq 1$, one can easily multiply any term in a model (corresponding to some biological process) with such a function. We here define two families of functions $f(x)$ that increase with $x$, are zero when $x = 0$, and approach a maximum $f(x) = 1$ when $x \to \infty$. Whenever one would need a different maximum in the model, one could simply multiply $f(x)$ with some parameter. Having increasing functions $0 \leq f(x) \leq 1$, one can easily define decreasing functions by taking $g(x) = 1 - f(x)$.

Hill-functions are a very conventional and convenient family of saturation functions:

$$ f(x) = \frac{x^n}{h^n + x^n} \quad \text{and} \quad g(x) = 1 - f(x) = \frac{1}{1 + (x/h)^n}, $$

in which you may recognize the classical Michaelis-Menten saturation function for $n = 1$ (see Fig. 13.5a). The “saturation constant” $h$ is the value of $x$ where $f(x)$ or $g(x)$ attains half of its maximal value. The exponent $n$ determines the steepness of the function. Whenever $n > 1$ the function is sigmoid (see Fig. 13.5b), and for $n \to \infty$ both $f(x)$ and $g(x)$ become step functions switching between zero and one at $x = h$. The slope of $f(x)$ in the origin is determined from its derivative, which for $n = 1$ equals

$$ \partial_x f(x) = \frac{1}{h + x} - \frac{x}{(h + x)^2}, $$

which delivers a slope of $1/h$ for $x = 0$. For $n > 1$ the derivative is

$$ \partial_x f(x) = \frac{nx^{n-1}}{h^n + x^n} - \frac{nx^{2n-1}}{(h^n + x^n)^2}, $$

which means that for $x = 0$ the slope is zero. An advantage of using Hill functions in mathematical models is that solving steady states corresponds to solving polynomial functions.
The exponential functions
\[ f(x) = 1 - e^{-\ln[2]x/h} \quad \text{and} \quad g(x) = e^{-\ln[2]x/h} . \] (13.14)

are as conventional as Hill functions. They may be more convenient for finding solutions of equations, but they are more cumbersome when it comes to finding steady states. Like Hill functions we have \( f(0) = 0 \). For finding the half maximal value of \( f(x) \) one solves \( 0.5 = e^{-\ln[2]x/h} \) to find that \( x = h \). The slope in the origin is determined from the derivative \( \frac{\partial}{\partial x} [1 - e^{-\ln[2]x/h}] = (\ln[2]/h)e^{-\ln[2]x/h} \) which for \( x = 0 \) gives a slope of \( \ln[2]/h \). The sigmoid form of the exponential function is known as the Gaussian distribution
\[ f(x) = 1 - e^{-\ln[2](x/h)^2} \quad \text{and} \quad g(x) = e^{-\ln[2](x/h)^2} . \] (13.15)

Thanks to our scaling with \( \ln[2] \) these sigmoid functions are also half maximal when \( x = h \) (and \( x = -h \)); see Fig. 13.5b.

Finally, in Section 7.5 we have presented the Holling I/II function that can be tuned between a discontinuous minimum function and a classical saturated Hill function with a single curvature parameter \( \gamma \). We have seen that discontinuous saturation functions can easily be written with minimum and maximum functions. For instance, \( f(x) = \min[1, x/(2h)] \) has its half-maximal value \( f(x) = 0.5 \) when \( x = h \), but has a sharp corner at \( x = 2h \). Another simple and convenient function is
\[ f(x) = 1 - (x/k)\alpha , \] (13.16)
which declines from one to zero over the interval \( x = 0 \) to \( x = k \). When \( \alpha = 1 \) the decline is linear, when \( \alpha > 1 \) the function is concave, and when \( \alpha < 1 \) it is convex.

### 13.5 Scaling

Models can be simplified by scaling variables and time such that one loses a number of parameters. Such scaled variables are said to be dimensionless. Reducing the number of parameters of a model can be very helpful to completely understand its behavior. The technique is explained by writing a dimensionless logistic growth model.

