Continuous Dynamical Systems

Computational Models for Complex Systems

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Introduction

We will see how to define ordinary differential equations (ODEs) in order to model the dynamics of systems whose state changes continuously.

- focus on population models (birth/death of individuals)

See also:

- Notes on a Short Course and Introduction to Dynamical Systems in Biomathematics by Urszula Foryś
  Available on the course web page
- Chapter 2 of A Guide to Numerical Modelling in Systems Biology by Peter Deuflhard and Susanna Roblitz
  Freely accessible if you are within the UniPi subnet
  Link available on the course web page
- Mathematical and Computer Modelling of Nonlinear Biosystems by Urszula Foryś
  Available on the course web page

Linear birth model, again

Let $N(t)$ denote the density of some population at time t.

We want to construct a mathematical model able to predict the density of the same population at time $t + \Delta t$, that is $N(t + \Delta t)$.

Assume that:

- all individuals are the same (no dinstinction by gender, age, ...)
- there is enough food and space for every individual
- each individual has λ children every σ time units
- there is no death in the interval $[t, t + \Delta t)$
- children do not start reproducing in the interval $[t, t + \Delta t)$

Linear birth model, again

We have seen that the model can be based on the following equation:

$$N(t + \Delta t) = N(t) + \lambda \frac{\Delta t}{\sigma} N(t)$$

from which we derived the discretized model corresponding to the following recurrence equation (with step Δt):

$$N_{t+1} = r_d N_t$$

where $r_d = \lambda \frac{\Delta t}{\sigma}$.

We have seen that discretization can lead to inaccuracies

- Let's consider $\Delta t \to 0$

Linear birth model, continuous version

The equation

$$N(t+\Delta t) = N(t) + \lambda \frac{\Delta t}{\sigma} N(t)$$

can be rewritten as

$$\frac{N(t+\Delta t) - N(t)}{\Delta t} = \frac{\lambda}{\sigma} N(t)$$

so that the left hand side turns out to be a difference quotient.

Now, let's consider the limit for $\Delta t \to 0$

$$\lim_{\Delta t \to 0} \frac{N(t+\Delta t) - N(t)}{\Delta t} = \lim_{\Delta t \to 0} r_c N(t)$$

with $r_c = \frac{\lambda}{\sigma}$.

Linear birth model, continuous version

$$\lim_{\Delta t \to 0} \frac{N(t+\Delta t) - N(t)}{\Delta t} = \lim_{\Delta t \to 0} r_c N(t)$$

The term on the left turns out to be the derivative of $N(t)$

- denoted $\dot{N}(t)$, or $\frac{dN}{dt}$

The term on the right does not depend on Δt. So, we obtain:

$$\dot{N}(t) = r_c N(t)$$

This is a so called Ordinary Differential Equation (ODE)

- relates the function N with its derivative $\dot{N}$
- time is continuous: t can take any value in $\mathbb{R}$

Linear birth model, continuous version

$$\dot{N}(t) = r_c N(t)$$

Finding a solution of the differential equation corresponds to finding a closed-form definition of $N(t)$ satisfying the equation

- a definition that depends only on t and some constants

For the linear growth model a solution can be found analytically.

Let's rewrite the equation as follows: $\frac{\dot{N}(t)}{N(t)} = r_c$

Since $\frac{\dot{N}(t)}{N(t)}$ is the derivative (w.r.t. t) of $\ln N(t)$ and r_c is the derivative of $r_c t + c$ for any constant c, we obtain

$$\ln N(t) = r_c t + c$$

that gives:

$$N(t) = Ce^{r_c t}$$

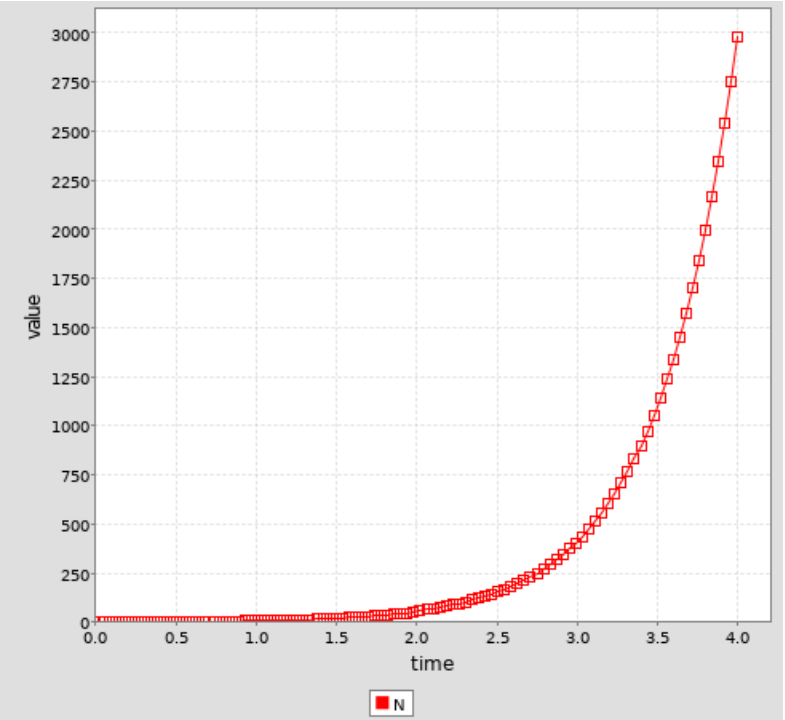
with e the Euler number and $C = e^c$ (typically $C = N(0)$).

Linear birth model, continuous version

$$N(t) = Ce^{r_c t}$$

The solution of the ODE tells us that the population shows an exponential growth over time

- $r_c = 2$
- $C = N(0) = 1$



Linear birth model, continuous version

This behaviour is qualitatively the same as that of the discretized model

- the population exhibits an exponential growth

What changes is the role of the growth rate:

discrete model:

$N_{t+1} = r_d N_t$

general term:

$N_t = {r_d}^t N_0$

continuous model:

$\dot{N}(t) = r_c N(t)$

solution:

$N(t) = Ce^{r_c t}$

The population grows if $r_d > 1$

$r_d = 1 + \lambda \frac{\Delta t}{\sigma}$

hence: $\frac{\lambda}{\sigma} > 0$

The population grows if $r_c > 0$

$r_c = \frac{\lambda}{\sigma}$

hence: $\frac{\lambda}{\sigma} > 0$

"Radioactive" decay

This example describes spontaneous decomposition (or decay, degradation) of substances

- it is called "radioactive" since this is has been considered initially for substances for which radioactivity can be measured

The idea is each molecule decays at a constant rate. So, the whole mass decreases with a rate which is proportional to the mass itself.

This is described by the following ODE:

$$\dot{N}(t) = -d_c N(t)$$

whose solution is

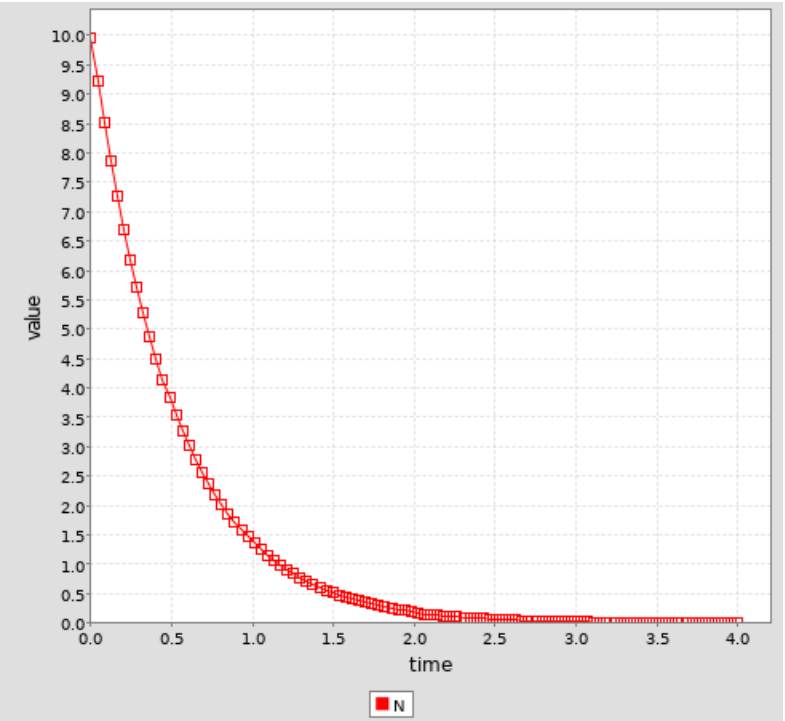
$$N(t) = N(0)e^{-d_c t}$$

"Radioactive" decay

$$\dot{N}(t) = -d_c N(t)$$

The negative exponent causes $N(t)$ to tend to zero

- $d_c = 2$
- $C = N(0) = 10$



Logistic equation, continuous version

A continuous version of the logistic equation can be defined as follows:

$$\dot{N}(t) = r_c N(t) \left(1 - \frac{N(t)}{K}\right)$$

where r_c is the continuous growth rate and K is the carrying capacity of the environment

A solution of this ODE is

$$N(t) = \frac{K}{1 + \left(\frac{K}{N(0)} - 1\right) e^{-r_c t}}$$

The solution tells us that $N(t)$ tends to K, since $e^{-r_c t}$ tends to 0

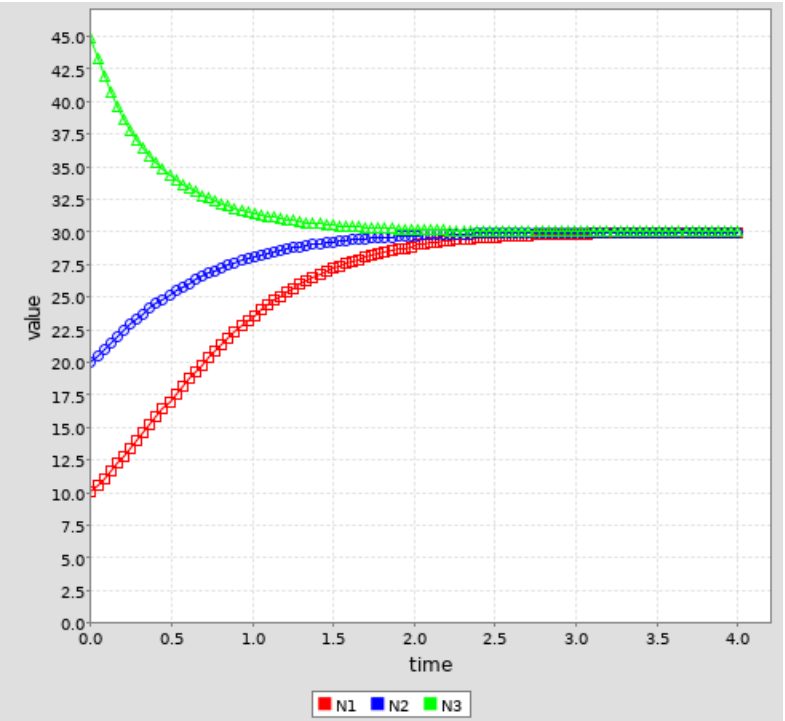
- the population converges to the carrying capacity of the environment

