

Classic Models in Ecology

Lecture 3

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28 January 2020

Classic models in ecology

in this lecture we will develop and explore a variety of classic models in ecology and epidemiology; these models illustrate many interesting dynamical patterns;

the models are:

- ▶ exponential and logistic models describing population growth;
- ▶ Lotka-Volterra competition and predator-prey models;
- ▶ SIR epidemiological models for the spreading of infectious diseases.

World population growth

let's upload some data on world population growth, and plot them...

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

# import historical world population data from 10000 BC to 1950
# data from united states census bureau
hpop=np.loadtxt("historical_population.csv", delimiter=";", skiprows=1)

# import modern world population data from 1950 to 2050
# data from united states census bureau
mpop=np.loadtxt("modern_population.csv", delimiter=";", skiprows=1)

plt.plot(hpop[:,0], hpop[:,1]/1e9, 'ob', label='historical')
plt.plot(mpop[:,0], mpop[:,1]/1e9, 'or', label='modern')

# add an arrow to the plot: plt.arrow(x, y, dx, dy, some arguments)
plt.arrow(2017, 5, 0, 1.65, head_width=3.0, head_length=0.3, fc="k", ec="k")

# add text to the plot: plt.text(x, y, string)
plt.text(2010, 4.5, "2017")
plt.text(1999, 4.0, "7.4 billions")

plt.xlim(1795,2055) # plot only data from 1800 to 2050

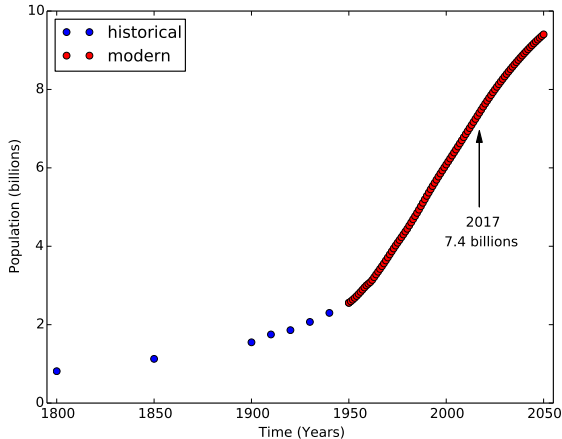
plt.xlabel("Time (Years)")
plt.ylabel("Population (billions)")