Write the logistic equation as
\[ \frac{dN}{dT} = rN[1 - N/k] , \] (13.17)
where \( r \) is the per capita maximum rate of increase, and \( k \) is the carrying capacity. The parameter \( r \) is a rate, with dimension \( 1/T \), and the parameter \( k \) has the dimension “biomass” or “number of individuals”. First scale the biomass such that the carrying capacity becomes one. We introduce a new variable \( n \) with the property \( n = N/k \) such that \( n = 1 \) when \( N = k \). Now substitute \( N = kn \) in Eq. (13.17), i.e.,
\[ \frac{dkn}{dT} = k \frac{dn}{dT} = rk[n - kn/k] , \] (13.18)
which simplifies into
\[ \frac{dn}{dT} = rn[1 - n] , \] (13.19)
which indeed has a carrying capacity \( \bar{n} = 1 \).
Figure 13.6: The function defined by Eq. (13.22) for three values of $h$. The inflection point is located at $R = \sqrt[3]{Kh^2}$.

Having lost one parameter one can scale time, $T$, such that the parameter $r$ disappears, i.e.,
\[ r \frac{dn}{dt} = rn[1 - n] , \]  \(13.20\)
implying that $t = rT$. This defines a new time scale for which
\[ \frac{dn}{dt} = n[1 - n] . \]  \(13.21\)

This non-dimensional form of the logistic growth equation proves that its solution is always the same sigmoid function. Thus, plotting $N(T)$ as a function of time, the only effect of choosing different parameter values of $r$ and $k$ is a scaling of the horizontal and vertical axis.

### 13.6 The resource nullcline with a sigmoid functional response

In Section 7.2 we wrote the resource nullcline of the Holling type III functional response as the following function
\[ N = \frac{r(h^2 + R^2)}{aR} \left( 1 - \frac{R}{K} \right) , \]  \(13.22\)
which has a vertical asymptote at $R = 0$ and is zero when $R = K$ (see Fig. 13.6). The derivative $f'$ of this function is negative when $R \to 0$ and around $R = K$. The function will be non-monotonic, and have a minimum and a maximum, when the derivative is positive in the inflection point. The first and second derivative with respect to $R$ are
\[ f' = \frac{r(KR^2 - 2R^3 - h^2K)}{aKR} \quad \text{and} \quad f'' = \frac{2r(h^2K - R^3)}{aKR^3} , \]  \(13.23\)
respectively. Solving $f'' = 0$ shows that the inflection point is located at $R = \sqrt[3]{Kh^2}$ (see Fig. 13.6). Substituting this value of $R$ into $f'$ and solving $f' > 0$ yields $h < \frac{K}{3\sqrt[3]{3}} \simeq \frac{K}{3}$, which says that the function is non-monotonic whenever the saturation constant $h$ is sufficiently small.
13.7 Mathematical background

Sketching functions

Most models in this course are analyzed graphically by sketching nullclines in phase space. Some experience with sketching functions is therefore required. To fresh up these techniques we here discuss the general approach, and give a few examples. Since most of the models have free parameters, we also have to sketch functions with free parameters. This implies that one cannot simply resort to a computer program or a graphical calculator.

The general procedure is:
1. Determine the intersects with the horizontal and vertical axes.
2. Check for vertical asymptotes, i.e., $x$ values leading to division by zero.
3. Check for horizontal asymptotes by taking the limit $x \to \infty$ and $x \to -\infty$.
4. Check where the function has positive values and where it has negative values.
5. We typically do not need to determine minimum values, maximum values, or inflexion points.

Example 1

Sketch the function

$$y = \frac{ax}{b-x} \quad (13.24)$$

in a graph plotting $y$ as a function of $x$:

a. For $x = 0$ one finds $y = 0$ as the intersect with the $y$-axis. This is the only intersect with the horizontal axis.

b. There exists a vertical asymptote at $x = b$. When $x \uparrow b$ one finds that $y \to \infty$, when $x \downarrow b$ one sees that $y \to -\infty$.

c. To find horizontal asymptotes one rewrites the function into

$$y = \frac{a}{b/x - 1} \quad (13.25)$$

Both for $x \to \infty$ and for $x \to -\infty$ one sees $y \to -a$. Thus, we find one horizontal asymptote at $y = -a$.

d. When $x < 0$ one sees that $y < 0$, when $0 \leq x < b$ one sees that $y \geq 0$, and when $x > b$ one finds $y < 0$. The function is sketched in Fig. 13.7a.