Logistic equation, continuous version

$$\dot{N}(t) = r_c N(t) \left(1 - \frac{N(t)}{K}\right)$$

The population converges to the carrying capacity of the environment

- $r_c = 2$
- $N(0) = 10$
- $K = 30$



Systems of ODEs

We considered examples of systems described by a single variable $N(t)$

When more than one variable has to be cosidered, we have to construct a system of ODEs

Let's consider a population of males and females, with fights among males

- $F(t)$ models females and $M(t)$ models males
- assume a small part of males die because of fights among them (death rate s_c)

We obtain the following system of ODEs

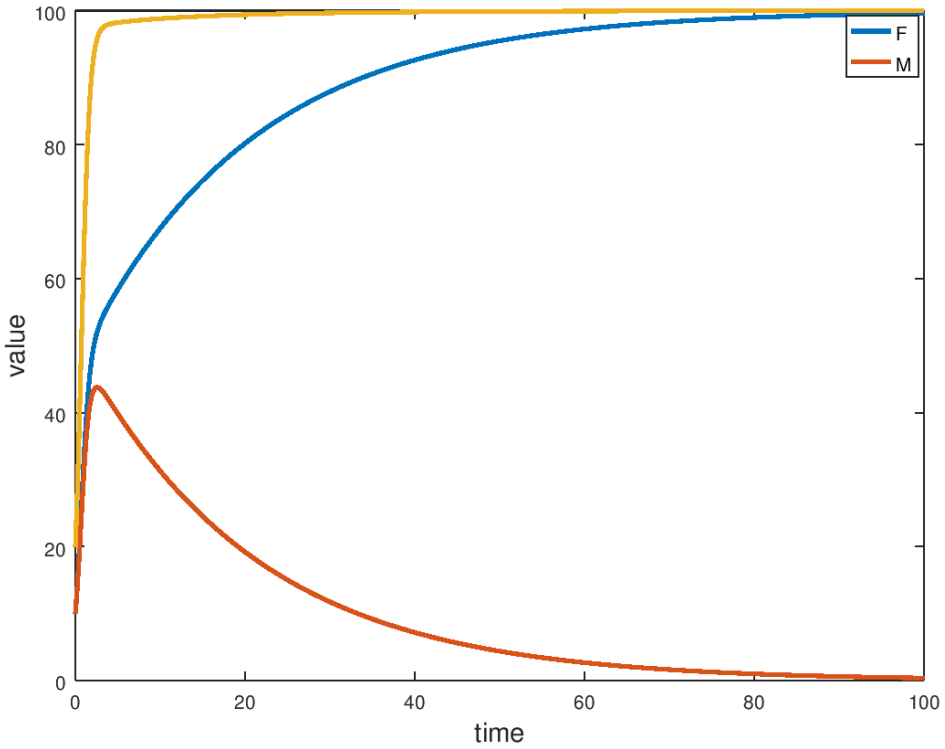
$$\begin{cases} \dot{F}(t) = r_c F(t) \left(1 - \frac{F(t)+M(t)}{K}\right) \\ \dot{M}(t) = r_c F(t) \left(1 - \frac{F(t)+M(t)}{K}\right) - s_c M(t) \end{cases}$$

where

- $r_d F(t)$ is used for both genders since both are generated by females
- $F(t) + M(t)$ describes the whole population size (to be related with the carrying capacity K)

Systems of ODEs

Dynamics of the systems of ODEs

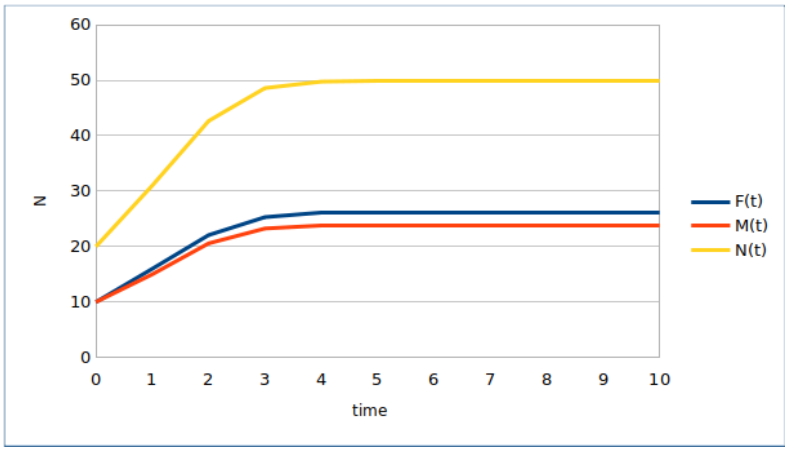


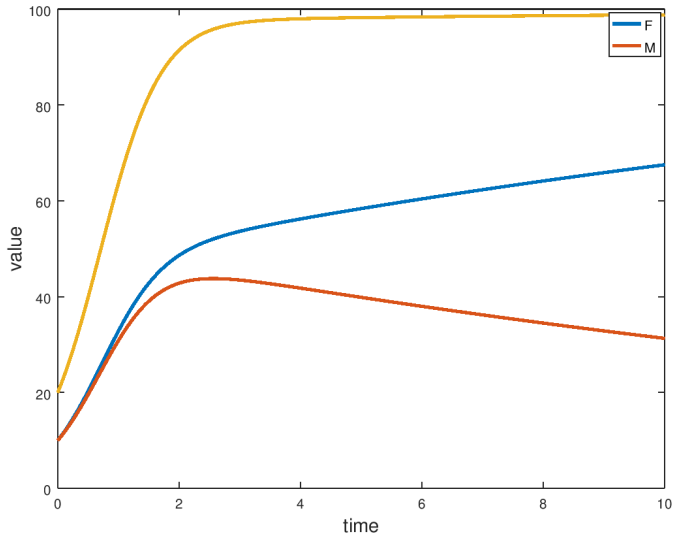
Recurrence Equations vs ODEs

Why the dynamics is so different from that of the recurrence relations we have seen in the previous lesson?

$$\begin{cases} F_{t+1} = r_d F_t \left(1 - \frac{F_t + M_t}{K}\right) \\ M_{t+1} = r_d F_t \left(1 - \frac{F_t + M_t}{K}\right) - s_d M_t \end{cases}$$

$$\begin{cases} \dot{F}(t) = r_c F(t) \left(1 - \frac{F(t) + M(t)}{K}\right) \\ \dot{M}(t) = r_c F(t) \left(1 - \frac{F(t) + M(t)}{K}\right) - s_c M(t) \end{cases}$$





Recurrence Equations vs ODEs

- Recurrence relations describe how to compute the next state
- ODEs describe derivatives: (the limit of) the difference between the current and the next state

Steady states are computed differently:

$$\begin{cases} F_t = r_d F_t \left(1 - \frac{F_t + M_t}{K}\right) \\ M_t = r_d F_t \left(1 - \frac{F_t + M_t}{K}\right) - s_d M_t \end{cases}$$

$$\Downarrow$$

$$M_t = F_t - s_d M_t$$

$$\Downarrow$$

$$F_t = (1 + s_d) M_t$$

$$\begin{cases} 0 = r_c F(t) \left(1 - \frac{F(t) + M(t)}{K}\right) \\ 0 = r_c F(t) \left(1 - \frac{F(t) + M(t)}{K}\right) - s_c M(t) \end{cases}$$

$$\Downarrow$$

$$0 = 0 - s_c M(t)$$

$$\Downarrow$$

$$M(t) = 0$$

Numerical solution of ODEs

Unfortunately, computing the solution of an ODE is not always possibile/simple

Very often, ODEs are studies by using numerical solvers (or numerical simulators)

- Numerical solvers do not compute the general function obtained by "integrating" the ODE
- They usually solve the initial value problem (or Cauchy problem)

Definition: Initial value problem

Given an ODE $\dot{N}(t) = f(N(t))$ and an initial value N_0 such that $N(0) = N_0$, compute a function $F(t)$ that is a solution of the ODE and such that $F(0) = N_0$

Actually, what we are usually interested in, are the values of $F(t)$ for $t \geq 0$

- hence, we want to perform a numerical simulation starting from $t = 0$

The Euler method

The Euler method is the simplest numerical simulation method

It is based on the idea of discretizing the dynamics of differential equations by time steps of constant length τ.

