Mathematical Biology

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Welcome

This is the webpage of **Mathematical Biology**! Here you will find all the material for the course. Stay tuned for regular updates!

Schedule

	Mon	Tue	Wed	Thu	Fri
13:30	Lecture A209				
14:30	Lecture A209	Lecture A224			
15:30		Lecture AZZ4	Lab A202		
16:30			Lab A202		

Figure 1: Schedule of the course

Next lectures

- Mon 16th, 2024 (A209): Introduction to Mathematical Biology
- Tue 17th, 2024 (A224): Population dynamics
- Wed 18th, 2024 (A202): Introduction to numerical solution of ODEs
- Mon 23rd, 2024 (A209): no lecture! Use the slot to review basic concepts of ODEs
- Tue 24th, 2024 (A224): no lecture! As above
- Wed 25th, 2024 (A202): Correction to first assignment
- ... TBA ...

Office hours

Any time Mon-Wed, please make an appointment by email first Works best right after the lectures

Exams

The exam will consist of a written test (50% of the final grade), an oral exam (20%), and a project presentation (30%). Specifically:

- Written Test: Exercises similar to those covered in class and available on the course website.
- Oral Exam: One question at the blackboard on the theoretical part of the course.
- **Project**: Conducted in groups of up to 2 students. Typically involves reading an article, or implementing or studying (presentation of the model, qualitative analysis, simulations) a model not covered in class. The presentation will last about 25 minutes (total, not per student) and will be part of a mini-workshop open to other students in the course and the public. A selection of possible projects and articles will be available on the website.

Topics

The course "Mathematical Modeling" has a dual purpose: on one hand, to introduce students to some basic mathematical models in various areas of biology (demography, ecology, infectious diseases, enzyme reactions, physiology, molecular networks); on the other hand, to provide fundamental knowledge in the analysis and numerical simulation of ordinary and partial differential equations.

Specifically, the first part of the course is dedicated to modeling using ordinary differential equations and introduces various analytical techniques (linearization, equilibria and their stability, bifurcation, regular and singular perturbations).

- Overview of ordinary differential equations (ODEs): Solution of linear equations; equilibria and linearized stability; phase plane, limit cycles; numerical schemes for solving ODEs.
- One- or two-dimensional models in demography, ecology, epidemiology, and immunology. Non-dimensionalization of variables and parameters.
- Slow-fast systems, enzyme reaction models and their simplification using perturbative methods.
- Bifurcation of equilibria and application to predator-prey systems and molecular networks. Simplified models of important biological phenomena, such as the cell cycle and glucose-insulin oscillations.
- Excitable systems: Hodgkin-Huxley equations (overview) and FitzHugh-Nagumo equations.
- Parameter estimation for differential models.

In the second part, partial differential equation models and some techniques for constructing or approximating solutions will be studied. Additionally, some of the most interesting phenomena

of reaction-diffusion equations (traveling wave solutions, Turing mechanism) will be presented in a biological context (morphogenesis).

- Dynamical systems on networks. Examples in epidemiology.
- Introduction to partial differential equations (PDEs): Solutions by separation of variables. Fourier series. The heat equation and Brownian motion. Eigenfunctions of the Laplacian. Numerical approximation.
- Skellam and Fisher equations: Waveform solutions; stationary solutions of the boundary value problem.
- Stability of stationary solutions of reaction-diffusion systems and Turing's mechanism for morphogenesis. Conditions for its validity and examples. Chemotaxis: The Keller-Segel model.

Part I Lectures

1 Bathtub model

1.1 The bathtub model

The models of Newtonian physics are made of differential equations built starting from the second law of the dynamics. The structure of the models discussed here is instead simpler; they are based on the "balance equation of the bathtub": if Q(t) is the quantity of a substance in the bathtub we have

$$\frac{\mathrm{d}Q}{\mathrm{d}t} = Q'(t) = I(t) - O(t),$$

where

- I(t) is the *input rate* (quantity that enters per unit time)
- Q(t) is the *output rate* (quantity that leaves per unit time).

To be more precise, the assumption is that, if $I_{(t,t+\Delta t)}$ is the quantity that enters in the interval $(t,t+\Delta t)$, we have $I_{(t,t+\Delta t)}=I(t)\Delta t+o(\Delta t)$, where $o(\Delta t)$ is a higher order infinitesimal than Δt . Hence:

$$I(t) = \lim_{\Delta t \to 0} \frac{I_{(t,t+\Delta t)}}{\Delta t}.$$

The input rate I(t) is like an instantaneous velocity: the quantity entered in a given time, when that time becomes very small. Hence I(t) is measured in $[C][t^{-1}]$ units where [C] represents the concentration of the quantity Q. Similarly for the exit rate O(t).

Let us start from a very simple example. Assume $I(t) = \Lambda$ constant input flux; $O(t) = \gamma Q(t)$, i.e. exit flux is proportional to the quantity present at the moment; the proportionality constant γ is often called the *exit rate* and has the dimension $[t^{-1}]$, the inverse of time. From these assumptions we get:

$$Q'(t) = \Lambda - \gamma Q(t), \tag{1.1}$$

supplemented with some initial condition

$$Q(0) = Q_0.$$

The solution is:

$$Q(t) = e^{-\gamma t} Q_0 + \frac{\Lambda}{\gamma} \Big(1 - e^{-\gamma t} \Big).$$

Exercise

Solve Equation 1.1 with the method you prefer.

Exercise

Solve Equation 1.1 with the general formula for linear ODEs, by first defining the matrix exponential (here, just a scalar function).

Note that if $\Lambda = 0$ (no input), the solution is simply

$$Q(t) = Q_0 e^{-\gamma t}.$$

This means that the survival time of a molecule initially present follows the exponential distribution:

$$\mathbb{P}[\text{a molecule present at time 0 is present at time } t>0] = \frac{Q(t)}{Q_0} = e^{-\gamma t}.$$

From the properties of the exponential distribution, we obtain that the mean survival time $\mathbb{E}[T] = 1/\gamma$; hence the exit rate γ can be interpreted as the inverse of the mean survival time.

To be more precise, let us define a continuous random variable T, which measures the lifetime of a particle present in the bathtub. Then, the cumulative distribution F(t) of T is given by

$$\begin{split} F(t) &= \mathbb{P}[T \leq t] \\ &= 1 - \mathbb{P}[T > t] \\ &= 1 - \mathbb{P}[\text{a molecule present at time 0 is present at time } t > 0] \\ &= 1 - e^{-\gamma t}. \end{split}$$

So, we indeed have an exponential distribution. The probability density function is:

$$f(t) = F'(t) = \gamma e^{-\gamma t},$$

and the expectation is:

$$\mathbb{E}[T] = \int_0^\infty t f(t) \mathrm{d}t = \frac{1}{\gamma}.$$



Exercise

Compute the above integral explicitly.

1.2 Malthus equation

The metaphor of the bathtub can be used to model the dynamics of a population. Neglecting all differences among individuals (due to age, sex, genetic,...) we can represent a population through its size N(t); this will increase through inputs due to births and outputs due to deaths (if immigration and emigration are not considered). Hence

$$N'(t) = B(t) - D(t),$$

where B(t) = births and D(t) = deaths.

Malthus model assumes

- within a (short) time period of length Δt , each individual gives, on average, birth to $\beta \Delta t$ new individuals; hence $B(t) = \beta N(t)$;
- within the same time period Δt , each individual has probability $\mu \Delta t$ of dying; hence $D(t) = \mu N(t)$.

We get the following equation

$$N'(t) = \beta N(t) - \mu N(t) = (\beta - \mu)N(t),$$

that represents the *Malthus model*. The parameter β is known as *fertility rate*, while μ is the *mortality rate*. Finally,

$$r = \beta - \mu$$

is the (instantaneous) growth rate and is also called Malthus parameter or biological potential of the population.

With the initial condition

$$N(0) = N_0$$

the evolution of the population is completely determined. In fact, the solution is

$$N(t) = N_0 e^{rt},$$

and we see that the population will go to extinction or will grow without limits if r < 0 or r > 0, respectively. If instead r = 0, the population size is constant (births and deaths compensate.)

```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

sns.set_theme("notebook", style="whitegrid")
t = np.linspace(0,1,100)

plt.plot(t,np.exp(1*t),label='r > 0')
plt.plot(t,np.exp(-1*t),label='r < 0')
plt.plot(t,np.exp(0*t),label='r = 0')
plt.grid()
plt.legend()
plt.xlabel('Time')
plt.ylabel('Population')
plt.show()</pre>
```

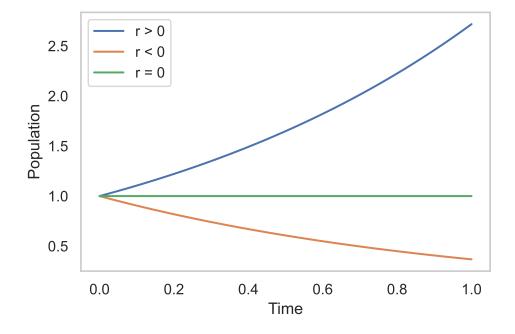


Figure 1.1: Example of solutions of Malthus equation

2 Population dynamics

This lecture is based on [@ip14, Section 1.1-1.4]

2.1 Population growth model

We have seen, using the bathtub analogy, that the fundamental balance equation of population dynamics take the form

$$N'(t) = B(t) - D(t) + I(t) - E(t),$$

where at time t we have that

- N(t) is the population,
- B(t) is the birth rate,
- D(t) is the death rate,
- I(t) is the immigration rate, and
- E(t) is the emigration rate.

