

Deterministic models

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Deterministic models

A brief caveat

Deterministic models

Structural equation and mathematical models

ODE models

ordinary differential equations (autonomous)

mass action

The most boring model

Consider the most boring model for a quantity $y(t)$

$$\frac{dy}{dt} = \lambda$$

with initial condition $y(0) = y_0$.

What function of t has slope λ for every t ? The straight line

$$y(t) = y_0 + \lambda t$$

Birth process

Recall the basic birth process, where the rate of growth in $y(t)$ is proportional to $y(t)$ itself,

$$\frac{dy}{dt} = \lambda y(t)$$

with initial condition $y(0) = y_0$, which has solution

$$y(t) = y_0 e^{\lambda t}$$

and $y(t)$ increases “exponentially”.

Death process

The “death” process is the same, but we let $\lambda = -\mu < 0$. Then

$$\frac{dy}{dt} = -\mu y(t)$$

with initial condition $y(0) = y_0$, which has solution

$$y(t) = y_0 e^{-\mu t}$$

and $y(t)$ decreases “exponentially” to zero.

Logistic growth I

Recall the exponential growth model

$$\frac{dy}{dt} = \lambda y(t)$$

with initial condition $y(0) = y_0$. Its solution is $y(t) = y_0 e^{\lambda t}$. As $t \rightarrow \infty$, $y(t) \rightarrow \infty$. This unbounded growth may be unrealistic due to resource constraints.

Suppose K is the “carrying capacity” of the medium, and λ is the intrinsic growth rate as above. Consider the model

$$\frac{dy}{dt} = \lambda y(t) \left(1 - \frac{y(t)}{K} \right)$$

with initial condition $y(0) = y_0$.

Logistic growth II

Recall

$$\frac{dy}{dt} = \lambda y(t) \left(1 - \frac{y(t)}{K}\right)$$

When is $dy/dt = 0$? When either $y(t) = 0$ or $y(t) = K$.

- ▶ If $y(t) < K$, then $dy/dt > 0$ and the population size increases.
- ▶ If $y(t) > K$ then $dy/dt < 0$ and the population size decreases.

The solution can be written down precisely:

$$y(t) = \frac{Ky_0}{y_0 + (K - y_0)e^{-\lambda t}}$$

```

ts = seq(0,10,by=0.01)
lam = 0.5
K = 0.8
y0s = c(0.05, 0.2,0.5,1)
plot(0,
      type="n",
      xlim=range(ts),
      ylim=c(0,1),
      ylab="Number of bacteria y(t)",
      xlab="Time t",
      bty="n")
text(10, K, "K=0.8", pos=3)
abline(h=K, lty="dashed", col="gray")
for(y0 in y0s) {
  ys = K * y0 / (y0 + (K-y0)*exp(-lam*ts))
  lines(ts, ys)
  text(1,ys[100], bquote(y[0] == .(y0)), pos=1)
}

```

Logistic growth: SI model

Consider a population of N individuals where every individual is *susceptible* or *infected* with an infectious disease. Let $S(t)$ be the number of susceptibles, and let $I(t)$ be the number of infectives. Then the system is characterized by

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

where $N = S(t) + I(t)$. We can rewrite as

$$\frac{dI}{dt} = \beta I(t)(N - I(t))$$

where initially we have $I(0) = i_0$ infectives. The carrying capacity is $K = N$ and $\lambda = \beta$ and $y_0 = I(0)$ above.

SIR model

Consider a population of N individuals where every individual is *susceptible* or *infected* or *recovered*. Let $S(t)$ be the number of susceptibles, $I(t)$ be the number of infectives, $R(t)$ the number of recovered. Then the system is characterized by

$$\frac{dS}{dt} = -\beta S(t)I(t)$$

$$\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t)$$

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

with initial condition $S_0, I(0), R(0)$ and conservation equation $S(t) + I(t) + R(t) = N$. This system does not have a solution that is easy to write down, but it is easy to understand!

Lotka-Volterra predator-prey dynamics

Let $x(t)$ be the number of prey, and let $y(t)$ be the number of predators.

- ▶ Having abundant food, prey reproduce naturally in proportion (α) to their number
- ▶ Prey die (are eaten) in proportion (β) to the product of their abundance and the number of predators
- ▶ Predators reproduce in proportion (δ) to the product of their number and the number of prey they can eat
- ▶ Predators die in proportion to their number

$$\frac{dx}{dt} = \alpha x(t) - \beta x(t)y(t)$$

$$\frac{dy}{dt} = \delta x(t)y(t) - \gamma y(t)$$

with initial conditions $x(0)$ and $y(0)$.

Pharmacokinetic models

ODE systems

many compartments, harder to solve analytically.

ODE solvers

Lots of ODEs can't be solved analytically. For (well-behaved) systems that have a unique solution, it is often possible to solve for $y(t)$ numerically, without having any calculus-style analytic insight into the structure of the solution. There are very fast computer algorithms for doing this.

We will focus on methods implemented in standard software packages.

SIR solution

```
library(deSolve)
sir.model <- function (t, x, params) {
  S <- x[1]
  I <- x[2]
  R <- x[3]
  with( as.list(params), {
    dS <- -beta*S*I
    dI <- beta*S*I-gamma*I
    dR <- gamma*I
    dx <- c(dS,dI,dR)
    list(dx)
  })}

times <- seq(0,120,by=1)
params <- c(beta=0.4,gamma=1/7)
xstart <- c(S=9999/10000,I=1/10000,R=0)
out <- as.data.frame( lsoda(xstart, times, sir.model, par
plot(out$time, out$I, ylab="Population proportion", xlab=
```

Lotka-Volterra solution

```
library(deSolve)
lv.model <- function (t, x, params) {
  X <- x[1]
  Y <- x[2]
  with( as.list(params), {
    dX <- alpha*X - beta*X*Y
    dY <- delta*X*Y - gamma*Y
    dx = c(dX,dY)
    list(dx)
  })}

times <- seq(0,120,by=1)
params <- c(alpha=1.1,beta=0.4,delta=0.1,gamma=0.4)
xstart <- c(X=0.5,Y=0.6)
out <- as.data.frame( lsoda(xstart, times, lv.model, para
plot(out$time, out$X, ylab="Population proportion", xlab=
  type='l', bty="n", col="red")
lines(out$time, out$Y, col="blue")
```

Our general-purpose ODE solver

Explain lsoda

see also example in lsoda help page for Lotka-Volterra system
Runge-Kutta methods and RK4.

DEsolve: <https://daphnia.ecology.uga.edu/drakelab/wp-content/uploads/2014/07/deterministic-models.pdf>

How to model ODEs

Left-hand side: derivatives of the things that you want to change

Right-hand side: the rates of change

Example: constructing SIR dynamics

ODEs are most interesting when there are interactions between compartments.

More sophisticated models

Vital dynamics/demography more health/disease states age structure seasonal forcing

A brief caveat

[\[Back: Introduction to Modeling\]](#) [\[Home\]](#) [\[Next: Stochastic models\]](#)

References

Brauer, Fred, Carlos Castillo-Chavez, and Carlos Castillo-Chavez.
2001. *Mathematical Models in Population Biology and
Epidemiology*. Vol. 40. Springer.