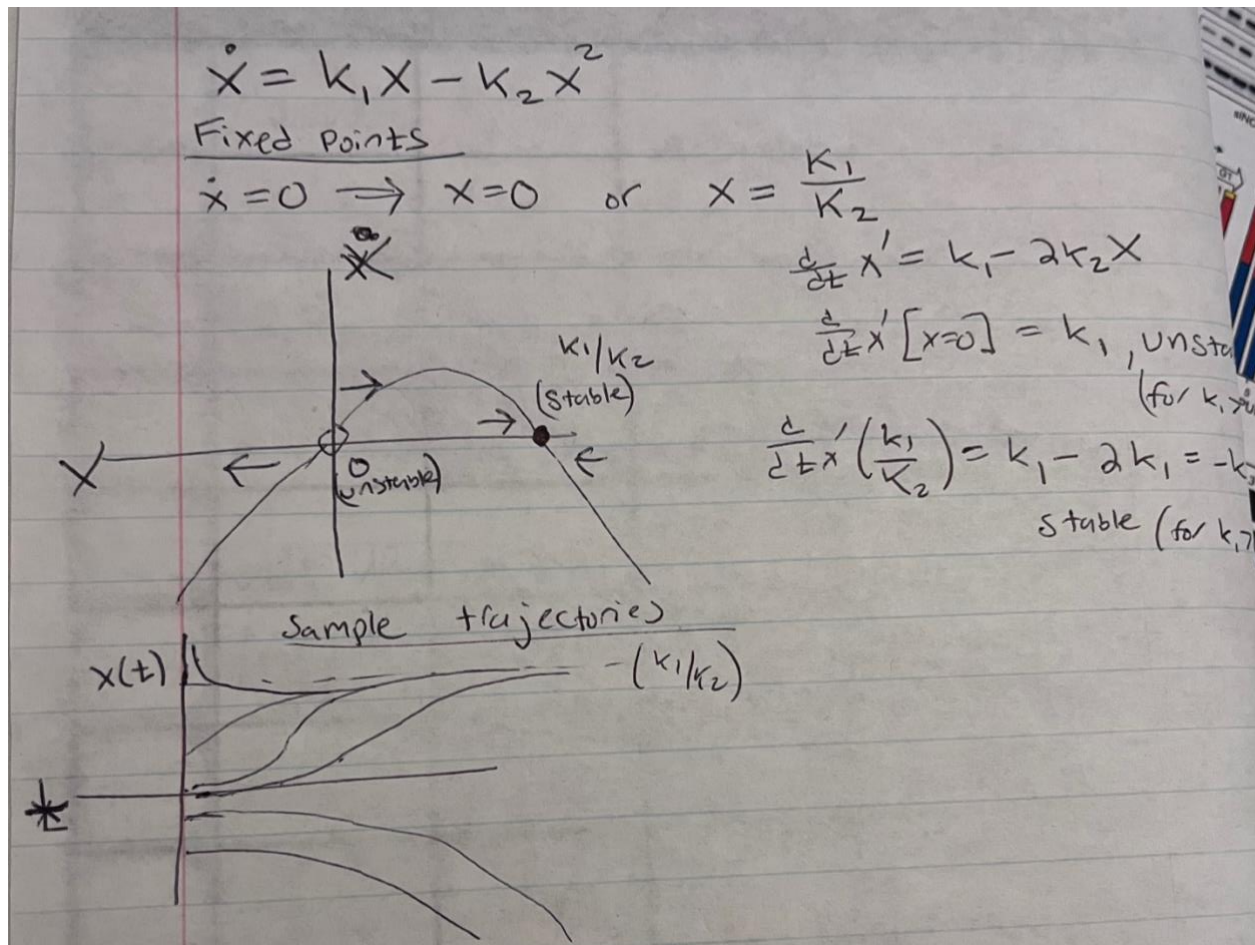


Dynamic Models in Biology

Lab 7

Jonathan Levine

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$$\text{let } J(t) = \beta + e^{-\gamma t}$$