There is also an integral interpretation, in fact:

$$N(t) - N(t_0) = \underbrace{\int_{t_0}^t B(s) \, \mathrm{d}s}_{\text{births}} - \underbrace{\int_{t_0}^t D(s) \, \mathrm{d}s}_{\text{deaths}} + \underbrace{\int_{t_0}^t I(s) \, \mathrm{d}s}_{\text{immigration}} - \underbrace{\int_{t_0}^t E(s) \, \mathrm{d}s}_{\text{emigration}}.$$

A population growth model is an ODE of the above form with some specific form for each term above. Note that we could provide functions above explicitly, as function of time alone. However, it should be clear that some of them like B(t) or D(t) should depend on N.

2.1.1 Malthus model

Quoting Thomas R. Malthus (1766-1834):

Population, when unchecked, increases in a geometrical ratio. Subsistence increases only in an arithmetical ratio. A slight acquaintance with numbers will show the immensity of the first power in comparison of the second.

Essay on the Principle of Population, 1798

Malthus' model is mathematical formulation of the above statement. We already derived Malthus model, but let us recall the hypotheses.

- 1. The population is *homogeneous*, that is all individuals are identical. We have a single class to represent them, that is N(t).
- 2. The population is *isolated*, so E(t) = I(t) = 0.
- 3. The habitat is *invariant*, so resources and life conditions are not affected by the environment nor the population itself.
- 4. The population is very large, so we can consider continuous functions.
- 5. On a short time scale Δt , each individual gives birth to $\beta \Delta t$ new individuals, $B(t) = \beta N(t)$.
- 6. On a short time scale Δt , each individual has probability $\mu \Delta t$ of dying, $D(t) = \mu N(t)$.

The non-negative parameters β and μ are the fertility and mortality rate, respectively. From hypothesis 4, we have that μ and β are constant. We introduce the *growth rate*

$$r = \beta - \mu$$

also called Malthus parameter or biological potential.

The Malthus' model reads:

$$N' = rN, \quad \Rightarrow \quad N(t) = e^{rt}N(0),$$

thus, when r > 0, the growth of population is geometrical and unbounded, as predicted by Malthus.

2.1.2 Expected life

We have seen that, in absence of births, the population goes like

$$N(t) = e^{-\mu t} N_0,$$

thus, we could say that the probability of surviving up to time t is $e^{-\mu t}$. Specifically, the *life* expectancy L is a random variable such that

$$\mathbb{P}[L > t] = e^{-\mu t}.$$

Thus, the cumulative distribution of L is

$$F_L(t) = \mathbb{P}[L < t] = 1 - \mathbb{P}[L > t] = 1 - e^{-\mu t},$$

and the probability density function is

$$f_L(t) = F'_L(t) = \mu e^{-\mu t}$$
.

We conclude that $L \sim \text{Exp}[\mu]$, the exponential distribution. The average life expectancy is:

$$\mathbb{E}[L] = \int_0^\infty s f_L(s) \, \mathrm{d}s = \int_0^\infty s \mu e^{-\mu s} \, \mathrm{d}s = \frac{1}{\mu}.$$

We have another interpretation of μ : it is the reciprocal of the expected life time.

2.1.3 Basic reproduction number

Let us rescale the equation and put it in non-dimensionalized form. This is a fundamental step in general, because

- 1. it reduces the number of parameters,
- 2. it removed scale effects (units are removed),
- 3. it highlights the determining factors of the model (maybe what matters is not this or that parameter, by their ratio or sum).

Here, we rescale as follows:

$$\tau = \mu t, \quad u = N,$$

so that time is now in units of "expected life time": $\tau = 1$ means $t = \mu^{-1} = \mathbb{E}[L]$. We have that

$$N' = \frac{\mathrm{d}N}{\mathrm{d}t} = \frac{\mathrm{d}u}{\mu^{-1}\mathrm{d}\tau} = \mu \frac{\mathrm{d}u}{\mathrm{d}\tau} = \mu \dot{u}.$$

We use the "dot" notation \dot{u} for the derivative for the non-dimensional form, just to remember that now the time is τ and not t. We finally obtain:

$$\dot{u} = \mu^{-1} N' = \frac{\beta}{\mu} N - N = (R_0 - 1) u,$$

where we defined the basic reproduction number

$$R_0 = \frac{\beta}{\mu} = \beta \mathbb{E}[L].$$

We could interpret it as the average number of newborns produced by one individual during his whole life. Note that R_0 is non-dimensional.



• Exercise

Why it does not make much sense to use the scaling $\tau = rt$?

2.1.4 Migration

In the presence of migration, say with a constant rate, we have the ODE:

$$N' = rN + m = f(N), \tag{2.1}$$

where m = I - E. If positive, there is a net immigration, otherwise emigration.

In order to study how the model will behave, we have 3 options:

- 1. Solve the problem analytically, that is finding $N(t) = \dots$ explicitly.
- 2. Solve the problem numerically, which is always possible.
- 3. Study the problem qualitatively.

The last option has the advantage that we can be generic, there is no need for a specific value of the parameters or the initial condition. The qualitative study consists in the following steps:

1) Fixed points of the system. A fixed point or equilibrium (see ?@def-equilibrium) is a constant solution of the ODE. We can find it by setting the right hand side to zero:

$$N' = 0 \Leftrightarrow rN + m = 0.$$

The model has a single equilibrium for

$$N=N^*=-\frac{m}{r}=\frac{m\mathbb{E}[L]}{1-R_0}$$

2) Biological feasibility. Equilibria must be biologically feasible. For this model, we need to check that N^* is non-negative, otherwise it doesn't make sense biologically speaking. Therefore

 $N^* \ge 0$, \Leftrightarrow m and r have opposite sign and $r \ne 0$.

3) Local stability. Informally, an equilibrium is locally stable when, starting from a neighborhood of it, the solution stays close to it for $t \to \infty$. It is asymptotically stable when the solution converges toward the equilibrium for $t \to \infty$. It is unstable otherwise. See ?@def-lyapunov for a more precise statement.

The local stability is determined by the sign of the derivative of the right hand side, that is $f'(N^*)$ for f(N) = rN + m. In general (see ?@sec-linearization),

- when $f'(N^*) < 0$, the equilibrium is asymptotically stable, and
- when $f'(N^*) > 0$, the equilibrium is unstable.

To see this in this specific case, let us define $w(t) = N(t) - N^*$. Then,

$$w' = N' = rN + m = r(N - N^*) = rw.$$

Note that f'(N) = r. We have that:

$$w(t) = w_0 e^{rt},$$

hence,

- if r < 0, then $w \to 0$ for all w_0 , so $N(t) \to N^*$. The equilibrium is locally asymptotically stable.
- if r > 0, then $w \to \infty$ and the equilibrium is unstable.
- 4) Global stability. What if we start very far away from the equilibrium? In this particular case, with a linear ODE, the local stability argument applies also globally, thus the equilibrium is globally attractive. But for general, nonlinear ODEs this may not be the case, so we perform the analysis anyway. Note that if $N(0) = N_0 > N^*$, then

$$N'(0) = rN(0) + m = r(N_0 - N^*) < 0,$$

so the derivative of the solution is negative (assuming r < 0). Furthermore, for $N(t) > N^*$, the derivative is always negative. So, the solution must be monotonically decreasing. But the solution is bounded from below by the equilibrium $N(t) = N^*$, so we conclude that:

$$N(t) \to N^*$$

for all $N_0 \ge N^*$. Symmetrically, when $N_0 < N^*$, the derivative is positive and stays positive for all t, so the solution is monotonically increasing. Hence:

$$N(t) \to N^*$$

for all N^0 . The equilibrium is therefore globally stable when r < 0.