plt.legend(loc='best') # add a legend anywhere in the plot

plt.savefig('pop.pdf') # save plot as a PDF figure
```

World population growth

that script should produce the following plot...



Models of population growth

exponential or Malthusian growth model

in any population, the number of individuals changes over time in response to resource availability, competition, predation, disease, weather, and chance events; the simplest model describing changes in population size is exponential growth model;

this model assumes that the environment is constant, and ignore any interactions with other species (no competing species, predators, parasites, etc.);

we have already encountered a special case of the exponential growth model in the tree-branching example; each branch gives rise to b new branches in the next time step, and branches were never lost ($d = 0$);

the exponential growth model assumes that the variable changes at a rate that is proportional to its current value.

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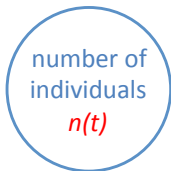
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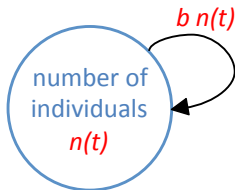
Models of population growth

exponential growth model - flow diagram and equation



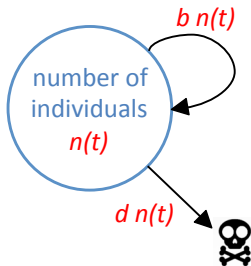
Models of population growth

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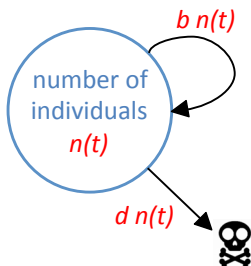
Models of population growth

exponential growth model - flow diagram and equation



Models of population growth

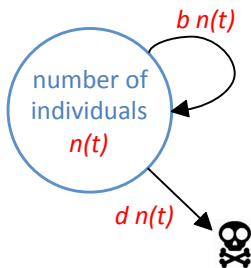
exponential growth model - flow diagram and equation



$$\frac{dn(t)}{dt} = b n(t) - d n(t)$$

Models of population growth

exponential growth model - flow diagram and equation

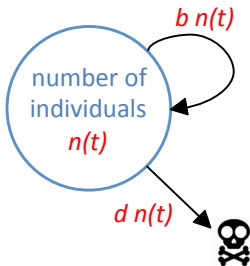


$$\frac{dn(t)}{dt} = b n(t) - d n(t)$$

$$\frac{dn(t)}{dt} = (b - d) n(t)$$

Models of population growth

exponential growth model - flow diagram and equation



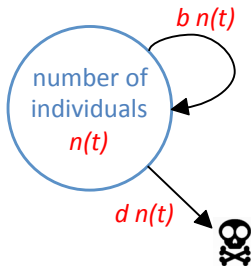
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$$\frac{dn(t)}{dt} = r n(t)$$

Models of population growth

exponential growth model - flow diagram and equation



$$\frac{dn(t)}{dt} = b n(t) - d n(t)$$

$$\frac{dn(t)}{dt} = (b - d) n(t)$$

$$\frac{dn(t)}{dt} = r n(t)$$

with r per capita rate of change of individuals or *net growth rate*.

Models of population growth

exponential growth model - analytical solution

$$\frac{dn(t)}{dt} = r n(t) \Rightarrow \frac{dn(t)}{n(t)} = r dt$$

$$\int_{n(0)}^{n(T)} \frac{dn(t)}{n(t)} = r \int_0^T dt \quad \text{with } n(0) \text{ population size at time } t = 0$$

$$\ln n(T) - \ln n(0) = r(T - 0)$$

$$\ln \left[\frac{n(T)}{n(0)} \right] = r T$$

$$\frac{n(T)}{n(0)} = e^{r T} \Rightarrow n(T) = n(0) e^{r T}$$

Models of population growth

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$$\frac{n(T)}{n(0)} = e^{r T} \Rightarrow n(T) = n(0) e^{r T}$$

Models of population growth

exponential growth model - python code

- ▶ import relevant libraries:

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import odeint
```

- ▶ create time array, set initial conditions, assign a value to r :

```
t = np.arange(0,250)      # time array (250 years)
y0 = 0.8                  # initial population size (0.8 billions)
r = 0.01                  # net growth rate (1% growth rate)
```

- ▶ define the function to be integrated and integrate:

```
def expgro(y, t):
    """ Exponential growth model """
    n = y
    dndt = r*n
    return dndt

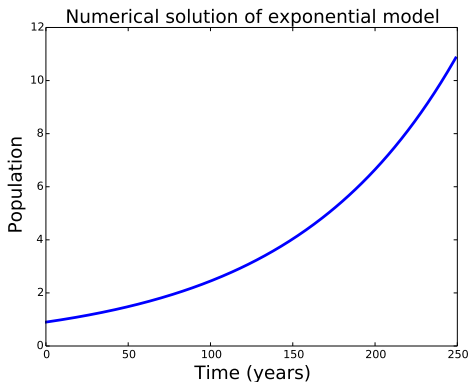
sol=odeint(expgro,y0,t) # integrate and save results into array
```


Models of population growth

exponential growth model - python code

- plot the results:

```
plt.plot(t,sol[:,0], linewidth=3)
plt.xlabel('Time (years)', fontsize=20)
plt.ylabel('Population', fontsize=20)
plt.title('Solution of exponential model', fontsize=24)
plt.savefig('ExpGrowth.pdf')
```