Example 2

Sketch the system

$$0 = \sigma + \frac{aX}{b+X} - cY \quad (13.26)$$

$$0 = -\alpha + \beta X - \gamma Y \quad (13.27)$$

in one graph. Because both equations can easily be solved for the $Y$ variable, it is most easy to draw $Y$ as a function of $X$. For the second equation one finds

$$Y = -\alpha/\gamma + (\beta/\gamma) X \quad (13.28)$$

which is a straight line with slope $\beta/\gamma$.

a. The intersect with the $Y$-axis $-\alpha/\gamma$, and that with horizontal axis $X = \alpha/\beta$.

b. No vertical asymptotes.

c. No horizontal asymptotes.

d. When $X < \alpha/\beta$ one finds $Y < 0$, otherwise $Y \geq 0$. 
For the first equation we also write $Y$ as a function of $X$

$$Y = \frac{\sigma}{c} + \frac{(a/c)X}{b + X}.$$  \hspace{1cm} (13.29)

\textbf{a.} The intersect with the vertical axis is $Y = \frac{\sigma}{c}$. That with the $X$ axis is $X = -b\sigma/\left(\sigma + a\right)$.

\textbf{b.} There exists a vertical asymptote at $X = -b$. When $X \downarrow -b$ one finds that $Y \rightarrow -\infty$ and when $X \uparrow -b$ we see $Y \rightarrow \infty$.

\textbf{c.} For the horizontal asymptotes one first writes

$$Y = \frac{\sigma}{c} + \frac{(a/c)}{b/X + 1},$$  \hspace{1cm} (13.30)

to see that for $X \rightarrow \infty$ and for $X \rightarrow -\infty$, $Y \rightarrow (\sigma + a)/c$.

\textbf{d.} One finds that $Y > 0$ if $X > -b\sigma/(\sigma + a)$ or if $X < -b$.

Although one does not know the parameters for this system, one can be sure that in the positive quadrant the two curves have to intersect. Thus, qualitatively, there is only one unique situation, which is depicted in Fig. 13.7b.

\section*{Useful mathematical formulas}

To fresh up your memory of earlier education in mathematics we provide a few standard formulas

$$\ln 1 = 0, \quad \ln xy = \ln x + \ln y, \quad \ln x/y = \ln x - \ln y, \quad e^{ix} = \cos x + i \sin x,$$  \hspace{1cm} (13.31)

and the two roots of the quadratic equation

$$ax^2 + bx + c = 0 \quad \text{are} \quad x_{\pm} = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}.$$  \hspace{1cm} (13.32)

The standard rules of differentiation are

$$[cx]^\prime = c, \quad [cx^n]^\prime = ncx^{n-1}, \quad [f(x) + g(x)]^\prime = f'(x) + g'(x),$$  \hspace{1cm} (13.33)
where the ’ means $\partial_x$, and

$$[f(x)g(x)]' = f'(x)g(x) + f(x)g'(x), \quad \left[ \frac{f(x)}{g(x)} \right]' = \frac{f'(x)}{g(x)} - \frac{f(x)g'(x)}{g(x)^2},$$  \hspace{1cm} (13.34)

and the famous chain rule

$$f'[g(x)] = f'(g) \cdot g'(x), \quad \text{e.g.,} \quad \sqrt{1 + ax}' = \frac{1}{2}(1 + ax)^{-\frac{1}{2}} = \frac{a}{2\sqrt{1 + ax}}. \hspace{1cm} (13.35)$$

**Trace and determinant**

In the accompanying Ebook (Panfilov et al., 2016) we explain that the eigenvalues of an arbitrary matrix

$$A = \begin{pmatrix} p & q \\ r & s \end{pmatrix}$$  \hspace{1cm} (13.36)

are the solutions of the characteristic equation

$$(p - \lambda)(s - \lambda) - rq = \lambda^2 - \lambda(p + s) + (ps - rq) = 0. \hspace{1cm} (13.37)$$
Defining the “trace” of the matrix as tr = p + s and the “determinant” as det = ps − rq, the characteristic equation simplifies into

\[ \lambda^2 - tr\lambda + det = 0 \]  

with solutions

\[ \lambda_\pm = \frac{tr \pm \sqrt{tr^2 - 4det}}{2} = \frac{tr \pm \sqrt{D}}{2}, \]

where \( D \equiv tr^2 - 4det \) is the “discriminant” of the matrix. If \( D < 0 \) the \( \sqrt{D} \) delivers imaginary solutions that correspond with oscillations \( (e^{ix} = \cos[x] + i\sin[x]) \).

