



Tutorials and worked examples for simulation,
curve fitting, statistical analysis, and plotting.
<http://www.simfit.org.uk>

The standard epidemic differential equation model considers the interaction between susceptible, infected, and resistant individuals as a development of a Lotka-Volterra type of interaction.

For $y_1(x)$ susceptible, $y_2(x)$ infected, and $y_3(x)$ resistant individuals in the population as functions of time x the scheme is as follows

$$\begin{aligned} f_1 &= \frac{dy_1}{dx} = -p_1 y_1 y_2 \\ f_2 &= \frac{dy_2}{dx} = p_1 y_1 y_2 - p_2 y_2 \\ f_3 &= \frac{dy_3}{dx} = p_2 y_2 \end{aligned}$$

where p_1 and p_2 are positive parameters, and the additional parameters $p_3 = y_1(0)$, $p_4 = y_2(0)$ and $p_5 = y_3(0)$ are the initial conditions. Here the number of susceptible individuals declines as a result of contact between themselves and those already infected, the number of infected individuals increases as a result of such contacts but declines resulting from the development of resistance, while resistance increases in proportion to the number of those infected. Note that the overall population $Y(x) = y_1(x) + y_2(x) + y_3(x)$ remains static as will be obvious from the conservation equation

$$\begin{aligned} \frac{dY}{dx} &= \frac{dy_1}{dx} + \frac{dy_2}{dx} + \frac{dy_3}{dx} \\ &= 0 \end{aligned}$$

while the Jacobian matrix required for stiff systems is defined as follows.

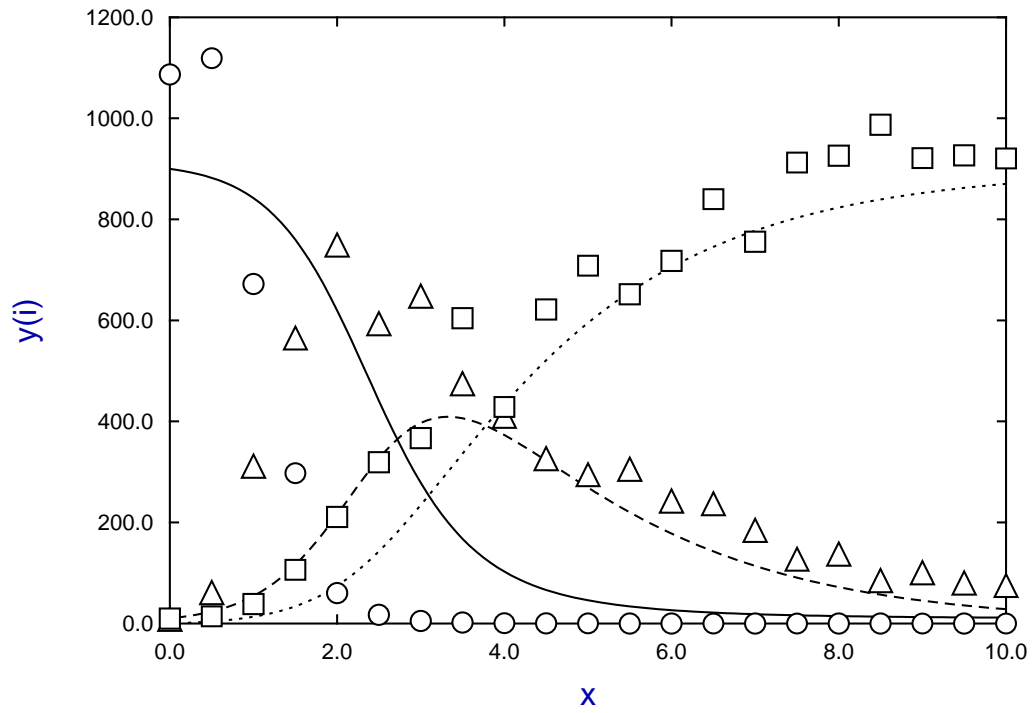
$$\frac{\partial f_i}{\partial y_j} = \begin{pmatrix} -p_1 y_2 & -p_1 y_1 & 0 \\ p_1 y_2 & p_1 y_1 - p_2 & 0 \\ 0 & p_2 & 0 \end{pmatrix}$$

Using SIMFIT program **deqsol** to fit the data contained in the default library file `epidemic.tfl` leads to the following results.