Models of population growth

let's plot population growth data and model results together

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import odeint

mpop=np.loadtxt("modern_population.csv", delimiter=";", skiprows=1)
hpop=np.loadtxt("historical_population.csv", delimiter=";", skiprows=1)

y0 = 0.8                      # initial population size (0.8 billions of people)
r = 0.01                      # net growth rate (1.0% per year)
t = np.arange(0,250)         # time array (250 years)

def expgro(y, t):
    """ Exponential growth model """
    n = y
    dndt = r*n
    return dndt

sol=odeint(expgro,y0,t) # integrate and save results into array

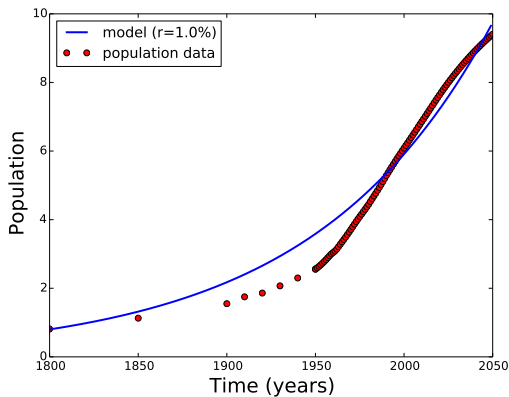
plt.plot(hpop[:,0], hpop[:,1]/1e9, 'or', label='population data', zorder=1)
plt.plot(mpop[:,0], mpop[:,1]/1e9, 'or', zorder=1)
plt.plot(t+1800, sol[:,0], '-b', label='model (r=1.0%)', linewidth=2, zorder=2)

plt.xlabel('Time (years)', fontsize=20)
plt.ylabel('Population', fontsize=20)
plt.xlim(1800,2050)          # plot from 1800 to 2050
plt.legend(loc='best')       # add a legend anywhere in the plot

plt.savefig('ExpGrowth2v.pdf') # save figure as Pdf file
```

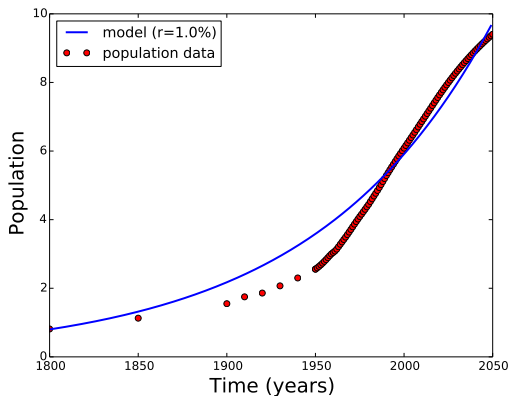
Models of population growth

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Models of population growth

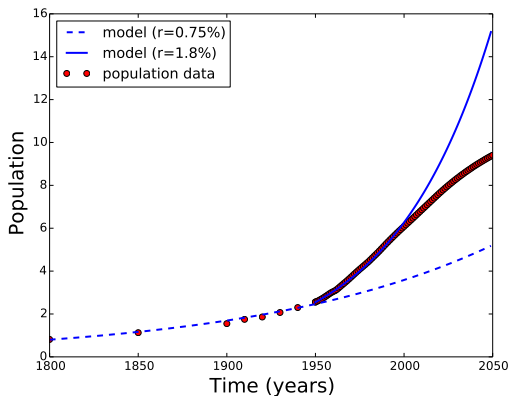
let's plot population growth data and model results together



it does not look like a perfect fit... it seems as if the first part of the data increase at a slower rate as compared to the second part of the data...

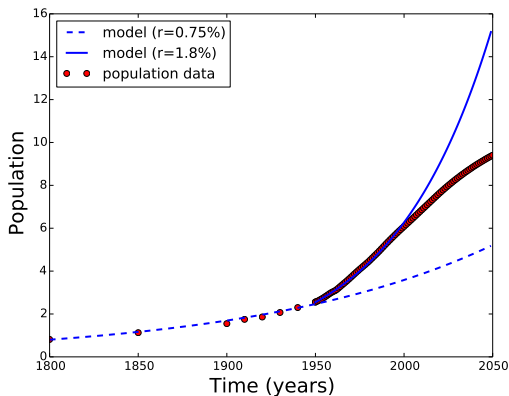
Models of population growth

let's plot population growth data and model results together



Models of population growth

let's plot population growth data and model results together



creating two distinct model results using two different net growth rates (r) produces much better fits; still the final part of the data does not seem to increase exponentially...

Models of population growth

obviously exponential growth cannot continue unabated;

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in fact, in the world population data we can observe that the increase is slowing down and most likely will, at some point in the future, cease completely...

Models of population growth

obviously exponential growth cannot continue unabated;

in fact, in the world population data we can observe that the increase is slowing down and most likely will, at some point in the future, cease completely...

what kind of models can account for the slowing rate of population growth?

Models of population growth

logistic or Verhulst growth model

many factors slow the rate of growth of a population, including declining resource availability, increased predation pressure, and a higher incidence of disease;

the logistic model describes these processes indirectly by assuming that the per capita rate of change of a variable, that is $\frac{1}{n} \frac{dn}{dt}$, decreases linearly as the variable increases in value, with no change occurring if the variable is at the *carrying capacity* K .

Models of population growth

logistic growth model

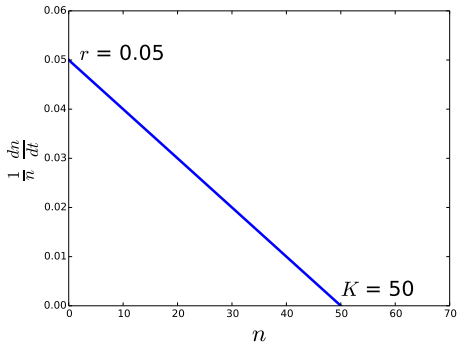
$$\frac{dn(t)}{dt} = r n(t) \left(1 - \frac{n(t)}{K} \right)$$

let's plot the per capita growth rate as a function of population size:

$$\frac{1}{n} \frac{dn}{dt} = r \left(1 - \frac{n}{K} \right);$$

when $n = 0$, then $\frac{1}{n} \frac{dn}{dt} = r$;

when $n = K$, then $\frac{1}{n} \frac{dn}{dt} = 0$.



Models of population growth

logistic growth model - python code

- ▶ import relevant libraries:

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import odeint
```