At each step, the solution of the differential equation is approximated by its derivative computed at the beginning of the time interval of length τ

Given an ODE

$$\dot{N}(t) = f(N(t))$$

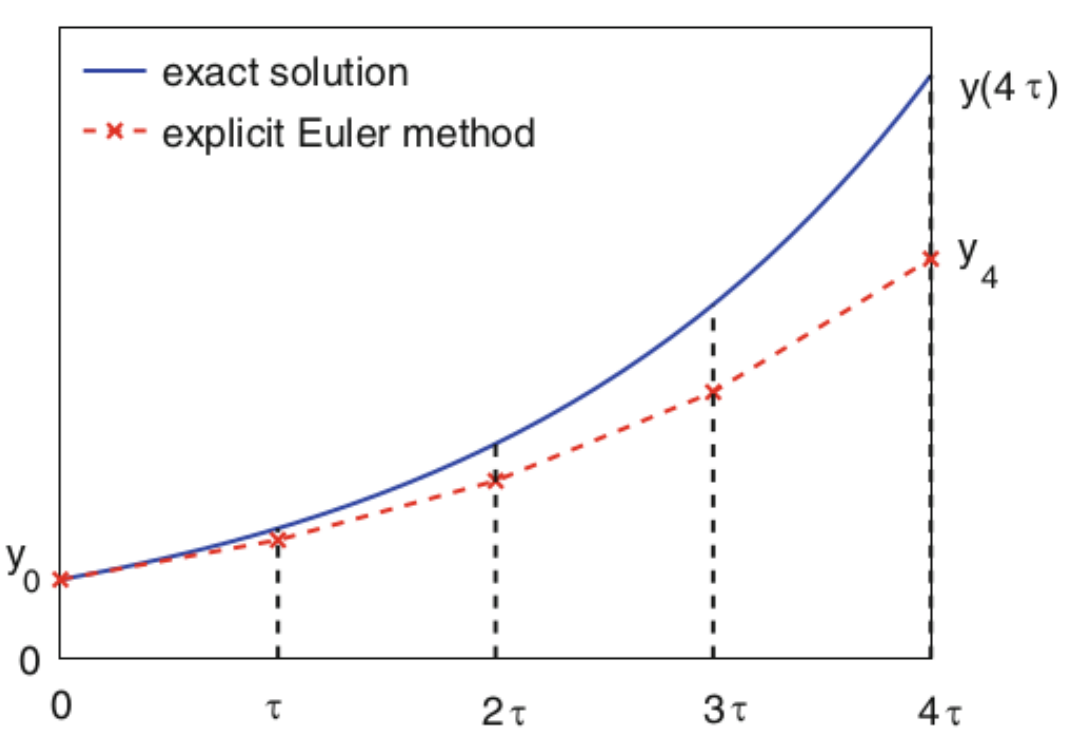
this corresponds to approximating its solution with the following recurrence relation (with $N_0 = N(0)$)

$$N_{k+1} = N_k + \tau f(N_k)$$

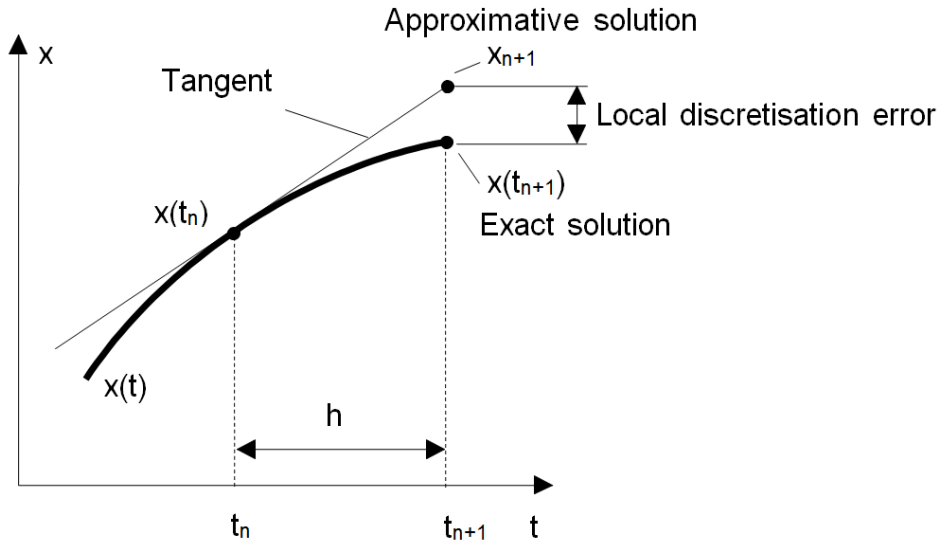
where N_k approximates $N(k\tau)$

The Euler method

Example of execution of the Euler method:



The Euler method: errors



Each step of the Euler method give rise to an error

- Local discretization error (or local truncation error) $|N(\tau) - N_1|$
- it is in the order $O(\tau^2)$

Errors accumulate: after k steps, namely at time $t = k\tau$, we have

- Global discretization error (or global truncation error) $|N(k\tau) - N_k|$
- it is in the order $O(k\tau^2) = O(\tau)$, since $k\tau = t$ is constant

Other "explicit" methods

A linear ($O(\tau)$) global discretization error often imply that a very small discretization step τ has to be used

- the computation becomes very slow (many steps)

Other methods have a global discretization error of a higher order (e.g. $O(\tau^p)$ for some p) which is better as long as $\tau \to 0$ (hence, it is smaller than one)

A few examples of such methods:

- Runge-Kutta methods: $p = 2$ in their original formulation, but can be higher
- Multistep methods (e.g. Adams methods): extrapolate the value of the next step from the values of the previous k steps. $p \approx k$

Other "explicit" methods

State-of-art methods can also:

- self-determine the step size τ based on thresholds on local and global discretization errors
- dynamically adjust the step size τ during their execution (e.g. Adaptive Runge-Kutta)

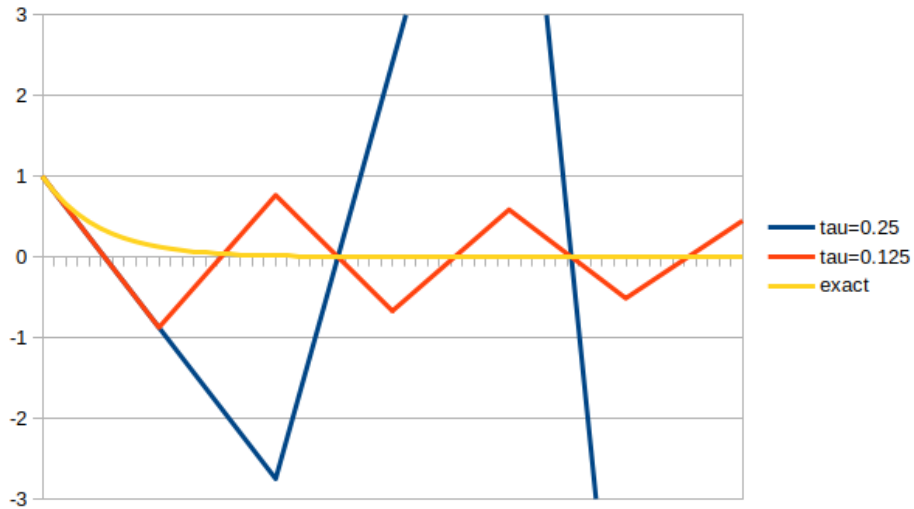
Instability and stiff systems

In some cases, explicit methods may become unstable, unless a very small step size τ is used.

Example:

$$\dot{N}(t) = -15N(t)$$

with $N(0) = 1$



Euler method with $\tau = 0.25$ and $\tau = 0.125$ compared with the exact solution

Instability and stiff systems

This kind of problematic systems are called stiff systems

There is no precise definition of stiffness

- Intuitively, the system contains some very fast term which causes very small step sizes to be used with explicit methods
- Sometimes, the combination of fast terms with slow terms in a system of ODEs make explicit methods unstable although the shape of the solution is smooth

Implicit Euler method

Implicit methods are often better suited for stiff systems.

Implicit variant of the Euler method:

At each step, the solution of the differential equation is approximated by its derivative computed at the end of the time interval of length τ

Given an ODE

$$\dot{N}(t) = f(N(t))$$

this corresponds to approximating its solution with the following equation (with $N_0 = N(0)$)

$$N_{k+1} = N_k + \tau f(N_{k+1})$$

where N_k approximates $N(k\tau)$

Implicit Euler method

$$N_{k+1} = N_k + \tau f(N_{k+1})$$

In this case the value of N_{k+1} is not explicitly expressed in terms of N_k, but it is implicitly espressed by means of an equation which could be difficult to solve

Hence, the computation of the single step requires more effort in implicit methods

But, often the local discretization error is smaller

- greater values of τ can be used
- with stiff systems it is often convenient to pay the extra time for the computation of each step

Other "implicit" methods

A few examples of implicit methods:

- Implicit Runge-Kutta methods
- Multistep methods (e.g. BDF methods)

Implementations of implicit methods often require the modeler to provide the Jacobian matrix (partial derivatives) of the funciton f

Also in these cases there are variants that can self-determine and dynamically adjust the step size τ according to threshold on the local and global discretizaton errors.

There exist methods that are able to automatically switch from explicit to implicit modes (and vice-versa)

- LSODE: switches between Adams and BDF
- CVODE: switches between Adams and BDF

Implementations

ODE solvers are available inside the main environments for numerical and mathematical computing (e.g. MatLab, Octave, Mathematica) and as libraries for the main programming languages (e.g. C, C++, Python)

Some implementations:

- `ode45`, `ode113`, `ode15s`, ... in MatLab
  see `https://www.mathworks.com/help/matlab/ordinary-differential-equations.html`
- `lsode` in Octave
- Sundials CVODE in C
- `odeint` in C++
- `scipy.integrate.odeint` and `scipy.integrate.ode` (interface to multiple solvers) in Python

Using the Octave solver

Let's see, for example, the Octave implementation of this system of ODEs

$$\begin{cases} \dot{A}(t) = 320s(A(t) - A(t)B(t) + B(t) - qA(t)^2) \\ \dot{B}(t) = 320(C(t) - B(t) - A(t)B(t))/s \\ \dot{C}(t) = 320w(A(t) - C(t)) \end{cases}$$

with $s = 77.27$, $q = 8.375 \cdot 10^{-6}$, $w = 0.161$.