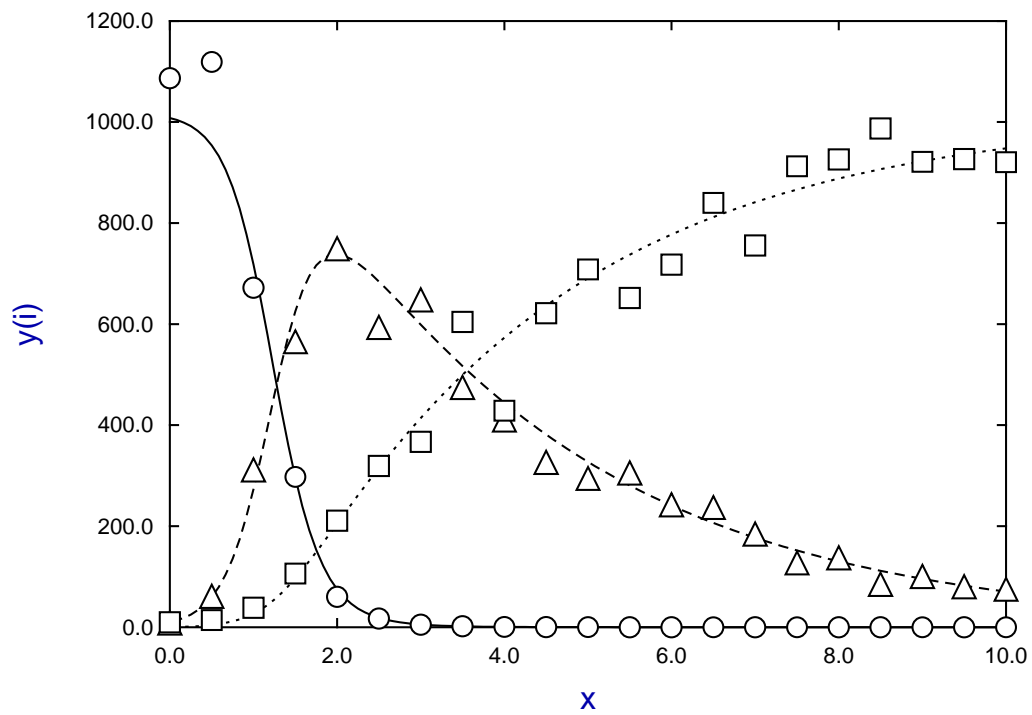
Best-fit parameters for the epidemic model							
Number	Low-Limit	High-Limit	Parameter	Std. Error	Lower95%cl	Upper95%cl	p
1	0	1	0.00389	0.00036	0.00355	0.00460	0.0000
2	0	2	0.30718	0.00919	0.28800	0.32558	0.0000
3	400	1400	1.00814	12.9747	982.169	1034.11	0.0000
4	0	50	10.2413	4.48755	1.25851	19.2241	0.0262
5	0	50	0.09828	0.09758	-0.09705	0.29361	0.3180 *

Note that the initial conditions were also fitted, and the nonzero p values for the corresponding estimates \hat{p}_4 and \hat{p}_5 indicates the unreliable nature of the fit to these parameters. The overlay before fitting, and then the final best-fit curve are displayed next, followed by the code for this model contained in the model file `deqmod3.tfl`.

Overlay of Initial Curves on Data



Data and Best-Fit Curves



```

%
differential equations: f(1) = dy(1)/dx = -p(1)y(1)y(2)
                      f(2) = dy(2)/dx = p(1)y(1)y(2) - p(2)y(2)
                      f(3) = dy(3)/dx = p(2)y(2)
y(1) = Susceptible, y(2) = Infected, y(3) = Resistant
Jacobian: j(1) = df(1)/dy(1) = -p(1)y(2)
          j(2) = df(2)/dy(1) = p(1)y(2)
          j(3) = df(3)/dy(1) = 0
          j(4) = df(1)/dy(2) = -p(1)y(1)
          j(5) = df(2)/dy(2) = p(1)y(1) - p(2)
          j(6) = df(3)/dy(2) = p(2)
          j(7) = df(1)/dy(3) = 0
          j(8) = df(2)/dy(3) = 0
          j(9) = df(3)/dy(3) = 0
initial condition: y0(1) = p(3), y0(2) = p(4), y0(3) = p(5)
%
3 equations
differential equation
5 parameters
%
begin{expression}
A = p(1)y(1)y(2)
B = p(2)y(2)
f(1) = -A
f(2) = A - B
f(3) = B
end{expression}
%
begin{expression}
C = p(1)y(2)
D = p(1)y(1)
j(1) = -C
j(2) = C
j(3) = 0
j(4) = -D
j(5) = D - p(2)
j(6) = p(2)
j(7) = 0
j(8) = 0
j(9) = 0
end{expression}
%
begin{limits}
  0    0.0025    1
  0    0.5       2
400  900       1400
  0    10        50
  0    0.1       50
end{limits}
begin{range}
121
0
10
end{range}

```