5) Phase portrait. The phase portrait of a dynamical system is the collection of all possible orbits. Here, the phase space is $\Omega = [0, \infty)$. The only equilibrium we have, N^* , is a barrier to other orbits, because orbits cannot intersect (See ?@prp-orbits). Therefore:

```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
sns.reset_defaults()
sns.set_context('notebook')
r,m = -0.5, 1.7
Neq = -m/r
f = lambda N: r*N + m
N = np.linspace(1.5, 5, 10)
fig, ax = plt.subplots()
ax.spines[["bottom"]].set_position(("data", 0))
ax.spines[["top", "right", "left"]].set_visible(False)
ax.xaxis.set_ticks([])
ax.yaxis.set ticks([])
ax.plot(1, 0, ">k", transform=ax.get_yaxis_transform(), clip_on=False)
ax.set_xlabel('N', loc='right', labelpad=10.0)
ax.plot(Neq,0,'r.',markersize=16, zorder=99)
ax.text(Neq, 3e-3, r'$N^*$', fontsize=12, ha='center', va='bottom')
ax.quiver(\mathbb{N}, 0*\mathbb{N}, f(\mathbb{N}), 0.0, \text{color='blue'}, \text{zorder=80})
ax.set_xlim((0,6))
ax.set_ylim((-1e-2,1e-2))
fig.subplots_adjust(left=0, right=1, top=0.1, bottom=0.05)
plt.show()
```

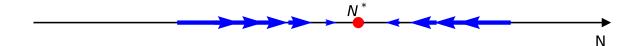


Figure 2.1: Phase space

For this problem we actually have the general solution

$$N(t)=(N_0-N^\ast)e^{rt}+N^\ast.$$

```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
r,m = -0.5, 1.7
Neq = -m/r
sns.set_theme("notebook", style="whitegrid")
t = np.linspace(0,10,100)
N = lambda N0: (NO-Neq)*np.exp(r*t) + Neq
fig, ax = plt.subplots()
ax.plot(t,N(Neq - 1), 'b', label='$N_0 < N^*$')
ax.plot(t,N(Neq + 1),'b',label='$N_0 > N^*$')
for delta in np.arange(0.1,0.9,0.1):
    ax.plot(t,N(Neq + delta),'b',lw=0.4)
    {\tt ax.plot(t,N(Neq - delta),'b',lw=0.4)}
ax.plot(t,N(Neq),'r-',lw=2,label='$N^*$')
ax.grid()
ax.legend()
ax.set_xlabel('Time')
ax.set_ylabel('Population')
plt.show()
```

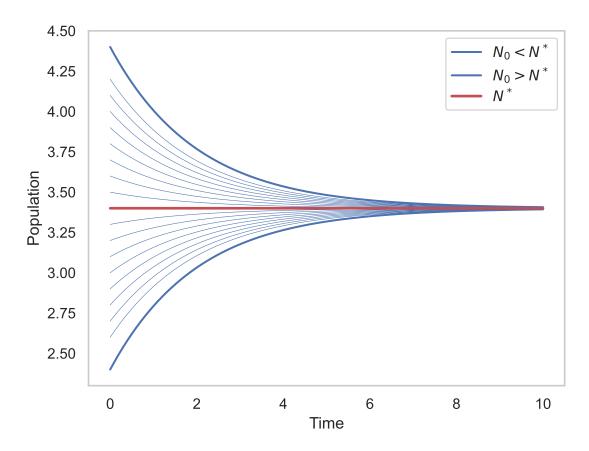


Figure 2.2: Example of trajectories

The case m < 0 and r > 0 is also interesting. Here, the equilibrium N^* is positive, but unstable. For $N_0 > N^*$ the population still grows exponentially, so emigration as no effect on the overall population. But for $N_0 < N^*$ the solution will become negative in finite time: the model is not correct. The reason is simple: the emigration m cannot be constant (like the immigration), it must depend on N as well.



2.1.5 Exogenous variability

By exogenous variability we mean variability in the parameter r that does not depend on the population. (Endogenous variability is when the parameters depend on internal variables like

N.) Thus, we consider the problem:

$$N' = r(t)N$$
,

for r(t) continuous function. An example could births and deaths that depend on climate or temperature. The solution is:

$$N(t) = N_0 e^{\int_{t_0}^t r(s) \,\mathrm{d}s}$$

We can also rewrite the solution as:

$$N(t) = N_0 e^{(t-t_0)\frac{1}{t-t_0} \int_{t_0}^t r(s) \, \mathrm{d}s},$$

showing that if the limit

$$r^* = \lim_{t \to \infty} \frac{1}{t - t_0} \int_{t_0}^t r(s) \,\mathrm{d}s$$

exists then the asymptotic behavior of the solution is:

$$N(t) \approx e^{r^*(t-t_0)}, \quad t \gg 1.$$

An interesting case is when r(t) is *periodic*, that is there exists T > 0 such that r(t+T) = r(t). In this case the above formula still applies, but we can "forget" the limit (check Assignment 4 for a proof) and take:

$$\bar{r} = \frac{1}{T} \int_0^T r(s) \, \mathrm{d}s,$$

and write the solution for any $t \ge t_0$ as:

$$N(t) = e^{\bar{r}(t-t_0)} N_{\pi}(t),$$

for some T-periodic function N_{π} . Note that

$$N(t_0 + kT) = e^{\bar{r}kT} N_\pi(t_0) = e^{k\bar{r}} N(t_0),$$

so after k periods the solution grows by a factor $e^{k\bar{r}}$. This factor is called Floquet multiplier.

3 Logistic model

This lecture is based on [@ip14, Section 1.5-1.6]

3.1 Logistic model

While populations can follow a phase of exponential growth for a limited amount of time, it seems impossible that this can go forever and that populations can grow to infinity. Indeed, we expect that there exists a negative effect of crowding, which can be stated in words as follows:

An increase of the population size produces a fertility decrease and a mortality increase; since resources are limited, if the population size exceeds some threshold level, the habitat cannot support the growth.

This simple statement tries to summarize the complex phenomenology of *intraspecific competition* due to many factors such as resource availability, habitat pollution and waste, predation increase, energy consumption for social organization.

The simplest way to include this effect into a model, is to suppose that fertility decreases and mortality increases linearly with the number of individuals; namely

$$\beta(N) = \beta_0 - \tilde{\beta}N,$$

$$\mu(N) = \mu_0 + \tilde{\mu}N,$$

where β_0 , μ_0 , $\tilde{\beta}$, and $\tilde{\mu}$ are non-negative constants. Hence:

$$B(N) = \beta(N)N = \beta_0 N - \tilde{\beta}N^2,$$

$$D(N) = \mu(N)N = \mu_0 N + \tilde{\mu}N^2.$$

The resulting equation is generally written, after simple algebraic steps, as

$$\begin{cases} N' = r \Big(1 - \frac{N}{K} \Big) N, \\ N(0) = N_0, \end{cases}$$

where $r = \beta_0 - \mu_0$ and $K = r/(\tilde{\beta} + \tilde{\mu})$. These parameters are usually called *intrinsic growth* rate and carrying capacity.

A couple of comments are necessary: first of all, either $\tilde{\beta}$ or $\tilde{\mu}$ can be 0, but not both, otherwise there is no effect of crowding and K is not well-defined. Note also that, if $\tilde{\beta} > 0$, the birth rate B(t) would become negative if N(t) is too large, which does not make sense biologically. However, this does not cause mathematical problems and the biological nonsense would occur only at population levels not normally reached, so we neglect this problem.

We will generally assume that r > 0, so that also K > 0. In that case, the behaviour of solutions to that equation displays a first phase of exponential growth, followed by convergence to the limiting value K. The general solution is

$$N(t) = \frac{KN_0}{N_0 + (K - N_0)e^{-rt}}.$$

When $N_0 < K/2$, the resulting sigmoid curve have been called *logistic curve*, so that equation is also named *logistic equation*.

The logistic equation is extremely common in experimental biology. Below, data fitted to a logistic for micro-organisms.

```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
sns.set_theme("notebook", style="whitegrid")
# from CRAN gauseR gause 1934 book f04.rda
t = [1.0, 2.0, 3.0, 4.0, 5.0, 5.0, 6.0, 6.0]
N = [22,129,334,374,376,356,397,367]
K = 375
r = 2.309
NO = 2.0
tt = np.linspace(0,6,1000)
logistic = K*NO/(NO + (K-NO)*(np.exp(-r*tt)))
plt.axhline(y=K,color='k',linestyle='--',linewidth=1.0)
plt.plot(tt, logistic, label='$\frac(K N_0){N_0+(K-N_0)e^{rt}}$')
plt.plot(t,N,'.',markersize=16,label='Data')
plt.xlabel('Days')
plt.ylabel('Number of individuals')
plt.title(f'Fit with K = \{K\}, N_0 = \{N0\}, r = \{r\}')
plt.annotate(f'K = {K}',(1,K),ha='center',va='bottom')
plt.legend()
```

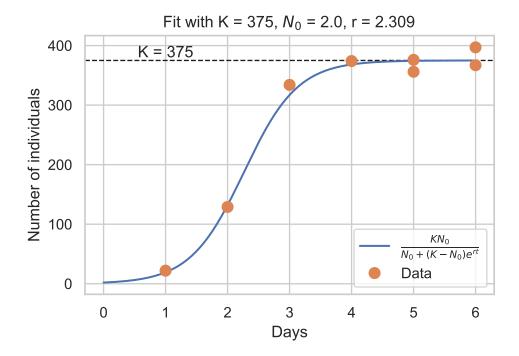


Figure 3.1: Fitting of *Paramecium caudatum* data using the logistic model. Data from (Gause 1934, fig. 4).