Summing the two eigenvalues \( \lambda_\pm \) yields

\[ \frac{tr + \sqrt{tr^2 - 4det}}{2} + \frac{tr - \sqrt{tr^2 - 4det}}{2} = tr \],

and the product gives

\[ \frac{tr + \sqrt{tr^2 - 4det}}{2} \times \frac{tr - \sqrt{tr^2 - 4det}}{2} = det \].

If this matrix was the Jacobian of a steady state, we now observe that to check for stability, i.e., \( \lambda_+ < 0 \) and \( \lambda_- < 0 \), it is therefore in many cases sufficient to know the values of the trace and the determinant. When \( det > 0 \) one knows that either both eigenvalues are negative or that they are both positive. Having \( det > 0 \) and \( tr < 0 \) one knows that they cannot be positive, and therefore that they are both negative and the steady state has to be stable. Summarizing an easy test for stability is \( tr[J] < 0 \) and \( det[J] > 0 \) (see Fig. 13.8).

Although we do not proof that here, this result for the trace and determinant are also true for high-dimensional matrices, i.e., \( \sum \lambda_i = \text{tr}(A) \) and \( \prod \lambda_i = \text{det}(A) \). The latter also tells you that the eigenvalues of a matrix in a triangular form, i.e., a matrix whose elements above or below the main diagonal are all zero, can be solved from the characteristic equation \( (A_{11} - \lambda)(A_{22} - \lambda) \ldots (A_{nn} - \lambda) = 0 \).

### 13.8 Parameter estimation

The interpretation of data comprised of longitudinal measurements of population densities can be improved by describing the data points with an appropriate mathematical model. The parameters of a mechanistic model that reasonably “fits” the data provide quantitative information on the biological processes implemented in the model, and that together apparently suffice to explain the data. Thus, it can be very useful to identify the models and parameters that can account for population dynamics described by the data. The main problem with most interesting models in biology is that they have complicated non-linear terms, and several parameters, which makes it difficult to find the “optimal” set of parameters by simple statistical procedures (such a linear regression).

There are several numerical techniques to fit complex models to data, and most of these are based upon clever gradient descent methods, where one makes an initial guess on the parameter values, and the algorithm subsequently makes small changes to all “free” parameters until it finds a direction in parameter space bringing the prediction of the model closer to the data.
This process of taking small steps through parameter space is repeated until a local minimum is found where small changes no longer improve the quality of the fit. Although this sound like a straightforward approach, it is difficult to know whether or not this local minimum corresponds to the true optimum, i.e., to the global minimum. Additionally, whether or not these methods find the optimum can crucially depend on the initial values of the free parameters, which are usually based upon a wild guess. Complex models typically have several local optima and gradient descent methods easily get stuck in a local minimum. It is therefore essential to have an informed initial guess, to limit the number of free parameters, and to try a variety of initial guesses.

Non-linear parameter fitting procedures attempt to reduce the distance between the model prediction and the data, and this distance is typically defined as the summed squared residuals (SSR). For instance, consider a data set of population densities, \( N(t) \), measured at various points in time, \( t \). Since we may have several measurements at each time point we will call them \( N(t_i) \), where \( i \) is the index of the data point, and \( t_i \) the time point at which the data point was measured. Having a mathematical model with a vector of parameters, \( p \), and an initial condition, \( S(0) \) (for state), we can predict the state of this model, \( S(t) \) for all time points, \( t_i \), in the data by numerically solving the model. The distance between the data, \( N(t_i) \), and the model prediction, \( S(t_i) \), for parameters, \( p \), can then be defined as

\[
SSR = \sum_{i=1}^{n} [N(t_i) - S(t_i)]^2,
\]

where we have \( n \) data points, and we sum the squared differences between each observed population density and the corresponding predicted density. Minimizing the SSR by an algorithm searching better parameter values is called a “least-squares” approach. Note that an appropriate model may require more variables than are available in the data, i.e., not all variables need to be observed, and we then have to match the corresponding variable(s) of the model to the observable(s) in the data. Once a gradient descent method has minimized the SSR and halts, the SSR is a measure for the quality of the fit of the model to the data.