- ▶ create time array, set initial conditions, assign values to r and K :

```
t=np.arange(0,800) # time array 250 years
n0=0.1           # initial population size (2.55 billions)
r=0.017          # set net growth rate (1.7% per year)
K=10.0           # set carrying capacity (10 billions)
```

- ▶ define the function to be integrated and integrate:

```
def loggro(n, t):
    """ Logistic growth model """
    dndt = r*n*(1-n/K)
    return dndt

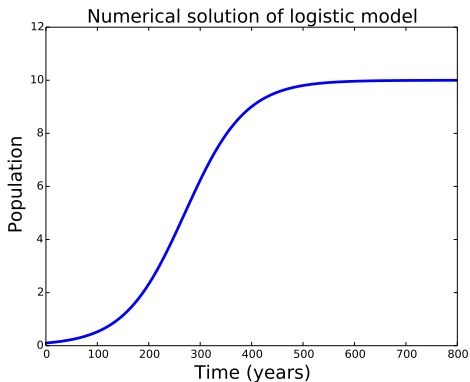
sol=odeint(loggro,n0,t) # inetgrate and save results into array
```

Models of population growth

logistic growth model - python code

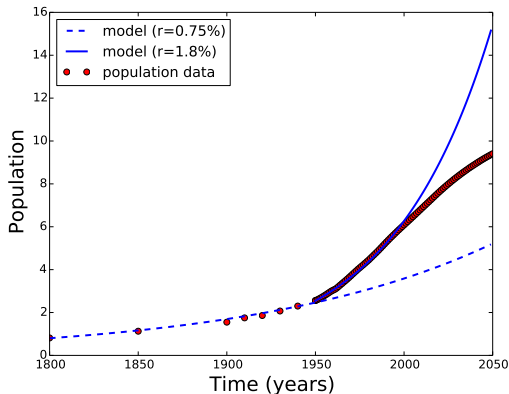
- plot the results:

```
plt.plot(t,sol[:,0], linewidth=3)
plt.xlabel('Time (years)', fontsize=20)
plt.ylabel('Population', fontsize=20)
plt.title('Solution of logistic model', fontsize=24)
plt.ylim(0,12)
plt.savefig('LogGrowth.pdf')
```