As before, we can non-dimensionalize the equation. Now we select:

$$\tau = rt, \quad u = \frac{N}{K},$$

so that u = 1 means that we are at carrying capacity. Substituting:

$$\dot{u} = u(1 - u).$$

The new equation has no parameters. Thus, the general solution of the logistic equation is just

$$N(t) = Ku(rt).$$

The absence of parameters in the non-dimensional equation means that its dynamic is always the same, up to a rescaling. We say that all parametric solutions (as we vary r and K) are topologically equivalent. Here, we cannot expect bifurcation, as we shall see.

3.2 Generalized logistic model

In general, we can take β and μ as generic functions of N, thus:

$$r(N) = \beta(N) - \mu(N)$$

is also a generic function of N. A generic growth model reads:

$$N' = r(N)N = f(N).$$

We can implicitly solve this equation, in fact:

$$N(t) = N(0)e^{\int_{t_0}^t r(N(s)) ds}$$

Thus, if N(0) > 0, then N(t) > 0 for all time. This is important to verify, since a population cannot be negative. Here, we need no further restriction on r(N) so to verify the condition.

How about equilibria? We have that $E_0 = 0$ is always an equilibrium. (Thus, since orbits cannot cross it, they positive stay positive foreover. This is another possible proof.) It is called extinction equilibrium. Its stability follows from:

$$f'(N)|_{N=E_0} = r'(0) \cdot 0 + r(0) = r(0).$$

The stability of E_0 is given by r(0), which is called *intrinsic growth rate*. It is the growth rate we observe for very small population size. When r(0) > 0 the extinction equilibrium is unstable. Equivalently, it is unstable when

$$R_0 = \frac{\beta(0)}{\mu(0)} > 1.$$

How to capture a general logistic effect? By general we mean what we quoted above: a population increase should correspond to a decrease of fertility and an increase of mortality. Thus:

$$r'(N) < 0$$
, and $\lim_{N \to \infty} r(N) < 0$.

The second hypothesis avoids the existence of positive horizontal asymptotes. Biologically, a sufficiently large population has always a negative growth rate.

We can now study more equilibria, those corresponding to r(N) = 0.

• If r'(0) < 0, then by monotonicity we conclude that r(N) < 0 for all N, so $E_0 = 0$ is the only equilibrium and the population is doomed.

• If r'(0) > 0, we have one additional (unique) equilibrium N^* , that we denote by K: that is, r(K) = 0. Since

$$f'(K)=r'(K)K+\underbrace{r(K)}_{=0}=r'(K)K<0,$$

this equilibrium is (globally) asymptotically stable. This equilibrium is also called *carrying* capacity.

The classic logistic equation has r(N) = r(1-N/K). The θ -logistic model (or Bernoulli model) has

$$r(N) = r(1 - (N/K)^{\theta}),$$

for $\theta > 0$. There are a multitude of models for r(N), some we will explore in the assignments (see also figure below). Nonetheless, the above hypotheses always imply a sigmoid growth, when $N(0) \in (0, K)$.

```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
sns.set_theme("notebook", style="whitegrid")
N = np.linspace(0, 1.2, 1000)
plt.plot(N, 1-N,label='$r=1-u$ (Verhulst)')
plt.plot(N, 1-N**2.0,
         label='$r=1-u^\\theta$ (Bernoulli, $\\theta=2$)')
plt.plot(N, (1-N)/(1+2*N),
         label='$r = \frac{1-u}{1+\alpha u}$ (Smith, $\alpha=2$)')
plt.plot(N, (np.exp(3*(1-N))-1)/(np.exp(3)-1),
         label='$r = \frac{e^{\sigma u}-1}{e^{\gamma u}-1}$ (Ricker, \$\gamma = 3\$)')
plt.plot(N[1:], -np.log(N[1:]), label='$r = -\log u$ (Gompertz)')
plt.ylabel('Growth rate')
plt.xlabel('N / K')
plt.ylim([-0.5, 1.5])
plt.legend()
```

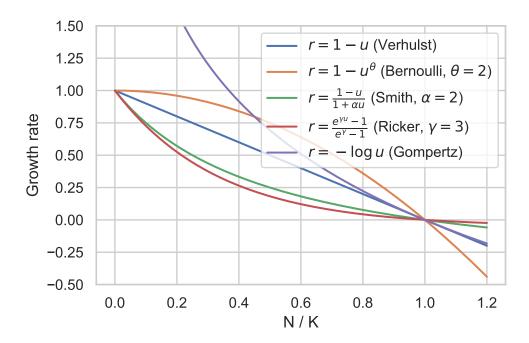


Figure 3.2: Different growth model giving a logistic effect. We set u = N/K, where K is the carrying capacity.

Exercise

Verify that the above models are "logistic", in the sense that they satisfy the hypotheses. Show that the Bernoulli model yields sigmoid solutions. (Hint: study N' and N''.)

Exercise

Integrate the Gompertz model, $\dot{u} = -u \log u$. This model is very common in the study of tumor cells proliferation. (Hint: set $u(t) = e^{w(t)}$.)

3.3 Allee effect

(Story time) The great auk was a bird that became extinct by the end of the 19th century. They were found at the northern Atlantic (Canada, Scotland, Iceland), usually on rocky islands. The overall population was composed by millions of individuals, before sailors and hunters started killing them for their meat, feathers, and oily fat.



Figure 3.3: The Great Auk (from Wikipedia) $\,$

As it could be expected, the auk population drastically reduced and the bird disappeared from many islands very quickly. Governments became aware of the situation in the 18th century, and some laws forbidden the hunt of the great auk, although with limited success.

Some species like the great auk are not able to fully recover, even in the absence of predation (or with a small one). In order for a species to go to excintion with no predation, say for

$$N' = r(N)N$$
,

we would need r(0) < 0, otherwise the equilibrium N = 0 is not stable. But this would lead to no further equilibria under the hypotheses of general logistic growth. Hence, we can further generalize the hypotheses as follows: the function r(N) is such that

- 1. there exists $N_m > 0$ such that r'(N) > 0 for $N < N_m$ and r'(N) < 0 otherwise;
- 2. $r(N_m) > 0$;
- $3. \ \lim_{N\to\infty} r(N) < 0.$

Therefore, we certainly have the equilibrium $K > N_m$ (the carrying capacity). However, if r(0) < 0, we also have another equilibrium at $T \in (0, N_m)$. In this case, we say that we have a *strong Allee effect*. On the other hand, for r(0) > 0 there are no further equilibria, thus we have a *weak Allee effect*.

Let us study the stability for r(0) < 0. Remember that

$$f'(N) = r'(N)N + r(N).$$

We have 3 equilibria:

- $N = E_0 = 0$, which is asymptotically stable, since f'(0) = r(0) < 0.
- $N = T \in (0, N_m)$, which is unstable, since f'(T) = r'(T)T > 0.
- $N = K > N_m$, which is asymptotically stable, since f'(K) = r(K)K < 0.

Hence, we have the following result: if N(0) < T, then $N(t) \to 0$ (extinction), otherwise if N(0) > T, then $N(t) \to K$ (survival). We call T the threshold population for survival.

```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
from scipy.integrate import solve_ivp

sns.set_theme("notebook", style="whitegrid")

r = 0.5
T,K = 0.2,1.0
f = lambda t,N: r*(N/T-1)*(1-N/K)*N
```

```
fig,ax = plt.subplots()
u0 = [0.1,0.15,0.25,0.3,0.6,0.8]
sol = solve_ivp(f,[0,8],u0,max_step=0.05)
ax.plot(sol.t,sol.y.T,lw=2.0)
ax.axhline(y=T,color='r',linestyle='--')
ax.grid(True)
ax.legend([f'$u_0 = {u}$' for u in u0])
plt.show()
```

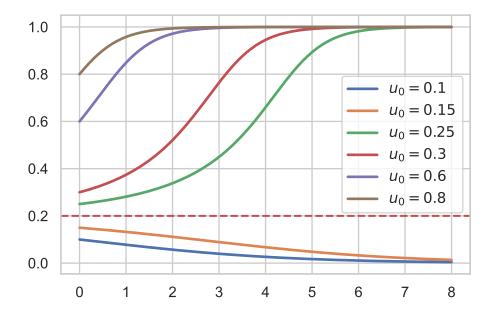


Figure 3.4: Solutions of the equation N'=rN(N/T-1)(1-N/K). Note the threshold value for N=T.