This is (a variant of) a well-known example of stiff system (the Oregonator)

Using the Octave solver

```
% workaround for scripts starting with a function definition
1;

%%% Function computing derivatives
function dX = dX(X,t)

  % model parameters
  s = 77.27;
  q = 0.000008375;
  w = 0.161;

  % variables used for the sake of readability
  A = X(1);
  B = X(2);
  C = X(3);

  % ODEs
  dA = 320 * s * (A - A*B + B - q*A*A);
  dB = 320 * (C-B-A*B)/s;
  dC = 320 * w * (A-C);

  dX(1) = dA;
  dX(2) = dB;
  dX(3) = dC;

endfunction

%(continues ...)
```

Using the Octave solver

```
%%% setting the simulation time and the number of points
t=linspace(0,2,1000);

%%% (or the time distance between two consecutive points)
%t=0:0.001:2;

%%% initial state
X0 = [1 1 2];

%%% These can be used to set global and local error tolerance
%lsode_options("absolute tolerance",1e-5);
%lsode_options("relative tolerance",1e-5);

%%% These can be used to force non-stiff or stiff integration
%lsode_options("integration method","non-stiff");
%lsode_options("integration method","stiff");

%%% Call the solver
X = lsode ("dX",X0,t);

%(continues ...)
```

Using the Octave solver

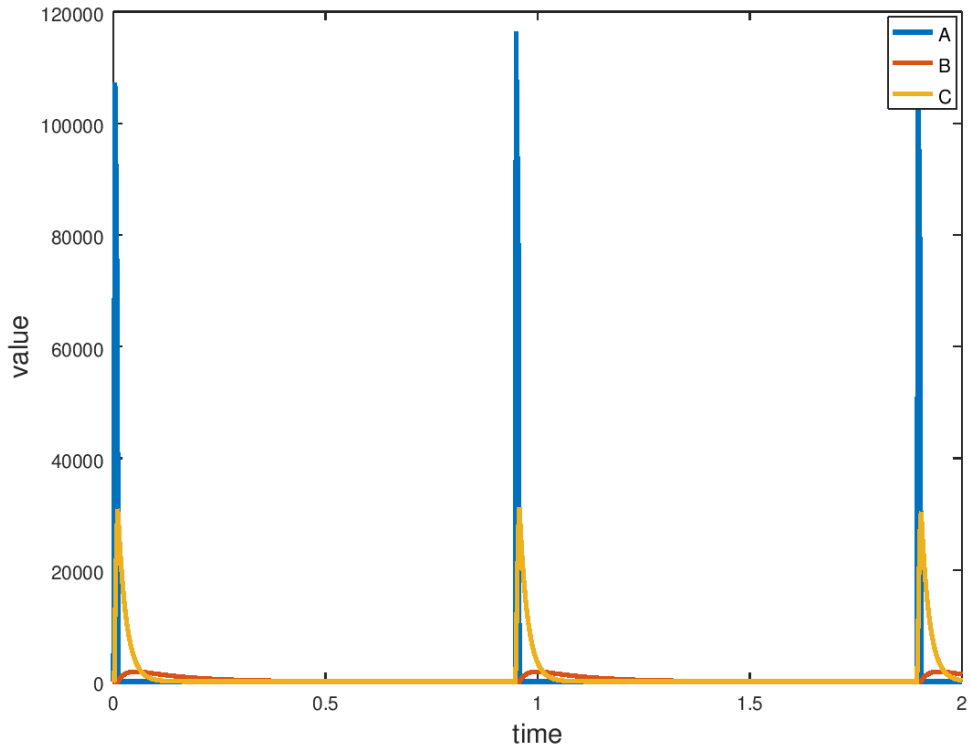
```
%%% Plot results
plot(t,X,"linewidth", 2);
xlabel ("time", "fontsize", 14);
ylabel ("value", "fontsize", 14);
legend("A","B","C");

%%% This would print the plot to a file
%print('graph.png','-dpng');

%%% Wait for the user to look at the graph
pause();
```

Using the Octave solver

Result:



Using the Octave solver

Comments:

- The system is stiff (because of the "fast" peaks)
  - try to force the solver to work in non-stiff mode
- In the case of stiff systems, the solver uses the Jacobian matrix (partial derivatives) to approximate the system behaviour at each step
- An approximate Jacobian matrix is computed automatically...
- ... but a function computing it precisely can be provided to the solver
  - this increases both accuracy and performance

Let's modify the previous implementation by passing the Jacobian matrix to the solver

Using the Octave solver

```
%%% Model parameters (global variables to be used in both the derivati
%%% and the jacobian functions)
global s = 77.27;
global q = 0.000008375;
global w = 0.161;

%%% Function computing derivatives
function dX = dX(X,t)

  global s q w; % use the global variables

  % variables used for the sake of readability
  A = X(1);
  B = X(2);
  C = X(3);

  % ODEs
  dA = 320 * s * (A - A*B + B - q*A*A);
  dB = 320 * (C-B-A*B)/s;
  dC = 320 * w * (A-C);

  dX(1) = dA;
  dX(2) = dB;
  dX(3) = dC;

endfunction

%(continues ...)
```

Using the Octave solver

```
%%% Function computing the Jacobian matrix
function J = jac(X,t)

  global s q w; % use the global variables

  % variables used for the sake of readability
  A = X(1);
  B = X(2);
  C = X(3);

  % partial derivatives
  dAdA = 320 * s * (1 - B - 2*q*A);
  dBdA = 320 * B / s;
  dCdA = 320 * w;
  dAdB = 320 * s * (-A + 1);
  dBdB = 320 * (-1 -A) / s;
  dCdB = 0;
  dAdC = 0;
  dBdC = 320/s;
  dCdC = 320 * w * (-1);

  J(1,1) = dAdA;   J(2,1) = dBdA;   J(3,1) = dCdA;
  J(1,2) = dAdB;   J(2,2) = dBdB;   J(3,2) = dCdB;
  J(1,3) = dAdC;   J(2,3) = dBdC;   J(3,3) = dCdC;

endfunction

%(continues ...)
```

Using the Octave solver

```
%%% setting the simulation time and the number of points
t=linspace(0,2,1000);

%%% (or the time distance between two consecutive points)
%t=0:0.001:2;

%%% initial state
X0 = [1 1 2];

%%% These can be used to set global and local error tolerance
%lsode_options("absolute tolerance",1e-5);
%lsode_options("relative tolerance",1e-5);

%%% These can be used to force non-stiff or stiff integration
%lsode_options("integration method","non-stiff");
%lsode_options("integration method","stiff");

%%% Pass both the functions to the solver
X = lsode ({@dX, @jac} ,X0,t);

%(continues ...)
```

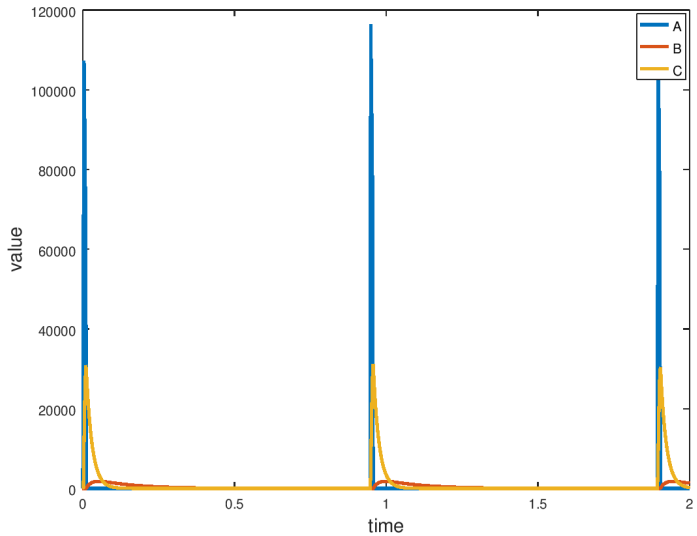
Using the Octave solver

```
%%% Plot results
plot(t,X,"linewidth", 2);
xlabel ("time", "fontsize", 14);
ylabel ("value", "fontsize", 14);
legend("A","B","C");

%%% This would print the plot to a file
%print('graph.png','-dpng');

%%% Wait for the user to look at the graph
pause();
```

Same result as before:



RELEVANT EXAMPLES OF ODE MODELS

Notation

It is no longer necessary to mention t in ODEs...

In the ODEs that follow
we will omit any explicit reference
to the time variable t

We will write:

- X for $X(t)$
- $\dot{X}$ for $\dot{X}(t)$
- X_0 for $X(0)$

The Lotka-Volterra model of prey-predator interaction

Independently proposed by Lotka in 1925 and Volterra in 1926

- By Lotka as a description of an hypothetical biochemical oscillator
- By Volterra as a description of two interacting populations

Volterra introduced this model to explain a strange phenomenon observed in the Adriatic sea after the First World War

- Ecologists (and fisherman) observed an increase in the population of some species of fish
- They expected the war to cause all populations to decrease...

Volterra's intuition was that prey and predator species have different (but related) dynamics.

- preys proliferate in the absence of predators

The Lotka-Volterra model of prey-predator interaction

Let us consider the following variables:

- V describes the size (or density) of the population of preys
- P describes the size (or density) of the population of predators

Basic observations on the inner dynamics of preys and predators (i.e. the dinamics of each population in isolation):

- In the absence of predators, preys can grow without any limitation.
- In the absence of preys, predators die.

From these observations, we obtain this preliminary system of ODEs:

$$\begin{cases} \dot{V} = rV & \text{exponential growth} \\ \dot{P} = -sP & \text{exponential decay} \end{cases}$$

where r is the growth rate of preys and s the death rate of predators.

The Lotka-Volterra model of prey-predator interaction

If both species are present in the enviroment, we observe hunting of predators on preys.

Assuming that meeting between individuals of both species is random, the number of meetings per time unit is proportional to both V and P

- namely it is proportional to the product VP

Not all predator-prey meetings result in a hunting...

- let a be the portion of meetings resulting in a hunting

Now, the more the predators eat, the more they can survive and reproduce

- let b denote the number of offsprings produced for each hunting

The Lotka-Volterra model of prey-predator interaction

We obtain the following system of ODEs (the Lotka-Volterra model):

$$\begin{cases} \dot{V} = rV - aVP \\ \dot{P} = -sP + abVP \end{cases}$$

that is

- preys decrease by a hunting rate aVP
- predators increase by a hunting and reproduction rate $abVP$

Predation is a direct form of interaction

- it is not mediated by the environment

The Lotka-Volterra model: coefficients

Let's play with the model!

We consider the following coefficients:

- Birth of preys: $r = 10$
- Death of predators: $s = 10$
- Hunting of predators on preys: $a = 0.01$
- Reproduction of predators: $b = 1$

We obtain:

$$\begin{cases} \dot{V} = 10V - 0.01VP \\ \dot{P} = -10P + 0.01VP \end{cases}$$

Before using a numerical solver... is there any steady state?