Models of population growth

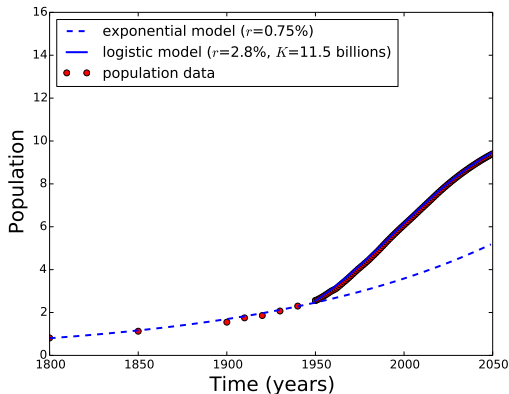
let's plot population growth data and model results together



creating two distinct model results using two different net growth rates (r) produces much better fits; still the final part of the data does not seem to increase exponentially...

Models of population growth

let's plot population growth data and model results together



using a logistic growth model for the second part of the data produces a much better fit! the growth of the world population may approach a carrying capacity in the future!

Species interaction

species do not exist in isolation from one another;

the simple models of exponential and logistic growth fail to capture the fact that the growth of a species must depend on its interactions with other species;

a complete model describing every species interaction would be prohibitively complex;

yet some insight can be obtained by focusing on specific types of interactions and how these interactions affect population growth;

in the following we will focus on the so-called predator-prey (or Lotka-Volterra) model.

Species interaction

Lotka-Volterra predator-prey model - flow diagram

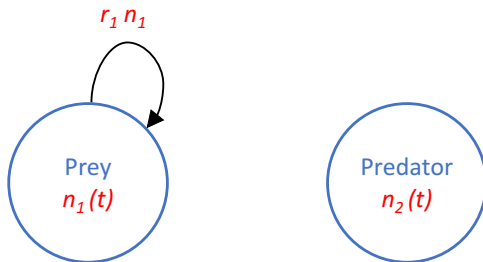
a classic species interaction model in ecology is called predator-prey (or Lotka-Volterra) model; the graphical representation is as follows:



Species interaction

Lotka-Volterra predator-prey model - flow diagram

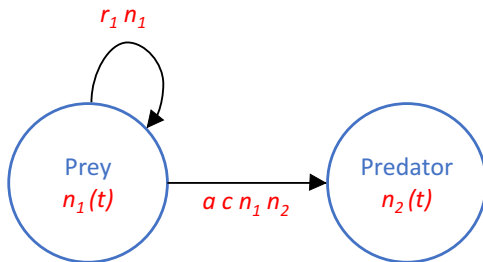
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Species interaction

Lotka-Volterra predator-prey model - flow diagram

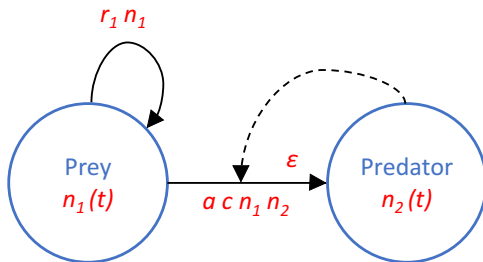
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Species interaction

Lotka-Volterra predator-prey model - flow diagram

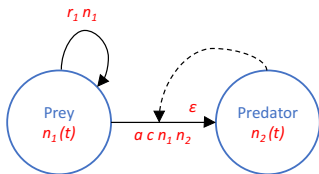
a classic species interaction model in ecology is called predator-prey (or Lotka-Volterra) model; the graphical representation is as follows:



Species interaction

Lotka-Volterra predator-prey model - equations

the equations can follow easily from the flow diagram:



$$\frac{dn_1}{dt} = r n_1 - a c n_1 n_2 \quad (\text{prey})$$

$$\frac{dn_2}{dt} = \epsilon a c n_1 n_2 - \delta n_2 \quad (\text{predator})$$

the Lotka-Volterra predator-prey model predicts that the number of prey and number of predators cycle over time, showing that species interactions can lead to interesting dynamical behaviour that might help explain the cyclic dynamics of several species.