The Allee effect may be found in other situations, for instance when the predation rate is a non-linear function of N.

4 Predation models

This lecture is based on [@ip14, Section 1.8-1.9]

4.1 Generalist predation

Predation is a fundamental topic in ecology and the main interaction between species. It must be understood in a broader sense: fishing, harvesting, hunting are all form of predation.

The simplest model of predation consists in formally increasing the mortality rate of N by an extra rate aP^* , that is

$$N' = r(N)N - aP^*N = f(N),$$

where $P^* > 0$ is the number of predators and a > 0 is the attack rate or effective killing rate. We note that the death rate aP^*N is proportional to both the number of predators P^* and the number of preys N, according to the law of mass action, as suggested by Volterra with the method of encounters. The idea is similar to collision theory for ideal gases.

This type of predation is also called *generalist*, in the sense that predators' survival does not depend on the survival of the prey population N. If the preys go to extinction, the predator will hunt something else. A *specialized* predator, on the other hand, will suffer from a low level of N, as we shall see next week.

The equilibria of the equation are: $N = E_0 = 0$, as usual, and the zeros of:

$$r(N) = aP^*$$
.

- If $aP^* > r(0)$, then we have no additional equilibria, because r'(N) < 0.
- If $aP^* < r(0)$, then there exists a second equilibrium $N^* > 0$.

The stability of the second equilibrium follows from

$$f'(N^*) = r'(N^*)N^* + r(N^*) - aP^* = r'(N^*)N^* - aP^* < 0,$$

because r'(N) < 0. So N^* is asymptotically stable.

The stability of E_0 is similar:

$$f'(E_0) = r'(0) \cdot 0 + r(0) - aP^* = r(0) - aP^* > 0,$$

meaning that it is unstable. Concluding:

- If $aP^* > r(0)$, we have one stable equilibrium $E_0 = 0$, thus the population will go to extinction. In fact, the predation level is high.
- If $aP^* > r(0)$, $E_0 = 0$ is unstable but we have another equilibrium $0 < N^* < K$ asymptotically stable. Thus, the predation is sustainable.

The case $aP^* = r(0)$ is delicate. We have a single equilibrium, $E_0 = 0$, but $f'(E_0) = 0$, so we cannot deduce the stability from the linearization (why?). By inspecting the sign of E_0 , we observe that f(N) < 0 for N > 0, so E_0 is attractive. However, for N < 0 we have that f(N) < 0, thus it is repulsive (biologically, we do not care because N < 0 is irrelevant.) This type of equilibrium is called saddle-node.

The point $aP^* = r(0)$ is a bifurcation point, specifically a transcritical bifurcation (See ?@sectransbif). Roughly speaking, the dynamic before and after the bifurcation point is topologically different: in one case we have one equilibrium, in the other 2 equilibria. Actually, we still have 2 equilibria for $aP^* > r(0)$, one being negative. Thus, what really happens is that as we increase aP^* the two curves of equilibria $(N = 0 \text{ and } N = E_0)$ crosses and swap stability.

```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
sns.set_theme("notebook", style="whitegrid")
with plt.xkcd(scale=0.5):
    fig, ax = plt.subplots()
    sns.despine()
    ax.xaxis.set_ticks([])
    ax.yaxis.set_ticks([])
    ax.plot([0,1],[0,0],'r-')
    ax.plot([0,1,1.2],[1,0,0],'b-')
    ax.plot([1,1.2],[0,-0.2],'r-',alpha=0.5)
    ax.plot([1],[0],'k.',markersize=16)
    ax.grid(False)
    ax.set_xlabel('$P^*$')
    ax.set_ylabel('$N^*$')
    ax.set_xlim([0,1.2])
```

```
[N,P] = np.mgrid[0.01:1.2:30j,0.01:1.2:30j]
D = N*(1-N) - P*N
ax.quiver(P,N,np.zeros_like(D),D,alpha=0.5)
plt.show()
```

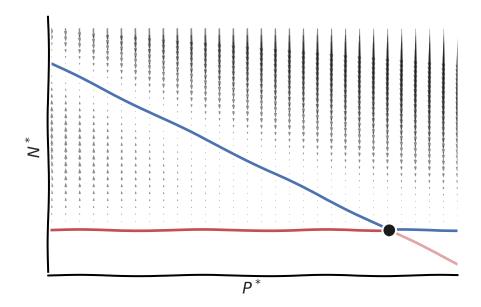


Figure 4.1: Bifurcation diagram for the model with generalist predation. In blue, the stable equilibrium, in red the unstable one. Beyond the bifurcation point (transcritical, in black) there is only one equilibrium.

4.2 Holling type predation models

More generally, we define the predation as:

$$N' = r(N)N - \pi(N)P^*,$$

where $\pi(N)$ is called *functional response*. The functional response can be interpreted as follows: $\pi(N)\Delta t$ is the number of preys killed in Δt units of time by a single predator.

For the simplest model, we have $\pi(N) = aN$. However, this is not realistic, because for very large N the predation rate cannot grow undefinitely, it must reach some limiting value. For instance, a predator needs some time to consume the prey, and this time cannot be reduced below a certain limit. Similarly, it is reasonable that at low density of preys, say when N is small, predation is harder.

In general, we can assume that:

- 1. $\pi(0) = 0$, no preys no predation, and
- 2. $\pi'(N) > 0$, the more preys, the higher the predation rate.

Holling (1965) proposed the following types of functional responses:

• Holling type I

$$\pi(N) = \begin{cases} aN, & 0 \le N \le N^*, \\ aN^*, & N > N^*. \end{cases}$$

This model is exactly like the linear one, but it assumes that for $N > N^*$ we have constant predation rate aN^* . The parameter a is called attack rate, and it measures, after an encounter between prey and predator, the success rate of predation. Note that the function $\pi(N)$ is not \mathcal{C}^1 but it is Lipschitz.

· Holling type II

$$\pi(N) = \frac{aN}{1 + a\tau N},$$

with $a, \tau > 0$. This is a smooth version of Holling type I. For small N, $\pi(N) \approx aN$, so the meaning of a is the same as above. For large N, we have that $\pi(N) \to 1/\tau =: \alpha$, which is called maximum killing rate. That is, α is the number of preys killed by one predator in a unit of time, when the number of preys is very large. Alternatively, we can interpret τ as the time required by the predator to consume the prey.

• Holling type III

$$\pi(N) = \frac{\alpha N^{\theta}}{\nu^{\theta} + N^{\theta}},$$

with $\alpha, \nu > 0$ and $\theta > 1$. The last type also accounts for a lower predation rate as low density of preys. In fact, for small N and $\theta > 1$ we have $\pi'(0) = 0$. For $N = \nu$, $\pi(\nu) = \frac{\alpha}{2}$, and for $N \to \infty$ we have $\pi(N) \to \alpha$, the maximum killing rate. Thus, ν is the number of preys at which the killing rate is exactly half of the maximum one.

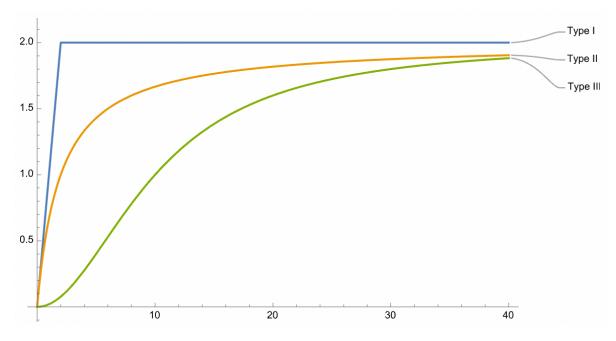


Figure 4.2: Different types of Holling predations

It is possible to justify Holling type II in a few ways. One, we will see in the completely different context of enzymatic reactions. A simpler one is as follows. In a time T, a single predator will spend $1/\pi(N)$ time in hunting. (Always keep in mind the bathtub example!) But the total time splits into T_s , the time spent seeking for a prey, and τ , the time needed to consume a prey. The time τ is fixed, no matter how large is N. The time T_s , however, is exactly $(aN)^{-1}$, because the more preys the easier is to catch them. Putting all together we have:

$$\frac{1}{\pi(N)} = T = \tau + T_s = \tau + \frac{1}{aN}, \quad \Rightarrow \quad \pi(N) = \frac{aN}{1 + a\tau N}.$$

4.3 Spruce budworm model



Figure 4.3: The effect of the spruce budworm on a forest.