The Lotka-Volterra model: steady states

A steady state is a combination of values for the variables that remains unchanged over time

In a steady state, all differential equations are equal to zero

So, we can find steady states of the Lotka-Volterra model by solving the following system of equations:

$$\begin{cases} 0 = 10V - 0.01VP \\ 0 = -10P + 0.01VP \end{cases}$$

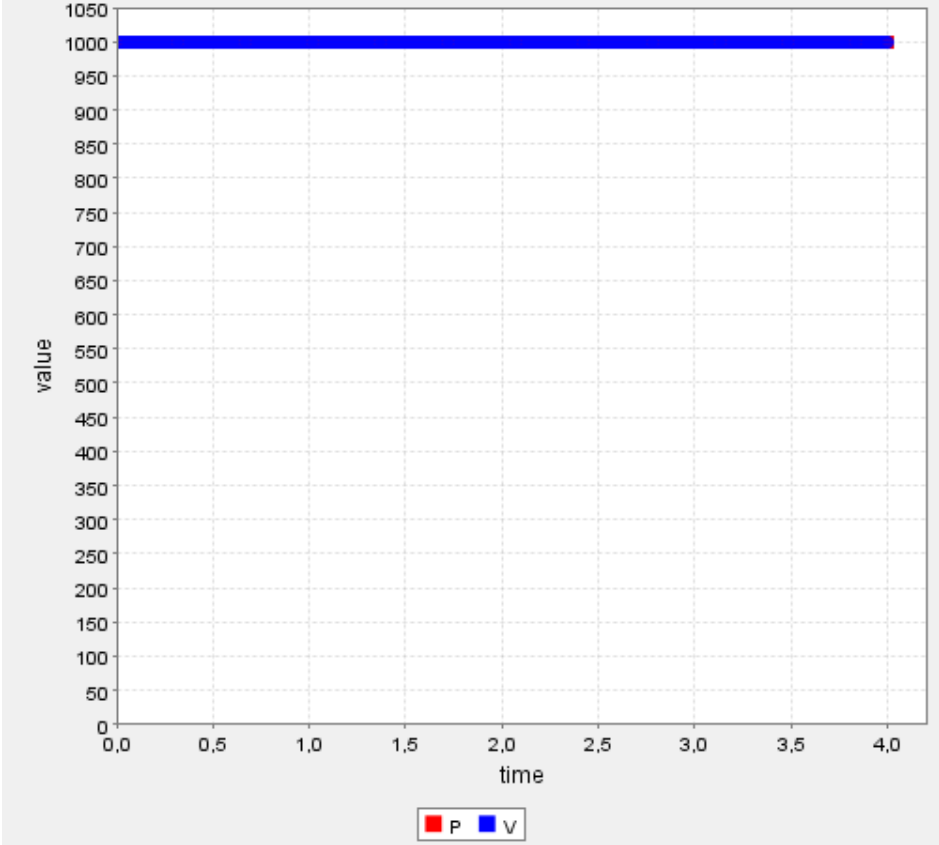
It has two solutions:

- $V = 0$ and $P = 0$ (empty population)
- $V = 1000$ and $P = 1000$

The Lotka-Volterra model: numerical solution

Let's use a numerical solver with the following initial conditions:

- $V_0 = 1000$
- $P_0 = 1000$

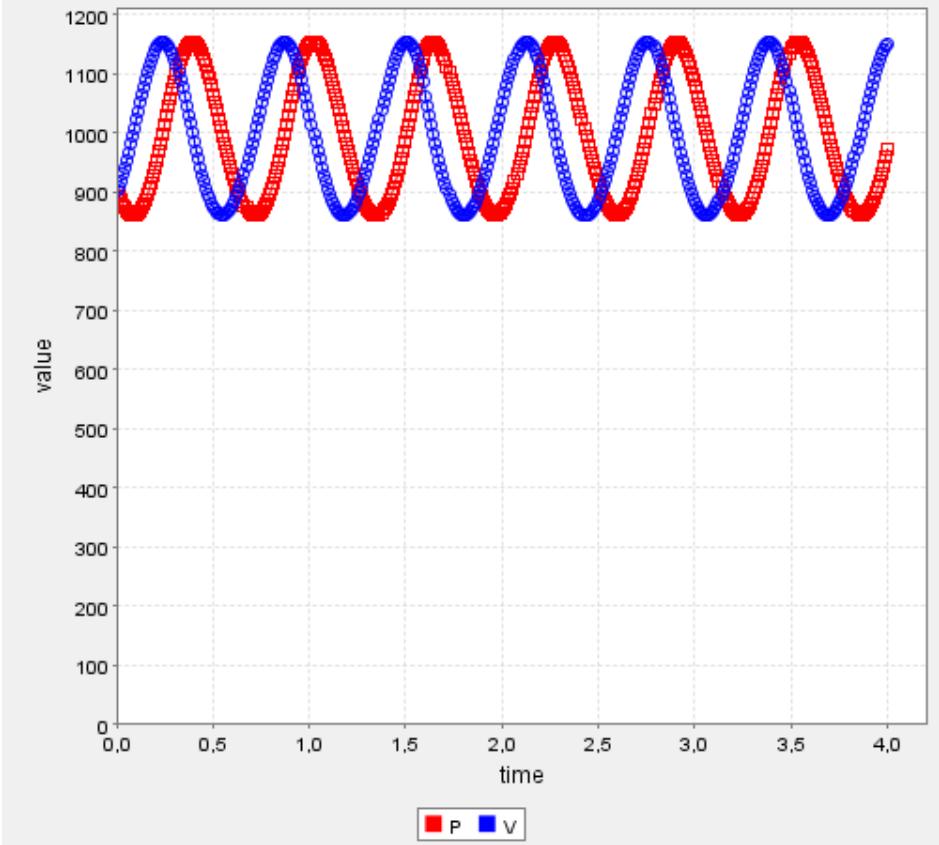


Both populations are actually stable

The Lotka-Volterra model: numerical solution

Let's use a numerical solver with the following initial conditions:

- $V_0 = 900$
- $P_0 = 900$

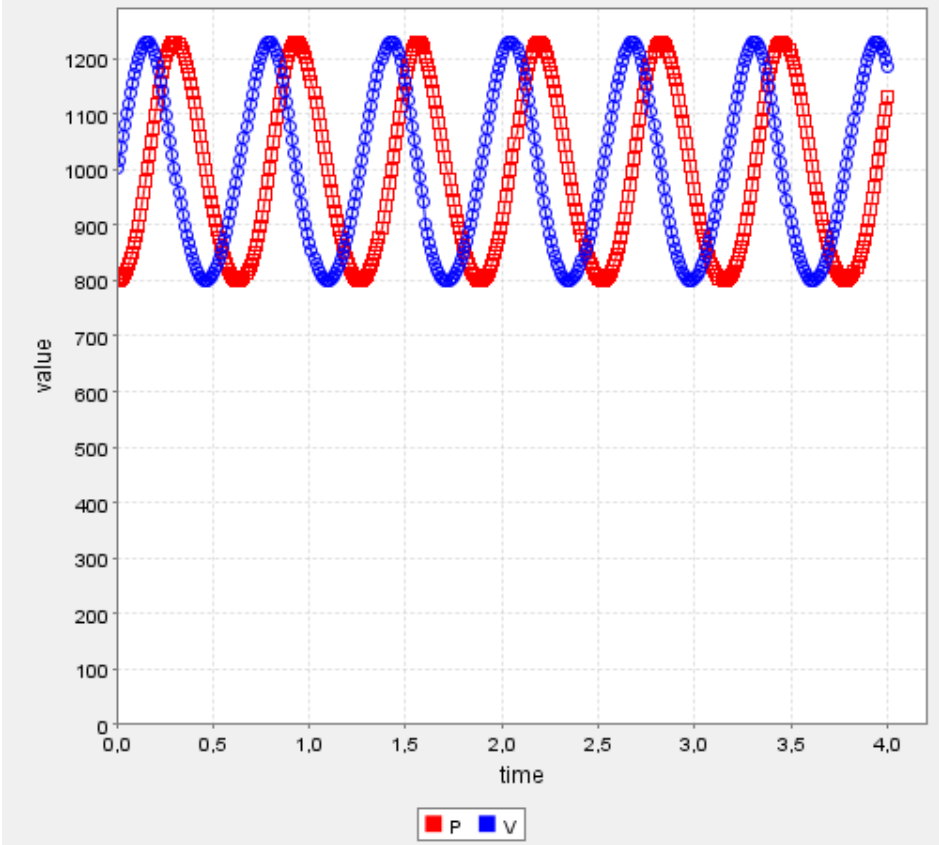


Oscillations around 1000 arise: first preys, then predators

The Lotka-Volterra model: numerical solution

Let's use a numerical solver with the following initial conditions:

- $V_0 = 800$
- $P_0 = 1000$



Same dynamics: oscillations around 1000

The Lotka-Volterra model: numerical solution

Back to the initial question:

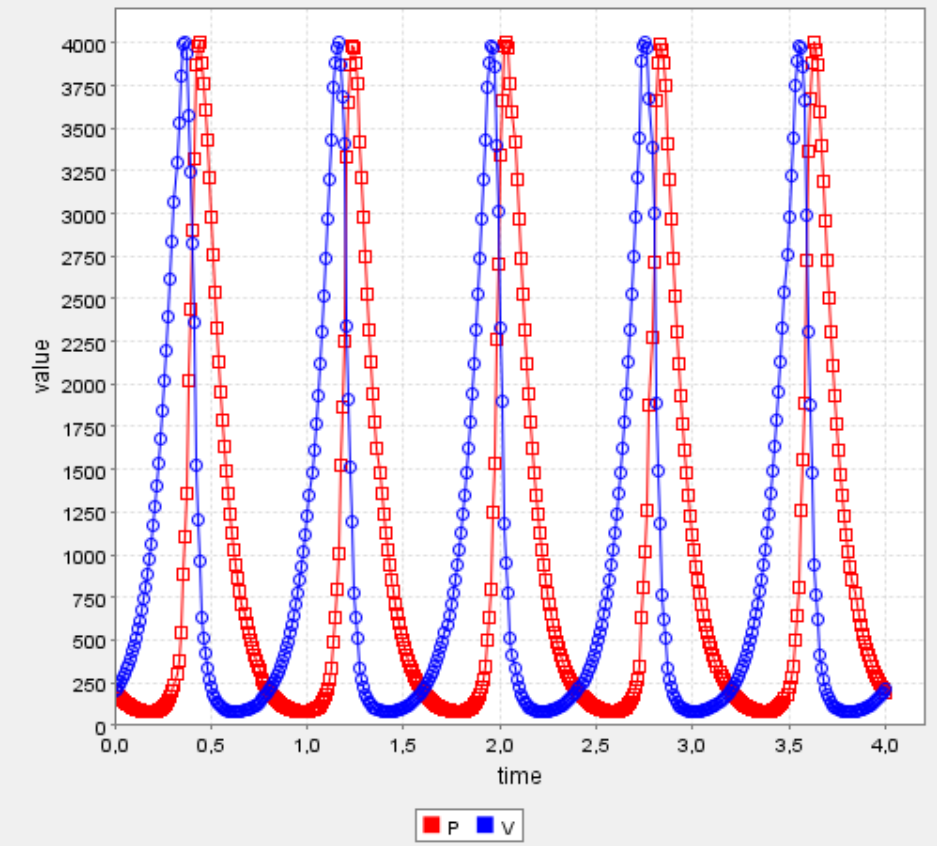
What happens if we significantly reduce the size of both preys and predators?

