
Dynamic Models in Biology, Computer Lab:

Parameter fitting: tumor growth data and model

In this lab, you will fit (made-up) data on tumor growth to determine parameters in a model.

1. Tumor growth

Model

Verhulst growth is described by:

$$\dot{x} = k_1x - k_2x^2,$$

where k_1 and k_2 are positive parameters.

Dynamics

Find the fixed points, sketch the phase space dynamics, and sketch trajectories.

Seems familiar?

The above should be familiar to you. Verhulst growth is the same as the logistic equation

$$\dot{x} = rx(1 - x/K).$$

Verhulst growth, or logistic growth, was originally developed (by Pierre-François Verhulst) to model population growth under conditions where there is competition for resources. The model is widely used for bacterial growth and has been used as a theoretical model for the growth of tumors.

Analytical solution

The *logistic function*

$$x(t) = \frac{\alpha}{\beta + \exp^{-\gamma t}},$$

is a solution to the model, with $k_1 = \gamma$ and $k_2 = \frac{\beta\gamma}{\alpha}$. (If you enjoy differentiation and algebra, you may show this by direct substitution of this equation into the differential equation).

Data and parameter estimation

The data file `tumor_growth_data.txt` contains made-up data mimicking the growth of

spherical tumor nodules grown in tissue. Modify the Matlab program `fitting_example.m` to fit a logistic function to this data. Run your program to get values for the parameters α , β , and γ .

Compute and plot the residuals. Any signs of trouble in the residuals?

Generate a QQ plot. Any signs of trouble in this plot?

Use the estimated values of α , β , and γ to determine k_1 and k_2 . Then use numerical integration to simulate the original differential equation and compare the simulated results to the data.