The spruce budworm is an insect that feeds on needles of balsam fir trees (see this website). If needles are removed, the tree dies. Historical data in Canada evergreen forests, where the budworm is present, shows that in most years the budworm density is very low. However, in a outbreak year, the budworm population spikes and can kill up to 80% of mature trees in the forest. The period of the outbreak is roughly 30-70 years.

The spruce budworm model has been introduced in Ludwig et al. (1978). They proposed a system of 3 variables:

- 1. N(t), the budworm density,
- 2. S(t), the habitat space for larvae, and
- 3. E(t), a measure of food energy reserves available to the budworm.

We focus here on the equation for N(t). In fact, S(t) and E(t) will vary very slowly compared to N(t), thus they can be assumed constant. (This argument can be made rigorous, as we shall see for enzymatic reactions.)

The equation for N(t) reads as follows:

$$N' = rN\left(1 - \frac{N}{K}\right) - \frac{\alpha P^*N^2}{\nu^2 + N^2}.$$

The first term is the logistic growth. The second one is the predation of the budworms due to birds. This is Holling type III. Note that the parameters are fixed numbers (they do not depend on time), but they will depend on S and E, somehow. Thus, it will be interesting to see what happens to the system as we change them.

Since we have too many parameters, we proceed with non-dimensionalization. Here we select:

$$\tau = \frac{t}{T}, \quad u = \frac{N}{\nu},$$

for some T > 0 to be selected. We have:

$$\frac{\nu}{T}\dot{u} = r\nu u \left(1 - \frac{\nu u}{K}\right) - \frac{\alpha P^* u^2}{1 + u^2},$$

thus by selecting

$$T = \frac{\nu}{\alpha P^*}, \quad \rho = \frac{r\nu}{\alpha P^*}, \quad q = \frac{K}{\nu}$$

we arrive at

$$\dot{u} = \rho u \left(1 - \frac{u}{q} \right) - \frac{u^2}{1 + u^2},$$

where we are left with only 2 parameters:

- ρ is proportional to the intrinsic growth rate, while
- q is the carrying capacity normalized to the half-saturation population ν .

4.3.1 Equilibria and stability

As usual, we start by looking for equilibria of the system, that is solutions of

$$\rho u \left(1 - \frac{u}{q} \right) - \frac{u^2}{1 + u^2} = 0.$$

We have that u=0 is an equilibrium. The others solve the equation

$$\rho\left(1 - \frac{u}{q}\right) - \frac{u}{1 + u^2} = 0,$$

which would lead to a 3rd-order polynomial equation, thus we can expect up to 3 real solutions. An analytical approach is not practical. However, equilibria are intersections of the two curves f(u) and g(u) where

 $f(u) = \rho \Big(1 - \frac{u}{q}\Big), \quad g(u) = \frac{u}{1 + u^2}.$

The function f(u) represents the per capita growth rate of u, whereas g(u) is the per capita death rate due to predation. Thus, solutions of the equation are equilibria of the system. Since the function g(u) does not depend on any parameters, we can fix it and simply change f(u), which is a segment.

```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
sns.set_theme("notebook", style="whitegrid")
u = np.linspace(0,12,1000)
fig,axs = plt.subplots(1,2,figsize=(9,3))
q = 4
uq = np.linspace(0,q,2)
axs[0].plot(u, u/(1+u**2))
for rho in np.linspace(0.2,0.8,10):
    pr = np.polynomial.Polynomial([g*rho,-g-rho,g*rho,-rho])
    rr = np.real(np.array([r for r in pr.roots() if np.isreal(r) and r >= 0]))
    axs[0].plot(uq,rho*(1-uq/q),'k',lw=0.5)
    axs[0].plot(rr,rho*(1-rr/q),'k.')
q = 10
uq = np.linspace(0,q,2)
axs[1].plot(u, u/(1+u**2))
for rho in np.linspace(0.1,0.8,6):
    pr = np.polynomial.Polynomial([q*rho,-q-rho,q*rho,-rho])
    rr = np.real(np.array([r for r in pr.roots() if np.isreal(r) and r >= 0]))
    axs[1].plot(uq,rho*(1-uq/q),'k',lw=0.5)
    axs[1].plot(rr,rho*(1-rr/q),'k.')
p = np.polynomial.Polynomial([q,0,-q,2])
rho = lambda u: q*u/((1+u**2)*(q-u))
        = np.real(np.array([r for r in p.roots() if np.isreal(r) and r >= 0]))
bif rho = rho(bif u)
for r,u in zip(bif_rho,bif_u):
```

```
axs[1].plot(uq,r*(1-uq/q),'r',lw=1.0)
axs[1].plot(u,r*(1-u/q),'r.',markersize=8)

for ax in axs:
    ax.grid(False)
    sns.despine()
    ax.xaxis.set_ticks([])
    ax.yaxis.set_ticks([])
    ax.set_xlabel('u',loc='right')
    ax.set_xlim(0,12)
    ax.set_ylim(0,1)

axs[1].yaxis.set_ticks(bif_rho)
axs[1].yaxis.set_ticklabels(['$\\rho_2$','$\\rho_1$'])

plt.show()
```

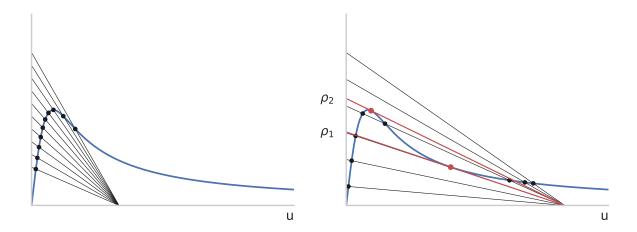


Figure 4.4: Equilibria for the spruce budworm model. On the left, the case of small q, on the right the case of large q.

We can see from the figure that when q is small, we only have a single equilibrium. When q is large, we can have 1, 2, or 3 additional equilibria, depending on ρ : given $\rho_1 < \rho_2$ we have:

- 1. If $\rho < \rho_1$, then there exists a single equilibrium $u_1^* \ll q$. This is the *refuge* equilibrium (low population). The equilibrium is globally stable, because f(u) g(u) > 0 for $u < u_1^*$ and f(u) g(u) < 0 for $u > u_1^*$.
- 2. If $\rho > \rho_2$, then there exists a single equilibrium u_3^* close to q. This is the *outbreak* equilibrium (large population). The equilibrium is globally stable, because f(u) g(u) > 0 for $u < u_3^*$ and f(u) g(u) < 0 for $u > u_3^*$.

3. If $\rho_1 < \rho < \rho_2$, then there exist 3 equilibria $u_1^* < u_2^* < u_3^*$. The stability of u_1^* and u_3^* is as above, but now locally. The equilibrium u_2^* is unstable.

The case 3. is the most interesting one. If $u(0) < u_2^*$, then $u \to u_1^*$, otherwise $u \to u_3^*$. This is again a threshold effect.

4.3.2 Bifurcation diagram

As we change ρ , we may have a different number of equilibria. Thus, there must be some bifurcation occurring. The equilibria are on the curve defined by

$$h(u,\rho)=\rho\Big(1-\frac{u}{q}\Big)-\frac{u}{1+u^2}=0.$$

The function $h(u,\rho)$ is smooth in ρ , since $\partial_{\rho}h \neq 0$ for $u \in [0,q)$. Thus we can write ρ as a function of u:

$$\rho(u) = \frac{qu}{(1+u^2)(q-u)}.$$

Since $h(u, \rho(u)) = 0$, the curve $(u, \rho(u))$ with $u \in [0, q)$ defines a curve of equilibria, shown below:

```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
sns.set_theme("notebook", style="whitegrid")
q = 12 #3*np.sqrt(3)
u = np.linspace(0, 0.9*q, 1000)
rho = lambda u: q*u/((1+u**2)*(q-u))
p = np.polynomial.Polynomial([q,0,-q,2])
bif_u = np.array([r for r in p.roots() if np.isreal(r) and r >= 0])
bif_rho = rho(bif_u)
rho_neg = p(u) < 0
with plt.xkcd(scale=0.5):
    fig, ax = plt.subplots()
    sns.despine()
    ax.xaxis.set_ticks([])
    ax.yaxis.set_ticks([])
```

```
ax.axhline(y=q,color='k',linestyle='--',linewidth=1.0)
ax.plot(rho(u),0*u,'r')
ax.plot(rho(u), u, 'b')
ax.plot(rho(u)[rho_neg], u[rho_neg], 'r')
ax.plot([0],[0],'k.',markersize=16)
ax.plot(bif_rho,bif_u,'k.',markersize=16)
ax.grid(False)
ax.set_xlabel('$\\rho$')
ax.set_ylabel('$\\rho$')
ax.set_ylabel('$\\rho$')
ax.fill_between(rho(u), q, where=rho_neg, facecolor='gray', alpha=.2)

if len(bif_u) > 0:
    ax.annotate(' $\\rho_2$',(bif_rho[0],bif_u[0]),ha='left',va='center')
    ax.annotate('$\\rho_1$ ',(bif_rho[1],bif_u[1]),ha='right',va='center')
ax.annotate('$q$',(rho(u).max(),q),ha='left',va='top')

plt.show()
```

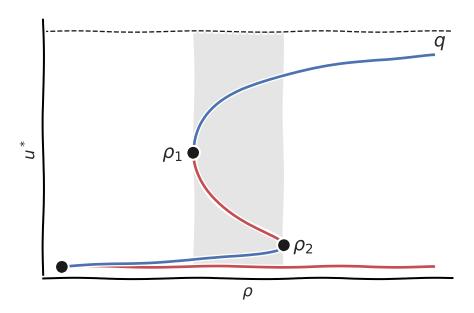


Figure 4.5: Bifurcation diagram with respect to ρ for the spruce budworm system, for q=12. In blue, the stable equilibrium, in red the unstable one. The shaded region is bistable.