- World war effect

The Lotka-Volterra model: numerical solution

Let's use a numerical solver with the following initial conditions:

- $V_0 = 200$
- $P_0 = 200$



Strong oscillations. At time 0.3 we have $\sim$ 3500 preys (much more than 1000) and only $\sim$ 500 predators.

The SIR epidemic models and the effects of vaccination

Epidemic phenomena (spread of infectuous diseases) are often studied by means of a SIR model

SIR stands for:

- **Susceptible**: individual that can be infected
- **Infected**: individual that has been infected and that can infect susceptible individuals
- **Recovered** (or Resistant): individual who passed the infection phase and cannot infect other individuals any more

First formulation of a SIR model was proposed by Kermack and McKendrick in 1927

The SIR epidemic models and the effects of vaccination

The dynamics of epidemic phenomena is described by means of ODEs

- One equation for each type of individual: variables S, I, R describe the ratios of each class of individual in the population

Assumptions of the (initial) model:

- the size of the population is constant in time (and normalized to 1), so it always hold $S + I + R = 1$
- only the transmission of infection is described: no reproduction, death, migration, etc...
- disease is transmitted by personal contacts beween individuals of I and S classes (horizontal transmission)
- contacts between individuals are random, i.e. the number of infections is proportional to both I and S
- after infection. individuals recover and become resistant to that disease

The SIR epidemic models and the effects of vaccination

Therefore, the model is described by the system of equations:

$$\begin{cases} \dot{S} = -\beta SI \\ \dot{I} = \beta SI - \gamma I \\ \dot{R} = \gamma I \end{cases}$$

where:

- β is the infection coefficient, describing probability of infection after the contact of a healthy individual with an infected one
- γ is the recovery coefficient, describing the rate of recovery of each infected individual (in other words, $1/\gamma$ is the time one individual requires for recovering)

The SIR epidemic models: role of parameters

$$\begin{cases} \dot{S} = -\beta SI \\ \dot{I} = \beta SI - \gamma I \\ \dot{R} = \gamma I \end{cases}$$

Note that:

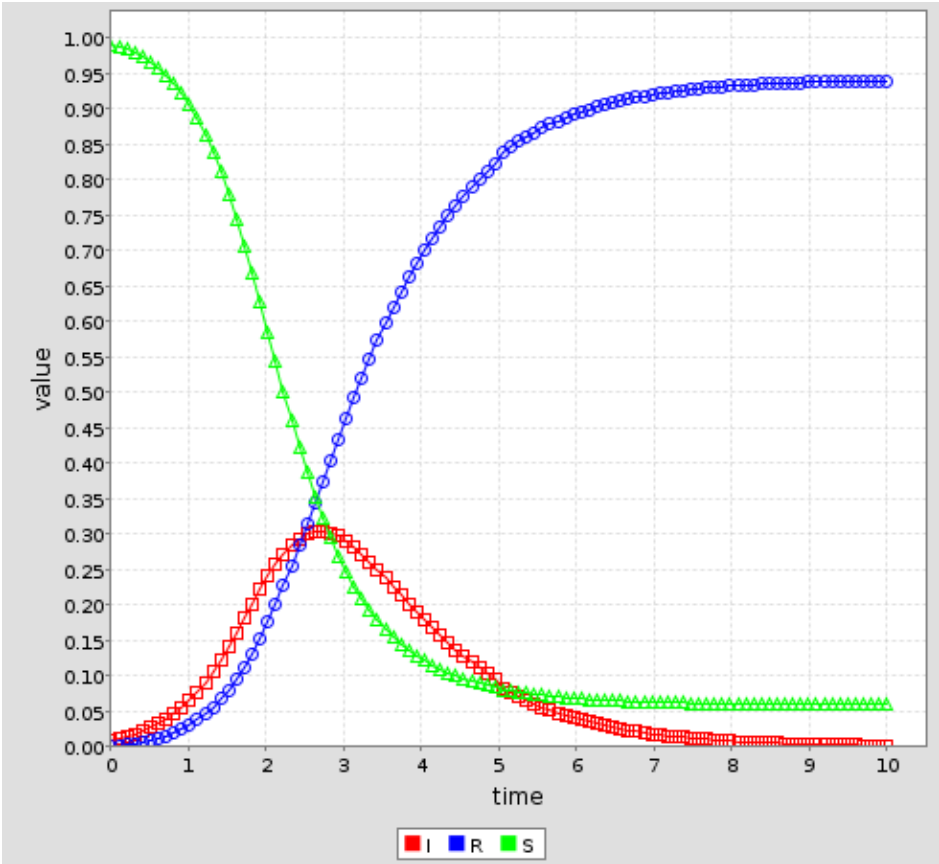
- R is the ratio of the population which got the disease in the past
- R is almost useless, it does not appear in the other equations and could be replaced by $1 - S - I$
- S can only decrease
- if $\beta < \gamma$ (i.e. $\beta/\gamma < 1$), I can only decrease (since $S \leq 1$)
- if $\beta > \gamma$ (i.e. $\beta/\gamma > 1$), the behavior of I depends on S. It initially increases if $S > \gamma/\beta$.

The SIR epidemic models: numerical solution

First case: $\beta/\gamma > 1$

- $S_0 = 0.99$
- $I_0 = 0.01$
- $R_0 = 0$

- $\beta = 3$
- $\gamma = 1$



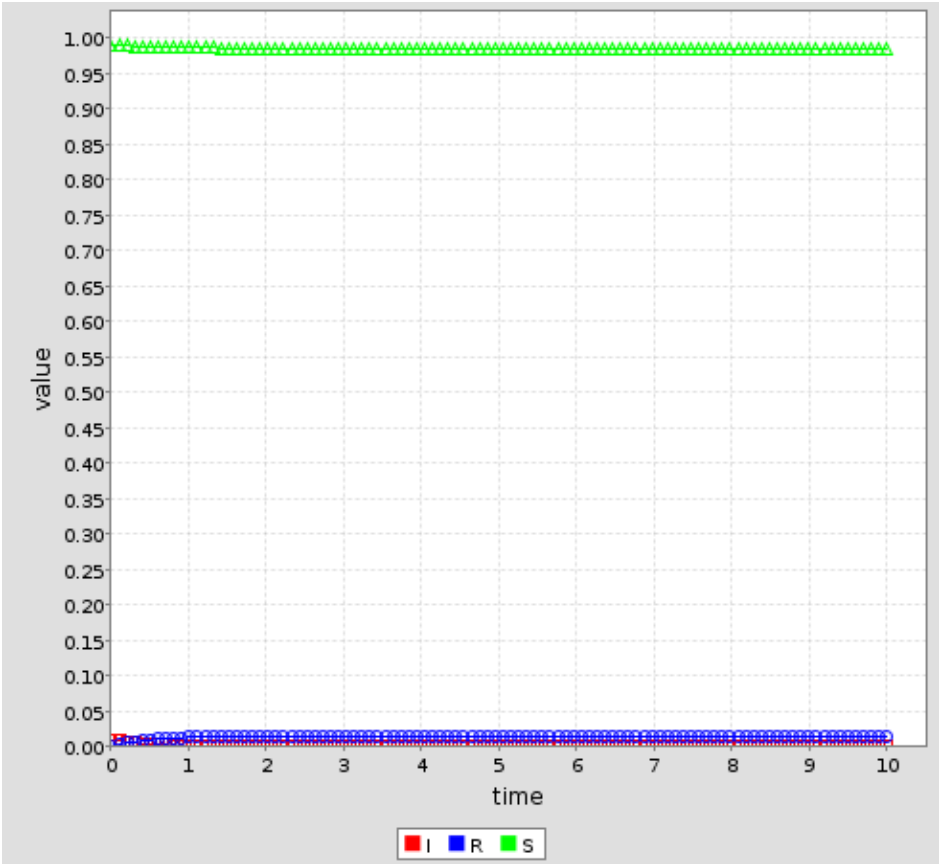
Spread of infection. 95% of the population gets the disease.

The SIR epidemic models: numerical solution

First case: $\beta/\gamma < 1$

- $S_0 = 0.99$
- $I_0 = 0.01$
- $R_0 = 0$

- $\beta = 1$
- $\gamma = 3$



The infection doesn't diffuse. $\sim 1\%$ of the population gets the disease.