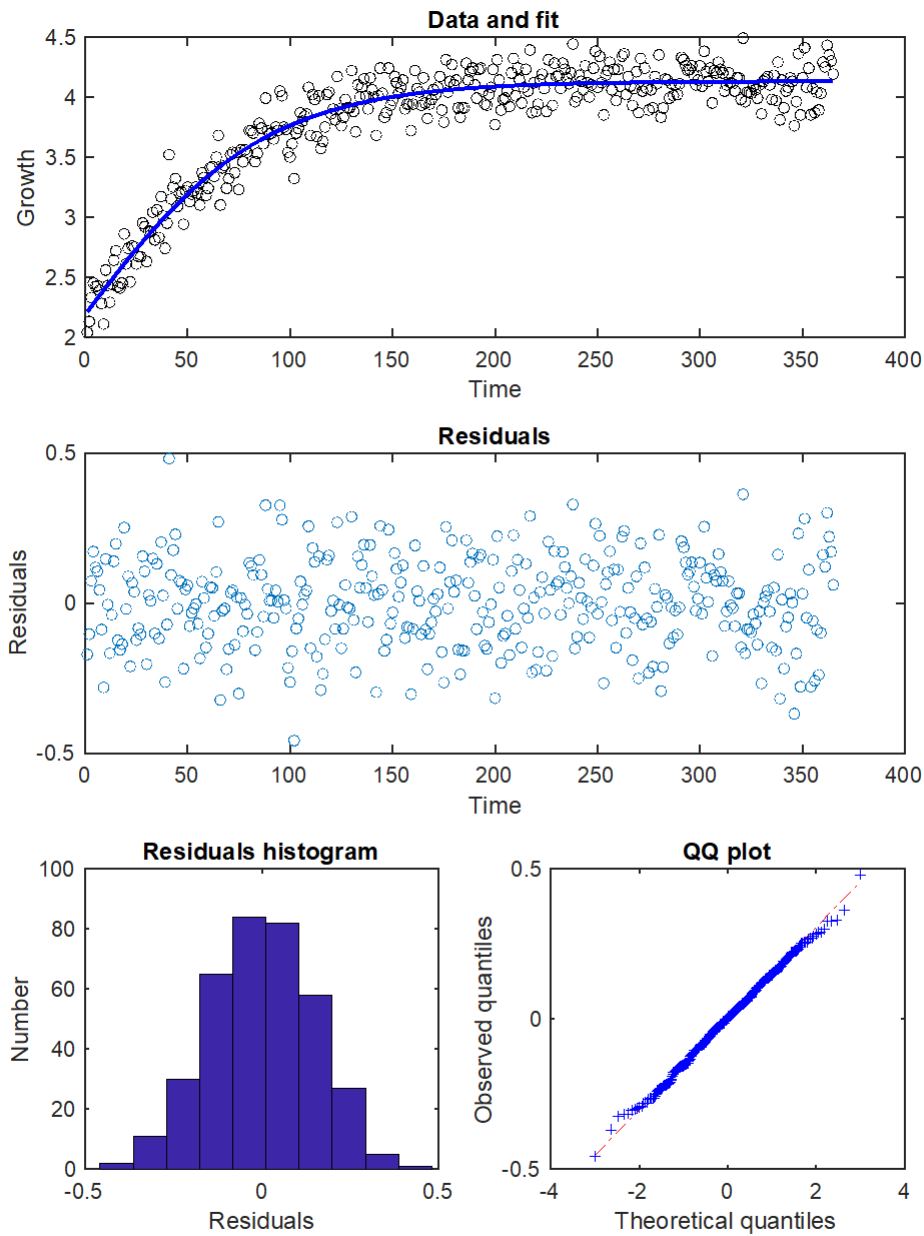
$$J'(t) = \gamma e^{-\gamma t}$$

$$x(t) = \frac{\alpha}{J(t)}$$

$$x'(t) = \alpha \frac{\gamma e^{-\gamma t}}{J(t)^2}$$

$$\dot{x} = k_1 x - k_2 x^2 = \frac{\alpha \gamma}{J(t)} - \frac{\beta \gamma \alpha}{J(t)^2} = \frac{J(t) \alpha \gamma - \beta \gamma \alpha}{J(t)^2} = \frac{\alpha \gamma \beta + \alpha \gamma e^{-\gamma t} - \alpha \gamma \beta}{J(t)^2} = \alpha \frac{\gamma e^{-\gamma t}}{J(t)^2} \blacksquare$$

You can see the model fits the data very well, and the residuals are normally distributed and the QQ plot looks good (points mostly along the unity line in red)



From this fit we get values for the parameters:

$$\alpha = 4.6536, \quad \beta = 1.1267, \gamma = 0.0221$$

This gives us $k_1 = 0.0221, k_2 = 0.0053$

Using these parameters to integrate over the relevant time interval (below) you can see that the least squares approach and the model integration are both good fits for the data, and are basically the same as each other. They differ slightly because of their initial condition (i.e. y intercept value) which is off by about .2 units in $x(t)$. If you vary the initial condition of the simulation, you would get fits of varying quality to the data (and if you set the intercept to exactly the logistic function at time 0 you would get a perfect fit to the least squares fit, because the parameters were taken from there).