The plot above is a bifurcation diagram. We can interpret it as follows: given $\rho = \bar{\rho}$, the equilibria are those corresponding to the intersections between $\rho = \bar{\rho}$ and the curve $\rho = \rho(u)$.

So, for $\rho < \rho_1$ we have one equilibrium, for $\rho_1 < \rho < \rho_3$ we have 3, and for $\rho > \rho_3$ we have one.

For $\rho = \rho_1$ or $\rho = \rho_2$, we have a tangent bifurcation (See **?@sec-tangbif**). As we can see, the curve of equilibria is always smooth, with no branching or crossing on another curve of equilibria, like in the case of transcritical bifurcation. However, there is a change in stability: in fact, the branch between ρ_1 and ρ_2 corresponds to u_2^* , which is unstable.

When varying also q, the tangent bifurcations points ρ_1 and ρ_2 moves as well. In particular, as q is reduced, the two bifurcation points will get closer until they meet for $q=3\sqrt{3}$. This point is another bifurcation, called *cusp bifurcation*. Beyond this point, the system is never bistable.

```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
sns.set_theme("notebook", style="whitegrid")
rho = lambda u,q: q*u/((1+u**2)*(q-u))
Q = []
R = []
for q in np.arange(1,15,0.01):
    p = np.polynomial.Polynomial([q,0,-q,2])
    bif_u = np.array([r for r in p.roots() if np.isreal(r) and r >= 0])
    if not len(bif_u): continue
    Q.append(q)
    R.append([rho(u,q) for u in bif_u])
R = np.array(R)
Q = np.array(Q)
q_{cusp} = 3*np.sqrt(3)
u_cusp = np.sqrt(3)
r_cusp = rho(u_cusp,q_cusp)
fig, ax = plt.subplots()
ax.plot(Q,R.min(axis=1),'r-')
ax.plot(Q,R.max(axis=1),'r-')
ax.plot(q_cusp, r_cusp, 'k.',markersize=16)
ax.fill_between(Q,R.min(axis=1),R.max(axis=1),color='r',alpha=0.2)
ax.set_xlim([2,None])
ax.set_ylim([0.2,0.8])
ax.set_ylabel('$\\rho$')
```

```
ax.set_xlabel('$q$')

ax.annotate(' Cusp point',(q_cusp,r_cusp),ha='left')
ax.annotate('Bistable region',(12,0.45),ha='center')
ax.annotate('Refuge region',(10,0.25),ha='center')
ax.annotate('Outbreak region',(12,0.65),ha='center')
plt.show()
```

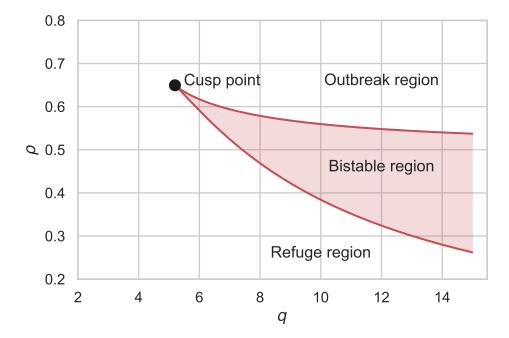


Figure 4.6: Bifurcation diagram with respect to (q, ρ) for the spruce budworm system. The shaded region is bistable. The cusp point is a bifurcation point of co-dimension 2. It occurs for $q = 3\sqrt{3}$.

If we plot the surface of equilibria in the space (q, ρ, u^*) , as the solution of the equation $h(u, \rho, q) = 0$, we obtain the plot below. This plot clearly shows the bistable region and the threshold value (in red).

```
import numpy as np
import pyvista as pv
pv.set_jupyter_backend('static')
n = 50
```

```
bnd = np.array([[0.1,0.1,0],[20,1.0,20]])
grid = pv.ImageData(dimensions=(n,n,n),
                    spacing=(bnd[1,:]-bnd[0,:])/n,
                    origin=bnd[0,:])
Q,R,U = grid.points[:,0],grid.points[:,1],grid.points[:,2]
vals = R*(1-U/Q)-U/(1+U**2)
sols = U.copy()
grid.point_data['sols'] = sols
out = grid.contour(1,scalars=vals,rng=[0,0])
out.compute_normals(inplace=True,auto_orient_normals=True)
out.point_data['normals_u'] = out.point_data['Normals'][:,2] > 0
plotter = pv.Plotter()
plotter.add_mesh(out,scalars='normals_u',cmap=['red','blue'],
                 smooth_shading=True)
plotter.set_scale(xscale=1, yscale=20, zscale=0.5)
plotter.remove_scalar_bar()
plotter.add_axes(xlabel='q',ylabel='rho',zlabel='u')
plotter.camera_position = [
    (41, -11, 24),
    (11, 11, 1.7),
    (-0.33, 0.4, 0.84),
plotter.show()
```

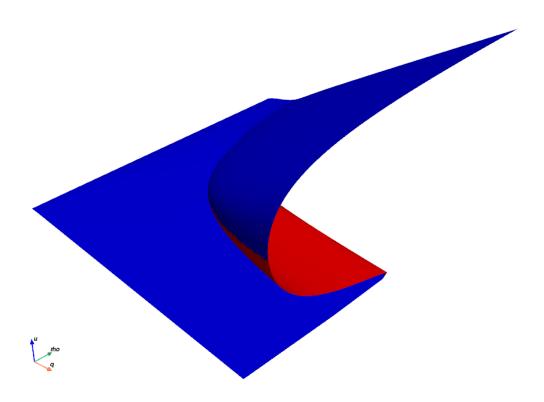


Figure 4.7: Bifurcation diagram with respect to (q, ρ) in 3D.

4.3.3 Hysteresis

Now that we have the bifurcation diagram, we can use it to find the periodic outbreaks. Remember that ρ and q are functions of S and E, but they vary very slowly compared to N(t). On the other hand, when N is at equilibrium, it does not vary anymore, so even slow and small variations of E and S could matter.

Suppose to start with small ρ , say $\rho < \rho_1$. The spruce budworms is at refuge state u_1^* . Now we slowly increase ρ . The equilibrium $u_1^*(\rho)$ will only slightly increase. Once we react the point $\rho = \rho_2$, the equilibrium u_1^* disappears, so $u \to u_3^*$ (outbreak), the only other stable equilibrium. Note the the outbreak is fast, even for a small change of ρ . For this reason, the tangent bifurcation is a *catastrophic bifurcation*. As we keep increasing ρ , the outbreak equilibrium keeps increasing, but again slowly.