The SIR epidemic models: influenza

Let's try to find parameters to describe the spread of influenza:

Flu usually takes more or less one week (say, 8 days)

- $\gamma = 1/8 = 0.125$

A person with flu usually infects more or less 1/5 of the persons he/she meets

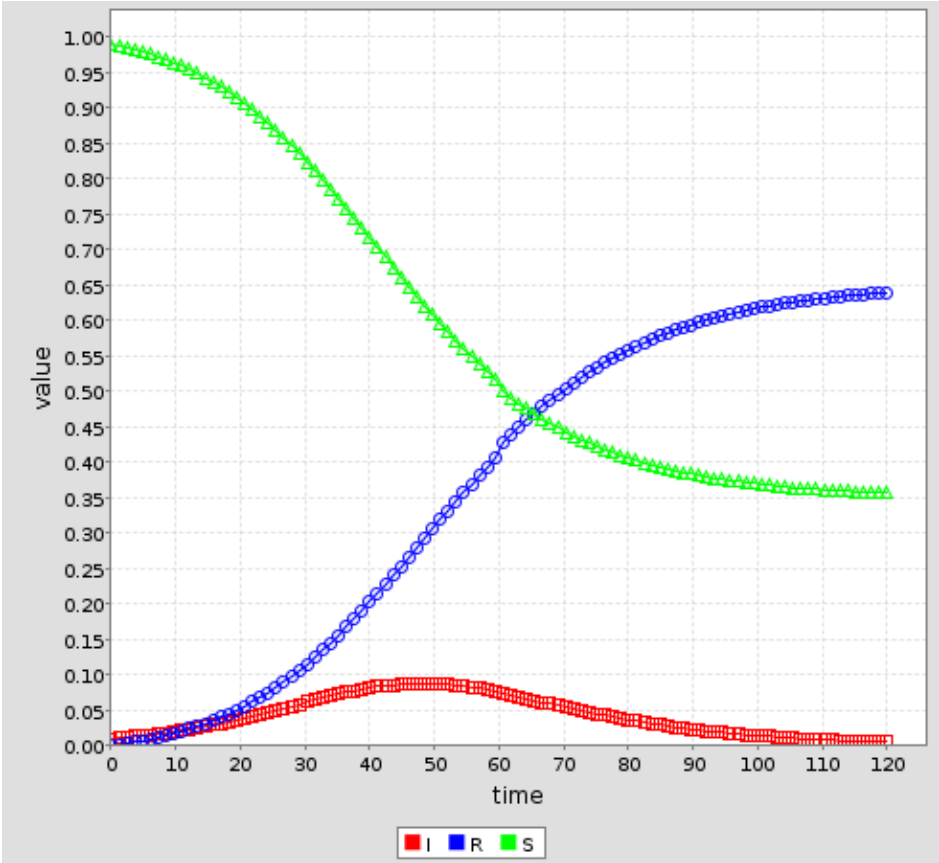
- $\beta = 1/5 = 0.2$

Flu epidemies usually cover winter (say, 120 days)

The SIR epidemic models: influenza

- $S_0 = 0.99$
- $I_0 = 0.01$
- $R_0 = 0$

- $\beta = 0.2$
- $\gamma = 0.125$



$\sim$ 65% of the population gets the disease, with a peak of infections at the end of the second month.

The SIR epidemic models and vaccination

The SIR model can be used to study the effects of vaccination

Vaccinations may require years to show their effect

- births and deaths cannot be ignored if we consider a long time span

Let's extend the SIR model with birth and deaths

The SIR epidemic models: births and deaths

Assumptions:

- for the sake of simplicity we would like the population size still to be constant over time (not too wrong: the size of the population of a country does not change significantly over 10-20 years...)
- No vertical transmission of the disease (from parents to children)
- Newborns are susceptible

Constant population size can be obtained by using the same coefficient μ for both birth and death

- This works since the population size is normalized to 1
- Let $N = S + I + R$, we have that $\dot{N} = \mu - \mu N$ has $N = 1$ as steady state

The SIR epidemic models: births and deaths

This is the extended model:

$$\begin{cases} \dot{S} = \mu - \beta SI - \mu S \\ \dot{I} = \beta SI - \gamma I - \mu I \\ \dot{R} = \gamma I - \mu R \end{cases}$$

As in the previous case, the dynamics of the model is governed by the ratio between the positive and negative coefficients in the equation of I

- if $\beta < (\mu + \gamma)$ (i.e. $\beta/(\mu + \gamma) < 1$), I can only decrease (since $S \leq 1$)
- if $\beta > (\mu + \gamma)$ (i.e. $\beta/(\mu + \gamma) > 1$), the behavior of I depends on S. It increases if $S > (\mu + \gamma)/\beta$.

In the previous case S could only decrease, but this is no longer true, since we have births

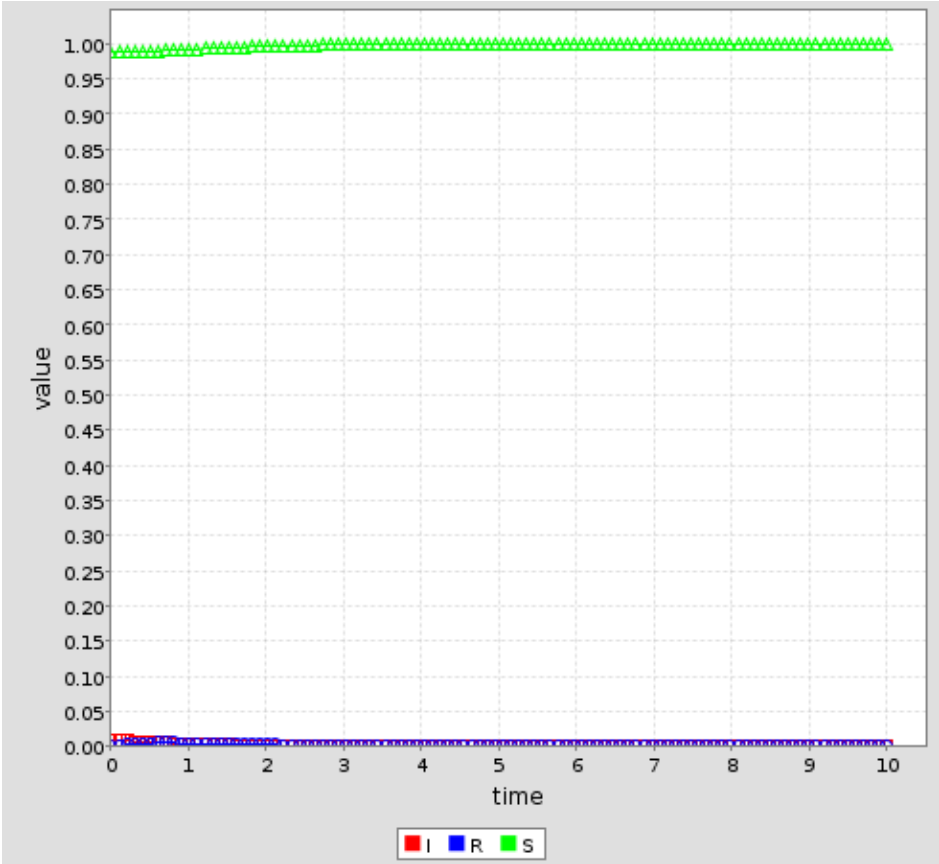
- births could maintain S above $(\mu + \gamma)/\beta$, which sustains infections (endemic state)

The SIR epidemic models: births and deaths

First case: $\beta/(\mu+\gamma) < 1$

- $S_0 = 0.99$
- $I_0 = 0.01$
- $R_0 = 0$

- $\beta = 3$
- $\gamma = 2$
- $\mu = 2$



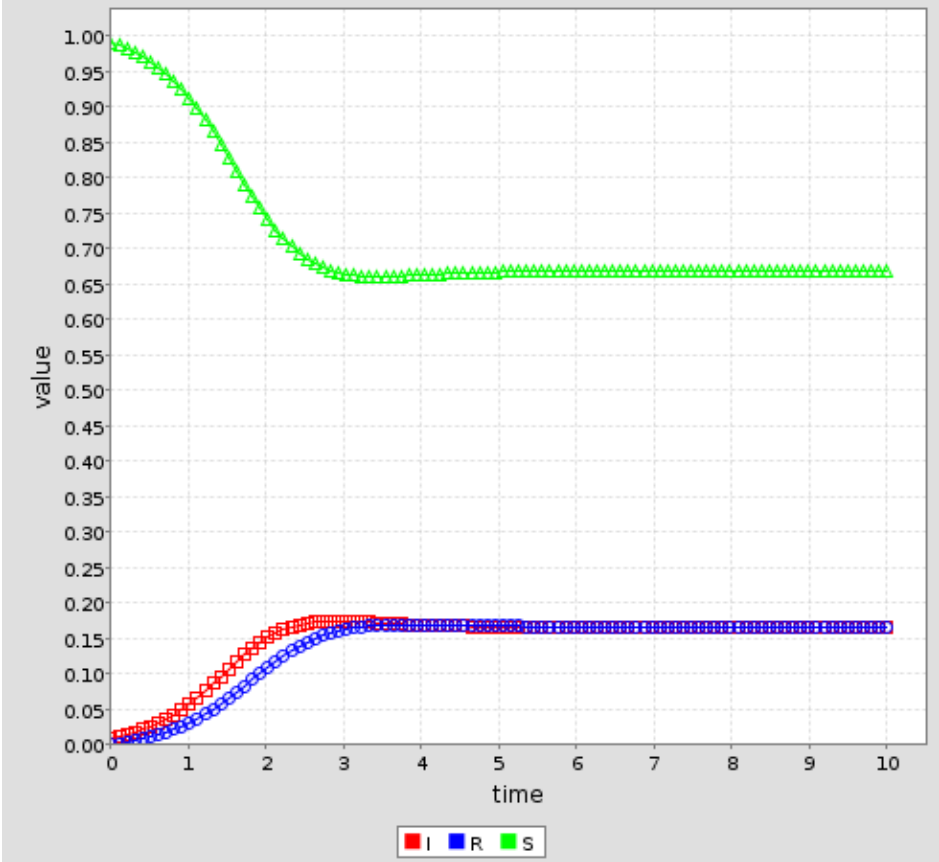
The infection doesn't diffuse. In the end, 100% of the population is susceptible (since recovered individuals die)

The SIR epidemic models: births and deaths

Second case: $\beta/(\mu+\gamma) > 1$

- $S_0 = 0.99$
- $I_0 = 0.01$
- $R_0 = 0$

- $\beta = 6$
- $\gamma = 2$
- $\mu = 2$



Endemic state! The population reaches a steady state in which $\sim 17\%$ of the population is infected.

The SIR epidemic models: vaccination

Let's further extend the model with vaccinations.

