Assignment 2: Figures and tables

Patient Alpha

Most likely sequence of hidden states for AGCGC: ['?', 'E', 'E', 'E', 'E']

Table 1: Viterbi probabilities for Patient Alpha's observed sequence AGCGC, where E=Exon and I=Intron

	t=0	t=1	t=2	t=3	t=4
Exon	0.125000	0.028125	0.006328	0.001424	**0.000320**
Intron	0.200000	0.008000	0.000960	0.000038	0.000021

Table 2: Backpointer indices for Patient Alpha's observed sequence AGCGC, where E=Exon and I=Intron

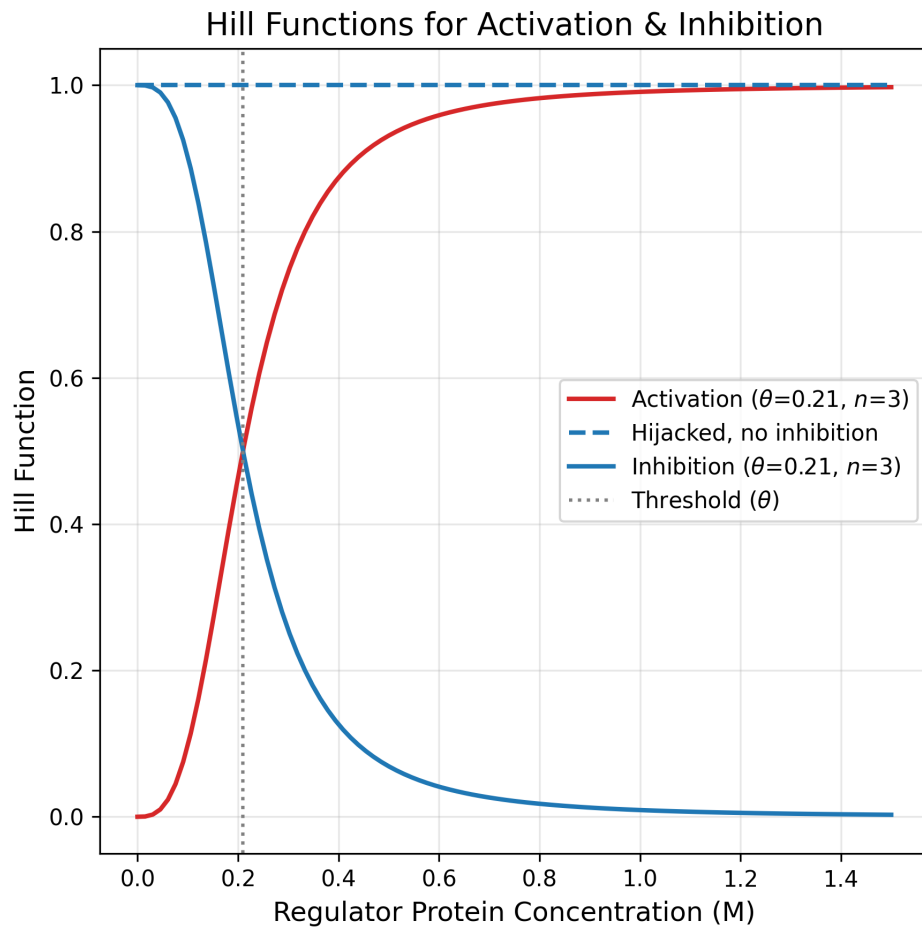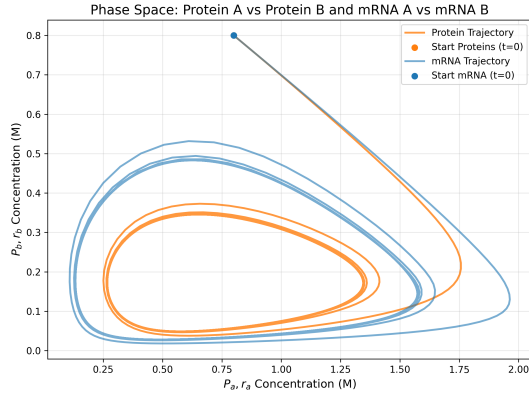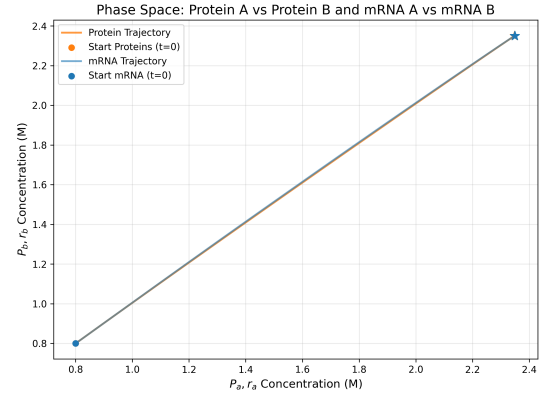|	t=0	t=1	t=2	t=3	t=4
Exon	?	**E**	**E**	**E**	**E**
Intron	?	I	I	I	E