Species interaction

Lotka-Volterra predator-prey model - python code

- import relevant libraries:

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import odeint
```

- create time array, set initial conditions, assign values to parameters:

```
t = np.arange(0,150) # time array 150 days
n0 = [500.0, 30.0]   # initial population sizes
r, a, c, epsilon, delta = 0.5, 1.0, 0.01, 0.02, 0.1 # parameters
```

- define the function to be integrated and integrate:

```
def pp(n, t):
    """ predator-prey model """
    n1, n2 = n
    dn1dt = r*n1 - a*c*n1*n2
    dn2dt = epsilon*a*c*n1*n2 - delta*n2
    dndt = [dn1dt, dn2dt]
    return dndt

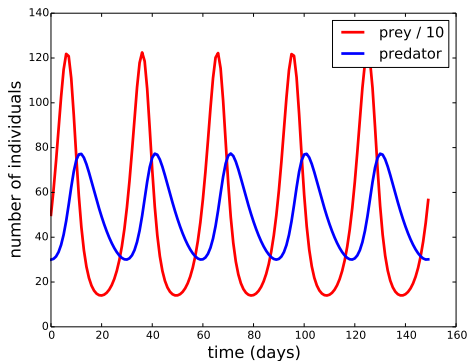
sol=odeint(pp,n0,t) # inetgrate and save results into array
```

Species interaction

nutrient-algal type of model - python code

- plot the results:

```
plt.plot(t,sol[:,0]/10.0, '-r', linewidth=3, label='prey / 10.0')
plt.plot(t,sol[:,1], '-b', linewidth=3, label='predator')
plt.legend(loc='best',fontsize=18)
plt.xlabel('time (days)', fontsize=20)
plt.ylabel('number of individuals', fontsize=20)
plt.savefig('np.pdf')
```



Epidemiological model of disease spreading

the final model that we derive describes the spread of a disease within a population;

this is an extension of the flu model that we explored in the previous lectures, but we now add more realism by accounting for births, deaths, recovery, and the gain and loss of immunity;

in the previous lectures we considered only two types of individuals, those susceptible to the flu and those infected with the flu;

we now allow for a third class of individuals: those who have recovered from the disease and are currently resistant.

Epidemiological model of disease spreading

Susceptible-Infected-Recovered (SIR) model



$$\frac{dS}{dt}$$

$$\frac{dR}{dt}$$

$$\frac{dI}{dt}$$

Epidemiological model of disease spreading

Susceptible-Infected-Recovered (SIR) model



$$\frac{dS}{dt} = \theta$$

$$\frac{dR}{dt}$$

$$\frac{dI}{dt}$$

Epidemiological model of disease spreading

Susceptible-Infected-Recovered (SIR) model



$$\frac{dS}{dt} = \theta - dS(t)$$

$$\frac{dR}{dt}$$

$$\frac{dI}{dt}$$

Epidemiological model of disease spreading

Susceptible-Infected-Recovered (SIR) model



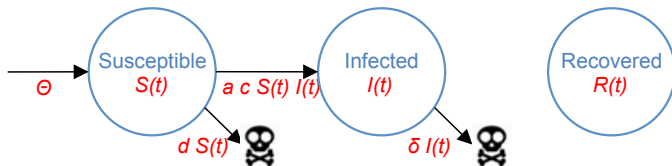
$$\frac{dS}{dt} = \theta - d S(t) - a c S(t) I(t)$$

$$\frac{dR}{dt}$$

$$\frac{dI}{dt} = a c S(t) I(t)$$

Epidemiological model of disease spreading

Susceptible-Infected-Recovered (SIR) model



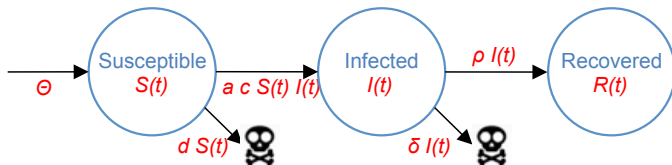
$$\frac{dS}{dt} = \theta - d S(t) - a c S(t) I(t)$$

$$\frac{dR}{dt}$$

$$\frac{dI}{dt} = a c S(t) I(t) - \delta I(t)$$

Epidemiological model of disease spreading

Susceptible-Infected-Recovered (SIR) model



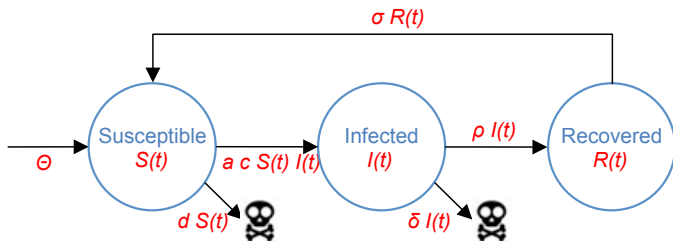
$$\frac{dS}{dt} = \theta - d S(t) - a c S(t) I(t)$$

$$\frac{dR}{dt} = \rho I(t)$$

$$\frac{dI}{dt} = a c S(t) I(t) - \delta I(t) - \rho I(t)$$

Epidemiological model of disease spreading

Susceptible-Infected-Recovered (SIR) model



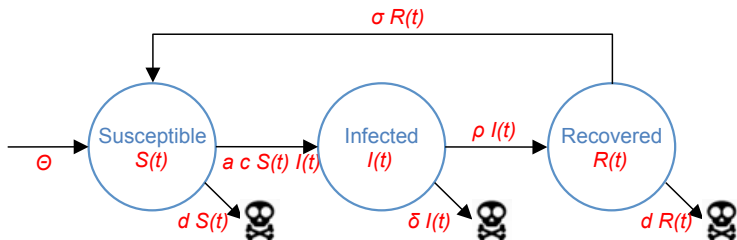
$$\frac{dS}{dt} = \theta - d S(t) - a c S(t) I(t) + \sigma R(t)$$

$$\frac{dR}{dt} = \rho I(t) - \sigma R(t)$$

$$\frac{dI}{dt} = a c S(t) I(t) - \delta I(t) - \rho I(t)$$

Epidemiological model of disease spreading

Susceptible-Infected-Recovered (SIR) model



$$\frac{dS}{dt} = \theta - d S(t) - a c S(t) I(t) + \sigma R(t)$$

$$\frac{dR}{dt} = \rho I(t) - \sigma R(t) - d R(t)$$

$$\frac{dI}{dt} = a c S(t) I(t) - \delta I(t) - \rho I(t)$$

Epidemiological model of disease spreading

Parameters of Susceptible-Infected-Recovered (SIR) model

Symbol	Description	Value (per day)
c	Contact rate per susceptible individual	1.0
a	Probability that the disease is transmitted upon contact	0.025
ρ	Recovery rate per infected individual	0.03
d	Death rate of healthy individuals (i.e. susceptible and recovered individuals)	0.1
σ	Rate of recovered individuals that become susceptible of being infected again	0.3
θ	Immigration rate of individuals entering the population of those that are susceptible of being infected	0.15
δ	Death rate of infected individuals	0.25

As for initial conditions, use: 85 susceptible, 10 infected, and 5 recovered.

Further reading



Sarah P. Otto & Troy Day 2007

A Biologist's Guide to Mathematical Modelling in Ecology and Evolution
Princeton University Press



US Census Bureau, Historical Estimates of World Population

https://www.census.gov/population/international/data/worldpop/table_history.php

Visited on: 20.09.2017



US Census Bureau, World Population 1950-2050

https://www.census.gov/population/international/data/worldpop/table_population.php

Visited on: 20.09.2017