Assumption:

- vaccination is done on a fraction p of the newborns
- this corresponds to assuming that a fraction p of newborns are already in the recovered state R

This results in the following model:

$$\begin{cases} \dot{S} = (1-p)\mu - \beta SI - \mu S \\ \dot{I} = \beta SI - \gamma I - \mu I \\ \dot{R} = p\mu + \gamma I - \mu R \end{cases}$$

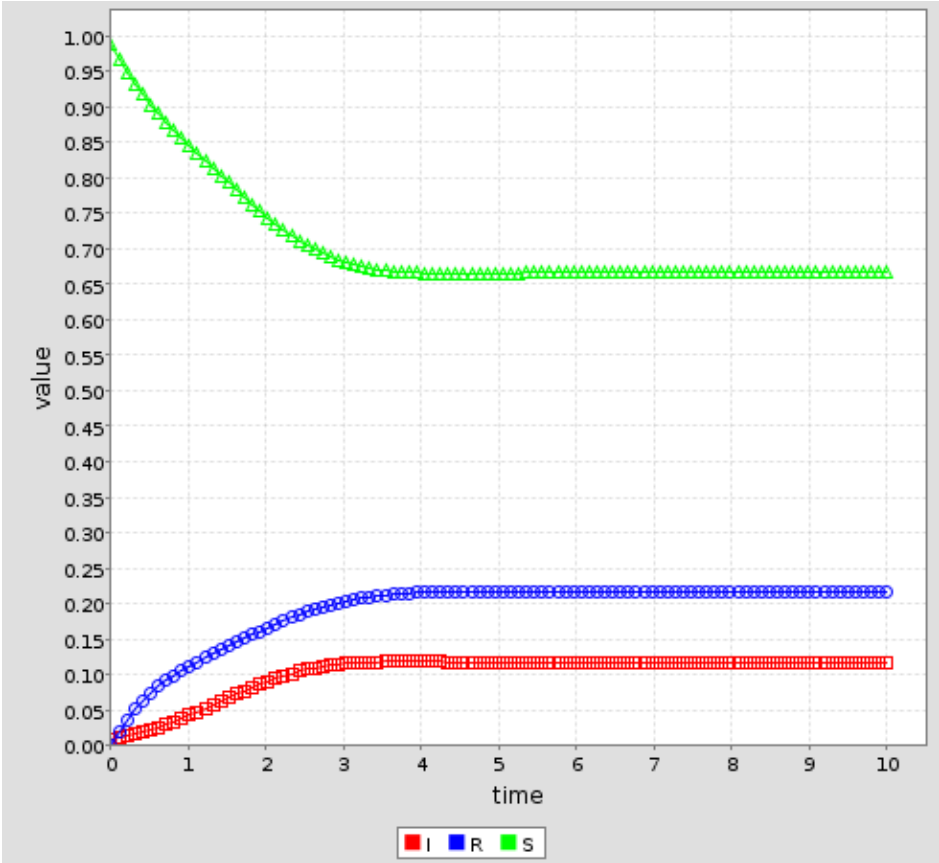
Let's perform some simulations by varying p.

The SIR epidemic models: births and deaths

First case: p small

- $S_0 = 0.99$
- $I_0 = 0.01$
- $R_0 = 0$

- $\beta = 6$
- $\gamma = 2$
- $\mu = 2$
- $p = 0.1$



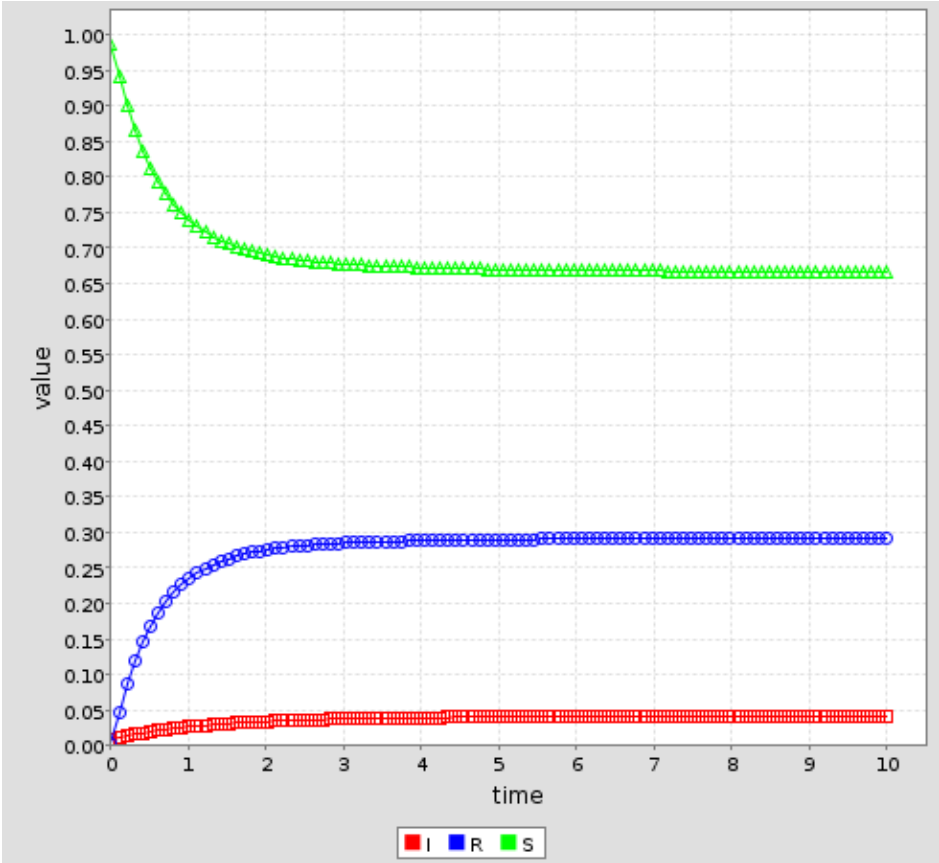
Still endemic state!

The SIR epidemic models: births and deaths

First case: p medium

- $S_0 = 0.99$
- $I_0 = 0.01$
- $R_0 = 0$

- $\beta = 6$
- $\gamma = 2$
- $\mu = 2$
- $p = 0.25$



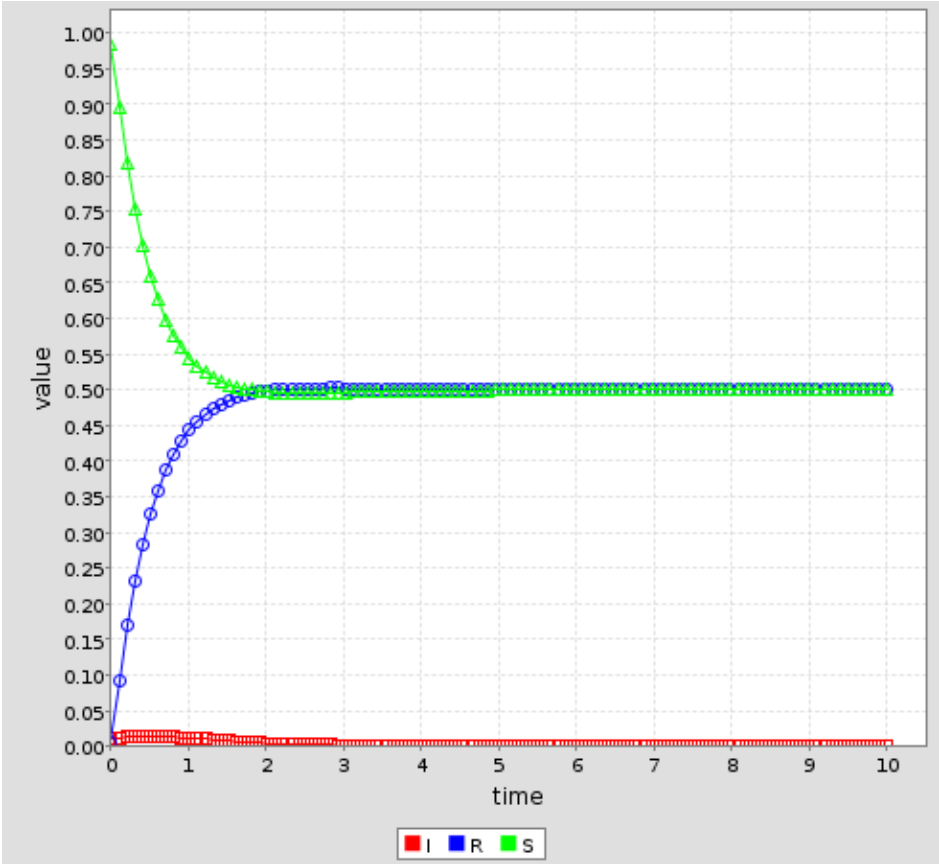
Endemic state, but with less infected.

The SIR epidemic models: births and deaths

First case: higher p

- $S_0 = 0.99$
- $I_0 = 0.01$
- $R_0 = 0$

- $\beta = 6$
- $\gamma = 2$
- $\mu = 2$
- $p = 0.5$



Healthy population! The disease has been eradicated.

The SIR epidemic models: vaccination threshold

So, which ratio of the newborns should be vaccinated in order to obtain disease eradication?

- p_c: threshold value of vaccination

The value of p_c can be computed analytically (see lecture notes) or simply by performing numerical simulations varying p.

- result:

$$p_c = 1 - \frac{\mu + \gamma}{\beta}$$

In the previous example $p_c = 1 - (2+2)/6 = 1/3$

The SIR epidemic models: application to measles

Let's consider measles ("morbillo")

For measles the following parameter values were estimated:

$$\mu = 0.02 \qquad \beta = 1800 \qquad \gamma = 100$$

which give the critical ratio of vaccine

$$p_c = 1 - \frac{0.02 + 100}{1800} \simeq 0.95$$

meaning that 95% of the newborns should be vaccinated in order to eradicate the disease

Lessons learnt

Summing up:

- ODEs can be used to describe dynamical systems whose state updates continuously
  - continuous dynamical systems
- Solving ODEs analytically is often difficult/impossibile
  - numerical solution of initial value problems helps
  - numerical solvers approximate ODEs by discretizing them (recurrence equations)
  - stiffness causes problems: implicit methods perform better in these cases
- ODEs are used extensively
  - Lotka-Volterra and SIR models are well-established examples

Limitations of continuous dynamical models

Continuous dynamical models based on ODEs describe THE behavior of the system, starting from an initial state

- often system may exhibit different behaviors starting from the same initial state
- this happens when some events happening within the system are somehow random
- in order to properly model these system, probabilisties have to be included in the model (probabilistic/stochastic model)

ODEs are not very modeler-friendly

- When the number of equations is high and each equation has many terms, understanding the model and manipulating it may become difficult
- more intutitive notations should be found

Exercises

- Define a variant of the Lotka-Volterra model with 3 kinds of individual: predator, prey and vegetation. Predators eat preys, preys eat vegetation, and vegetation (in the absence of preys) grows exponentially
  - compute the steady states
  - try to perform numerical simulation by varying coefficient values and initial quantities of predators, preys and vegetation
- Extend the "influenza" model with vaccination
  - the vaccination rate could be constant in time or (better) could be described by a logistic function with K corresponding to the number of individuals who choose to vaccinate (typically within few weeks)
- A lot of variants of the SIR model exist
  - look at the Wikipedia page "Compartmental models in epidemiology"