One major problem with non-linear parameter fitting procedures is that there may be several local minima, and that not all parameters need to be “identifiable”. The methods will nevertheless halt and report an SSR with an associated set of “optimal” parameter values. For instance, if one were to fit the birth-death model, \( \frac{dN}{dt} = (b - d)N \), to the densities of a population that is growing exponentially by equivalent birth and death events, the values of \( b \) and \( d \) are nevertheless not identifiable because the observed time series of population densities only contains information on the net replication rate \( r = b - d \). Thus, the only identifiable parameters would be \( r \) and the initial condition \( N(0) \). The estimates for \( b \) and \( d \) can take any value depending on their initial guesses, and these values will be correlated because \( b = r + d \). This is a trivial example, as in complex models it can be very difficult to determine which parameters are identifiable.

It is therefore essential to quantify the potential variation of parameter estimates, and to check for such correlations. An excellent approach to obtain such “confidence intervals” on the parameter estimates is “bootstrapping”, which basically means that new data sets are created by sampling the original data (with replacement). Fitting the model to many of these different “new” data sets provides a variety of values for every free parameter. Sorting these, one can exclude the outliers (that are apparently due to outliers in the data), and report the range of parameter values that is typically obtained, e.g., a 95% confidence interval for a parameter corresponds to the range of its values observed in 95% of the fits to the bootstrapped data. Since bootstrapping provides a variety of estimates for each parameter, one can also check for
pairwise correlations between parameters by plotting their individual estimates as a function of each other (R provides the `pairs()` function for this).

Full textbooks have been written on this important topic, and this section is nothing more than a short introduction. We end by saying that Eq. (13.8) may (or should) involve normalization of the data, e.g., by taking the logarithm of the data and the prediction, and that it may (or should) be weighted by the variance of the data. The latter is typically done in “maximum likelihood” methods (that are favored by statisticians). Fortunately, as long one is fitting a single data set, least-square and maximum likelihood methods are expected to give identical results (provided the errors in the data are distributed normally). A more recent development is to use Bayesian inference methods, and for this the http://mc-stan.org/ platform is gaining popularity. In this course we use the least-square methods implemented in FME (Soetaert & Petzoldt, 2010), which you can easily call by the `fit()` function in Grind. The parameter bootstrap in `fit()` allows you to bootstrap the data (setting bootstrap=500 will make 500 re-sampled data sets, and will probably take a while).

13.9 Exercises

**Question 13.1. Sketch a few functions**
In this course we sketch nullclines from models with free parameters. It is very important therefore to know how to sketch arbitrary functions with free parameters.

a. Sketch \( y = \frac{h}{k+x} \).

b. Sketch \( y = \frac{x}{n+x} \).

c. Sketch \( aA - bLA - cL = 0 \) plotting \( L \) as a function of \( A \), and plotting \( A \) as a function of \( L \).

d. Sketch \( 0 = aY(1-Y) - \frac{bYX}{c+Y} \). Hint: think beforehand which variable can best be expressed as a function of the other variable.

e. Sketch \( y = a \sqrt{\frac{1-x}{Y}} - d \) assuming that \( a > d \).

f. Sketch \( y = a\sqrt{x}(1-x) \). What is the derivative when \( x = 0 \)? At what value of \( x \) will \( y \) have a maximal value?

**Question 13.2. Linearization**
Consider the function \( f(x) = x^2 \).

a. What is the derivative \( \partial_x f(x) \)?

b. Use linearization around \( x = 3 \) to estimate the function value at \( x = 3.1 \). What is the true value at \( x = 3.1 \)?

**Question 13.3. Scaling**
Scale the Lotka-Volterra predator prey model by introducing non-dimensional population densities, and scale time by the natural rate of increase of the prey.

a. Write the new model.

b. How many parameters did you lose?
Bibliography


