

# Differential equation models

## Interval methods and error analysis

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- Given a mathematical model with parameters and a set of measurements
- Try to show that
  - either  
no parameter value gives agreement with data
  - or  
there exist some parameters that give agreement with data



- Protein 1 is changed into Protein 2 with velocity  $v_1$ .
- Protein 2 is changed into something else with velocity  $v_2$

$$\dot{x}_1 = -v_1(x_1)$$

$$\dot{x}_2 = -v_2(x_2) + v_1(x_1)$$

$x_i$  protein concentration,  $v_i$  reaction velocity



$$\dot{x} = f(x, \theta), \quad y = h(x), \quad x(0) = x_0$$

- $x$  state vector (typically concentrations)
- $\theta$  parameter vector (typically reaction rates)
- $y$  measured variable



Suppose there are uncertain output measurements so that it is known that

$$y(t_i) \in I_i = [ \underline{I}_i, \bar{I}_i ], \quad i = 1, \dots, N$$

or equivalently

$$\underline{I}_i \leq y(t_i) \leq \bar{I}_i, \quad i = 1, \dots, N$$

The width of the intervals  $I_i$  define the measurement uncertainty.



- A model is rejected if there is no choice of parameter vector  $\theta$  for which all  $y(t_i)$  lie in the prescribed intervals.
- Usually  $\theta$  is required to lie in some prescribed set  $\Theta$ . (For instance reaction rates are positive.)



The model is simulated using an algorithm of the form

$$x_{k+1} = x_k + h_k \Phi(x_k, \theta, h_k)$$

(For an Euler method  $\Phi = f(x_k, \theta)$ )

For every measurement there are usually several time steps so that

$$h_1 + \dots + h_{N_i-1} = t_i \quad (1)$$

- Thus  $x_{N_i}$  is an approximation of  $x(t_i)$ .



If the parameters lie in a box:

$$\underline{\theta}_i \leq \theta_i \leq \overline{\theta}_i$$

then the equation

$$x_{k+1} = x_k + h_k \Phi(x_k, \theta, h_k)$$

can be used together with interval arithmetic to compute an outer approximation of the solution:

$$\underline{x}_k \leq \theta_k \leq \overline{x}_k$$





The approximation error over a time interval  $T$  is

$$\|E\| \leq h^p \frac{C'}{L} (e^{LT} - 1)$$

- $L$  is the logarithmic norm of  $f_x$
- $Ch^{p+1}$  is the error from one step.  $C$  is an expression in the derivatives of  $f$  and depends on  $\theta$ . For most numerical methods (e.g. Runge-Kutta of various orders) it can be calculated explicitly.



Now define the extended intervals

$$I_i^e = [\underline{y}_i, \overline{y}_i] = [\underline{I}_i - C_{N_i}, \overline{I}_i + C_{N_i}]$$

Consider the numerical solution  $y_i = h(x_i)$

- If  $y_i \notin I_i^e$  then  $y(t_i) \notin I_i$ .
- Using interval calculations this rejection criterion can be extended to all parameter values in a box.



Similarly one can define contracted intervals

$$I_i^c = [\underline{y}_i^c, \overline{y}_i^c] = [\underline{I}_i + C_{N_i}, \overline{I}_i - C_{N_i}]$$

- If  $y_i \in I_i^c$  then  $y(t_i) \in I_i$ .
- Using interval calculations this acceptance criterion can be extended to all parameters in a box.



- Protein 1 is changed into Protein 2 with velocity  $\theta_1 x_1$ .
- Protein 2 is changed into something else with velocity  $\theta_2 x_2$

$$\dot{x}_1 = -\theta_1 x_1$$

$$\dot{x}_2 = -\theta_2 x_2 + \theta_1 x_1$$

In matrix form:

$$\dot{x} = \underbrace{\begin{bmatrix} -\theta_1 & 0 \\ \theta_1 & -\theta_2 \end{bmatrix}}_A x$$



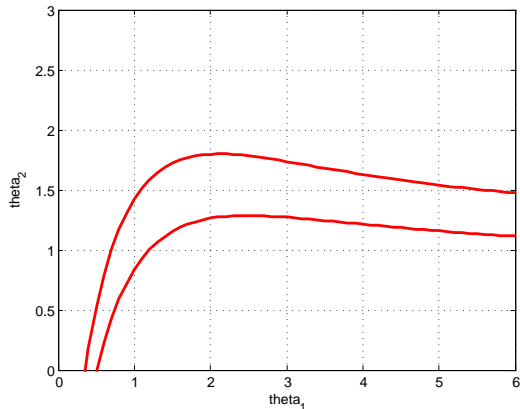
With initial state  $x(0) = (1 \ 0)^T$

$$y(t) = x_2(t) = \frac{\theta_1}{\theta_1 - \theta_2} \left( e^{-\theta_2 t} - e^{-\theta_1 t} \right)$$

$y$  is measured.



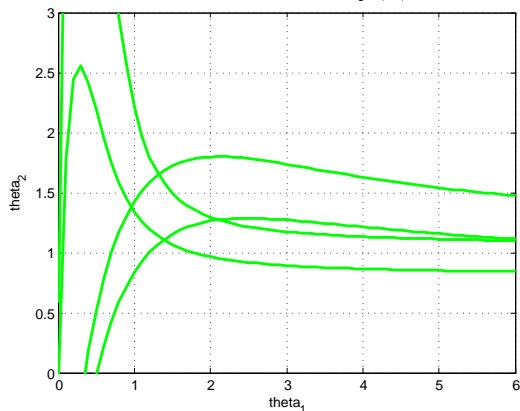
Supposer we know that  $0.3 \leq y(1) \leq 0.4$



The parameters are restricted to a strip in  $\theta_1 - \theta_2$ -space.



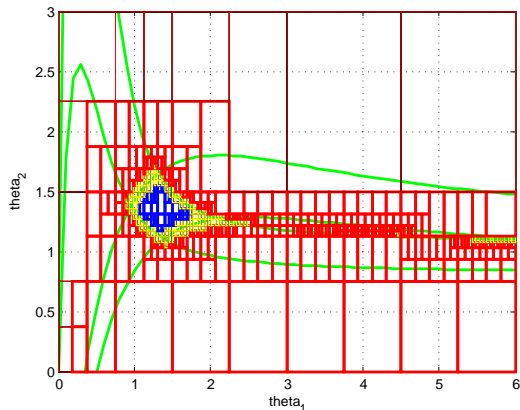
Suppose we know that  $0.3 \leq y(1) \leq 0.4$  and  $0.015 \leq y(4) \leq 0.04$



The exact solution can only be calculated in very special cases. Instead one can use the numerical solution and interval calculations to tile the parameter space into boxes in which the model is either rejected or accepted.







red rectangles: rejected  
blue rectangles: accepted  
yellow rectangles: undecided



Using interval arithmetic together with numerical differential equation solvers it is possible to rigorously accept or reject models at least in simple examples.