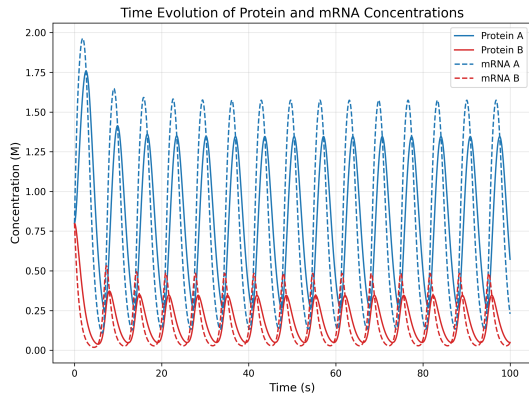Figure 1: Activation and Inhibition Hill Functions
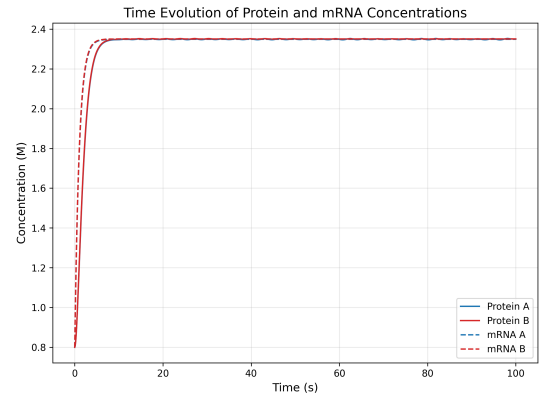
(a) Healthy State

(b) Hijacked State

Figure 2: Phase Portrait of Proteins and mRNAs concentrations for Patient Alpha
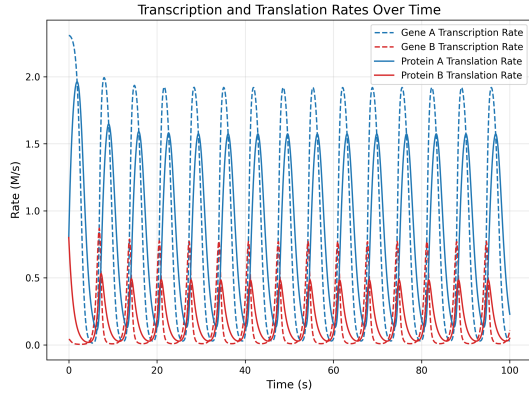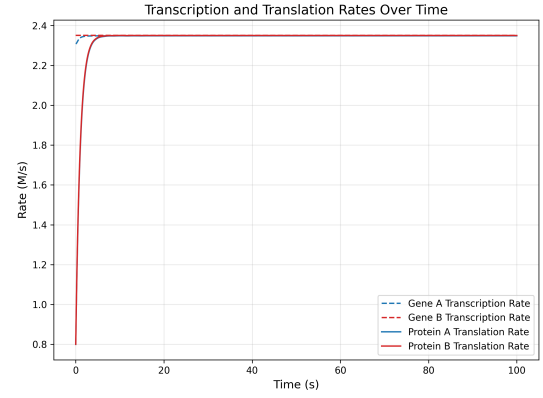

(a) Healthy State

(b) Hijacked State

Figure 3: Concentration of Proteins and mRNAs overtime for Patient Alpha

(a) Healthy State

(b) Hijacked State

Figure 4: Translation and Transcription Rates overtime for Patient Alpha

Healthy states results were validated against Polynikis A, Hogan SJ, di Bernardo M. Comparing different ODE modelling approaches for gene regulatory networks. *J Theor Biol.* 2009;261(4):511-530. doi:10.1016/j.jtbi.2009.07.040

Patient Beta

Most likely sequence of hidden states for AUUAU: ['?', 'I', 'I', 'I', 'I']

Table 3: Viterbi probabilities for Patient Beta's observed sequence AUUAU, where E=Exon and I=Intron

	t=0	t=1	t=2	t=3	t=4
Exon	0.125000	0.028125	0.006328	0.001424	0.000328
Intron	0.200000	0.064000	0.020480	0.006554	**0.002097**

Table 4: Backpointer indices for Patient Beta's observed sequence AUUAU, where E=Exon and I=Intron

