Question 1

Consider a gene whose protein product inhibits its own transcription:

If m is the amount of mRNA and p is the amount of protein product of this gene, then a simplified system of linear differential equations for this system is:

$$\frac{dm}{dt} = \alpha_0 - m - \alpha \cdot p$$

$$\frac{dp}{dt} = \beta(m - p)$$

In this model, α_0 represents the basal level of mRNA production, α represents the degree to which the protein product inhibits the mRNA production, and β represents the speed of the feedback control that regulates protein levels. As with a similar model developed in the course, we'll assume that β is sufficiently large that mRNA and protein are effectively always in equilibrium, so m = p. Thus:

$$\frac{dm}{dt} = \alpha_0 - m - \alpha \cdot m$$

What is/are the steady state solutions for this model?

Draw a one dimensional phase portrait for this model.

For what parameter values is/are the steady state solution(s) stable? Explain.

For what parameters values is the model biologically reasonable? Explain.

Question 2

The concentration of sucrose recorded in a chemostat is shown in the figure below. An exponentially decaying oscillation is apparent.
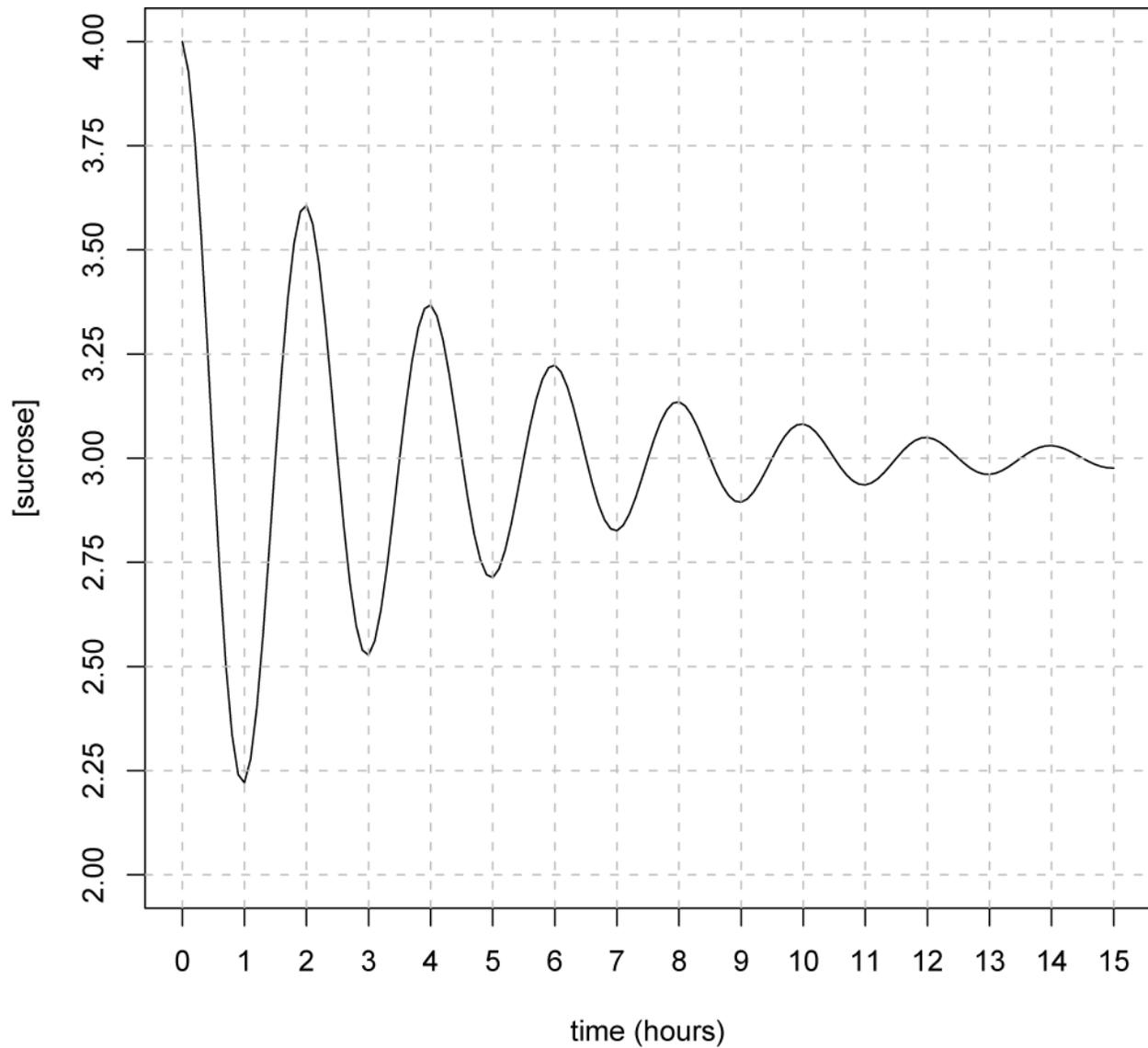
Estimate the period of the oscillation?

Estimate the time constant of the decay?

Assuming that the experimental system could be reasonably represented as a system of linear differential equations, estimate one eigenvalue that the system would be expected to have. Explain your reasoning.

Question 3

In the Hodgkin-Huxley model, potassium and sodium channels are modeled as bi-state channels that are either open or closed.

$$O \underset{\beta}{\overset{\alpha}{\rightleftharpoons}} C$$
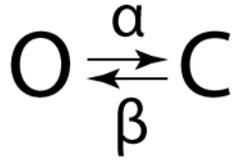
It appears that we should be able to write linear differential equations such as…

$$\frac{dC}{dt} = -\beta C + \alpha O$$

$$\frac{dO}{dt} = \beta C - \alpha O$$

…and solve these systems analytically by computing the eigenvectors and eignevalues of the resultant matrix.

Why can't this approach be used?

Are there any experimental conditions where a model of such a system be solved analytically? Explain?

Question 4

In a biomarker study, you have used qPCR to determine the transcription levels of five candidate genes across many samples. You analyze this data using principal components analysis in Matlab, which reports that the eigenvalues of the covariance matrix are…

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0.8450
0.8620
0.9756
1.0253
1.0614
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Do the results of the PCA suggest that you can reduce the amount of data that you need to analyze? Why or why not? How would you proceed?