Since ρ is the intrinsic growth rate, we can assume that ρ will now start to decrease, because

there are too many spruce budworm consuming the resources. As we go back, decreasing ρ , we follow a specular path, jumping at $\rho = \rho_1$ from the outbreak to the refuge equilibrium. We go back to the original situation.

```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
sns.set_theme("notebook", style="whitegrid")
q = 12
u = np.linspace(0, 0.9*q, 1000)
rho = lambda u: q*u/((1+u**2)*(q-u))
p = np.polynomial.Polynomial([q, 0, -q, 2])
bif_u = np.array([r for r in p.roots() if np.isreal(r) and r >= 0])
bif_rho = rho(bif_u)
rho1 = bif_rho.min()
rho2 = bif_rho.max()
p1 = np.polynomial.Polynomial([q*rho1,-q-rho1,q*rho1,-rho1])
p2 = np.polynomial.Polynomial([q*rho2,-q-rho2,q*rho2,-rho2])
u0 = p1.roots().min()
u1 = bif_u.min()
u2 = p2.roots().max()
u3 = bif_u.max()
rho_neg = p(u) < 0
with plt.xkcd(scale=0.5):
    fig, ax = plt.subplots()
    sns.despine()
    ax.xaxis.set_ticks([])
    ax.yaxis.set_ticks([])
    ax.plot(rho(u), u, 'k', lw=1.0)
    for lb,ub in [[u0,u1],[u2,u3]]:
        uu = np.linspace(lb,ub,100)
        ax.plot(rho(uu),uu, 'r')
    for lb,ub in [[u1,u2],[u3,u0]]:
        ax.plot([rho(lb),rho(ub)],[lb,ub], 'r')
    ax.plot([rho(.7*u0+.3*u1)], [.7*u0+.3*u1], 'r>')
```

```
ax.plot([rho(0.5*(u2+u3))],[0.5*(u2+u3)],'r>')
ax.plot([rho2],[0.5*(u1+u2)],'r^')
ax.plot([rho1],[0.5*(u3+u0)],'rv')
ax.grid(False)
ax.set_xlabel('$\\rho$')
ax.set_ylabel('$\\rho$')
ax.annotate(' $\\rho_2$',(bif_rho[0],bif_u[0]),ha='left',va='center')
ax.annotate('$\\rho_1$ ',(bif_rho[1],bif_u[1]),ha='right',va='center')
ax.annotate('$q$',(rho(u).max(),q),ha='left',va='top')
```

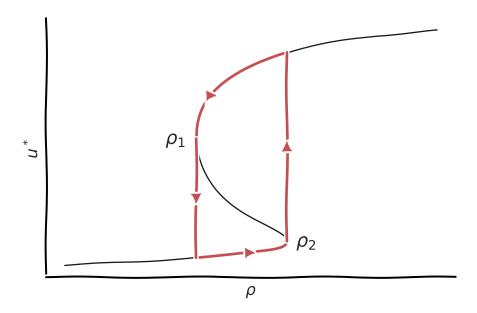


Figure 4.8: Bifurcation diagram with respect to ρ for the spruce budworm system. In blue, the stable equilibrium, in red the unstable one. The shaded region is bistable.

The result is a *hysteresis loop*, which could explain the periodic outbreaks.

We will analyze this model more in depth during the Lab session.

References

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Part II Assignments

Solving ODEs

The logistic model

Consider the following model for a population:

$$N' = \beta(N)N - \mu(N)N,$$

where $\beta(N)$ is the *fertility rate* and $\mu(N)$ is the *mortality rate*. We assume here both are function of the population size N as follows:

$$\beta(N) = \beta_0 - \tilde{\beta}N,$$

$$\mu(N) = \mu_0 + \tilde{\mu}N.$$

1. Show that the model can be written as

$$N' = r\left(1 - \frac{N}{K}\right)N. \tag{1}$$

- 2. Prove that the ODE, supplemented with an initial condition $N(0) = N_0$, has a unique local solution. Hint: verify the hypotheses of the Cauchy-Lipschitz theorem.
- 3. Consider u(t) = 1/N(t). Show that u(t) satisfies a linear ODE. Solve it, then use the solution to solve the original ODE in N(t) with the initial condition $N(0) = N_0 > 0$.
- 4. Make the change of variables as follows: $\tau = rt$ and y = N/K. Find the corresponding equation in $y(\tau)$.

Blow-up of solutions

It may be considered reasonable that, for a sexual species, births are proportional to the number of encounters, hence, disregarding the mortality process, we have the equation

$$N'(t) = \beta N^2(t).$$

1. This equation can be solved by the method of separation of variables. Show that the solutions of this equation with N(0) > 0 tend to infinity in a finite time. (Blow-up of solution.)

2. Let us correct the equation, introducing deaths:

$$N'(t) = \beta N^2(t) - \mu N(t).$$

Discuss how the dynamics changes. In particular, does the equation still have the problem of solutions going to infinity in a finite time? *Hint: do not solve analytically the equation*.

3. Solve the above equation analytically and confirm the qualitative analysis of the previous point.

mRNA

Zeisel et al. considered the following system for the concentration of mRNA. The variables are M(t), the concentration of mature mRNA, and P(t), the concentration of precursor mRNA:

$$\begin{cases} P'(t) = b(t) - \alpha_1 P(t), \\ M'(t) = \alpha_1 P(t) - \alpha_2(t) M(t). \end{cases}$$

where b(t) is the (gene-specific and time-dependent) production rate, α_1 is the conversion (splicing) rate of pre-mRNA to mRNA, $\alpha_2(t)$ the (time-dependent) degradation rate of mRNA.

- 1. Assume $b(t) \equiv b$ and $\alpha_2(t) \equiv \alpha_2$ are constant. Find the explicit solution given $P(0) = P_0$ and $M(0) = M_0$. Hint: use the method of variation of constants.
- 2. Assume now that $\alpha_2(t) \equiv \alpha_2$ and

$$b(t) = \begin{cases} \bar{b} & t < \bar{t}, \\ 0, & t > \bar{t}. \end{cases}$$

Show that M(t) tends to 0 as $t \to \infty$. At which rate does it decay?

Thorium-Uranium dating

The thorium-uranium method for dating rocks is based on the fact that Uranium-234 decays into Thorium-230 which in turn decays into other elements. Set t = 0 the rock formation time and denoting U(t) (resp. T(t)) the amount of Uranium-234 (resp. Thorium-230) in the rock at time t (measured in years), the following differential equation system is written:

$$\begin{cases} U'(t) = -aU(t), \\ T'(t) = aU(t) - bT(t), \\ U(0) = U_0, \\ T(0) = 0, \end{cases}$$

where $a\approx 5.9\cdot 10^{-6}\,\mathrm{years^{-1}}$, $b\approx 1.9\cdot 10^{-5}\,\mathrm{years^{-1}}$, U_0 represents the initial (generally unknown) amount of Uranium-234. Note that, based on geological principles, it is believed that there was no thorium at the time of rock formation.

- 1. Solve the equation for U(t).
- 2. How can the quantities of a and b be interpreted? From the data provided can we infer the half-life of Uranium-234 and Thorium-230?
- 3. Calculate T(t), solution of the second differential equation.
- 4. Compute

$$\lim_{t\to\infty}\frac{T(t)}{U(t)}.$$

5. Explain why it is possible to estimate the rock age from the knowledge of T/U at current time, but it is not possible from the knowledge of T alone. Hint: study the function T(t)/U(t).

Population dynamics

Periodic solutions

Consider the time dependent Malthus model

$$\begin{cases} N(t) = r(t)N(t), \\ N(0) = N_0. \end{cases} \tag{4.1} \label{eq:4.1}$$

with periodic Malthus parameter: r(t+T)=r(t) and denote by \bar{r} the average over one period:

$$\bar{r} = \frac{1}{T} \int_0^T r(s) \, \mathrm{d}s. \tag{4.2}$$

1. After showing that the function

$$\pi(t) = \int_0^t r(s) \, \mathrm{d}s - \bar{r}t$$

is periodic with period T, prove that

$$\bar{r} = \lim_{t \to \infty} \frac{1}{t} \int_0^t r(s) \, \mathrm{d}s.$$

2. Show that the solution of the ODE is

$$N(t) = e^{\bar{r}t} N_{\pi}(t),$$

where $N_{\pi}(t)$ is a periodic function.

3. Modify the ODE by adding a time-dependent migration

$$N'(t) = r(t)N(t) + m(t), (4.3)$$

assuming both r(t) and m(t) continuous and periodic with period T. Using Equation 4.2, show that, if $\bar{r} < 0$, then the function

$$N_{\infty}(t) = \int_{-\infty}^{t} e^{\int_{s}^{t} r(\sigma) \, \mathrm{d}\sigma} m(s) \, \mathrm{d}s$$

is well-defined, is a solution to the ODE, and is periodic with period T.

4. Show that if $\bar{r} < 0$, then the solution to Equation 4.3 with initial condition $N(0) = N_0$ is

$$N(t) = e^{\int_0^t r(\sigma)\mathrm{d}\sigma} N_0 + \int_0^t e^{\int_s^t r(\sigma)\mathrm{d}\sigma} m(s)\,\mathrm{d}s$$

and is such that $\lim_{t\to\infty}(N(t)-N_\infty(t))=0.$

Logistic model

Consider the logistic equation

$$N'(t) = r \Big(1 - \frac{N}{K}\Big) N.$$

- 1. Find the equilibria of the ODE and study their stability.
- 2. Study the global stability of the equilibria.
- 3. Would it make sense to assume r < 0 and K > 0?

Global well-posedness

Consider the following ODE model:

$$N'(t) = (\beta N^2 - \mu N)(1 - \gamma N).$$

Find all non-negative equilibria and discuss their stability. From the direction field conclude that all solutions are bounded, and hence solutions are globally defined (no blow-up in finite time).