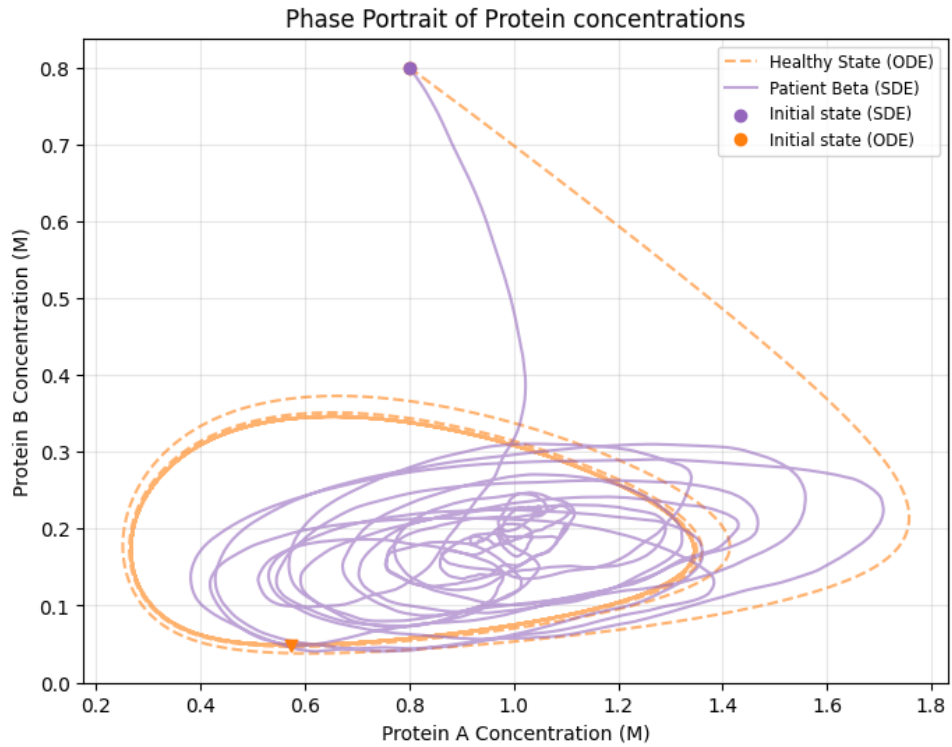|	t=0	t=1	t=2	t=3	t=4
Exon	?	E	E	E	I
Intron	?	**I**	**I**	**I**	**I**

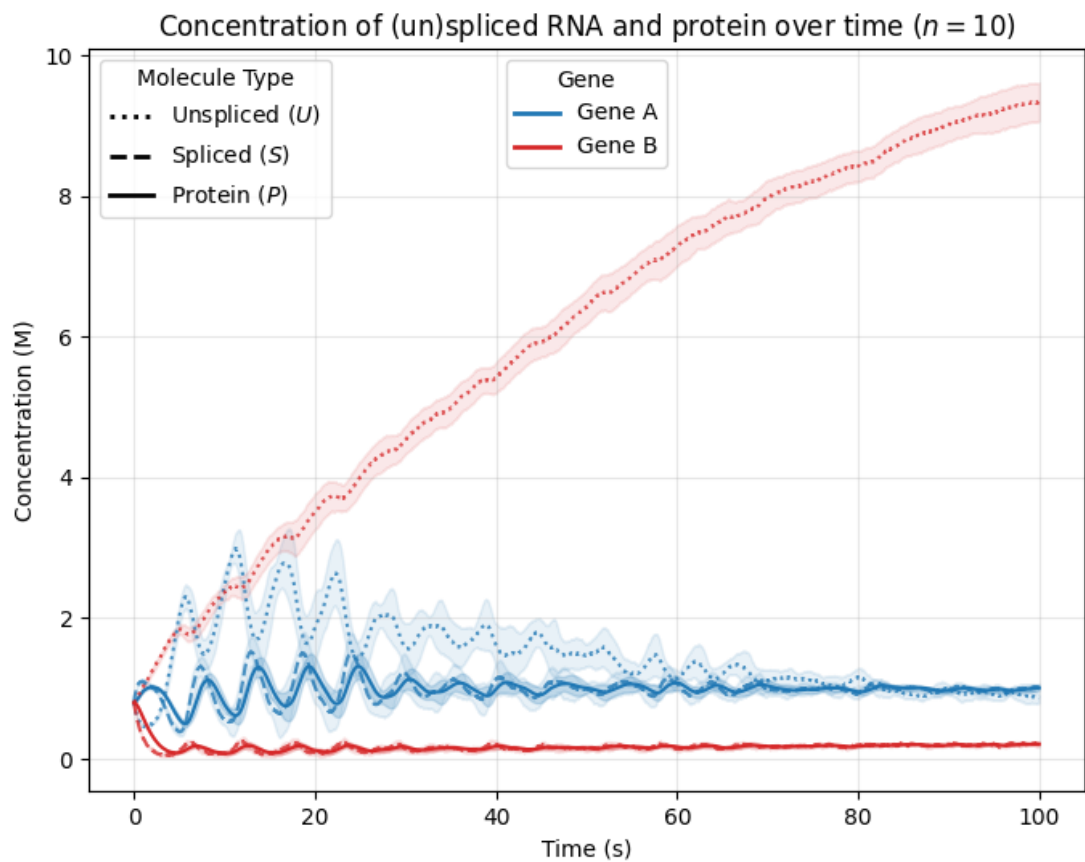Figure 5: Phase Portrait of the Protein concentrations of Patient Beta

Figure 6: Comparison of the (average) concentration of protein over time from ODE versus 10 SDEVelo simulations with 95% confidence interval
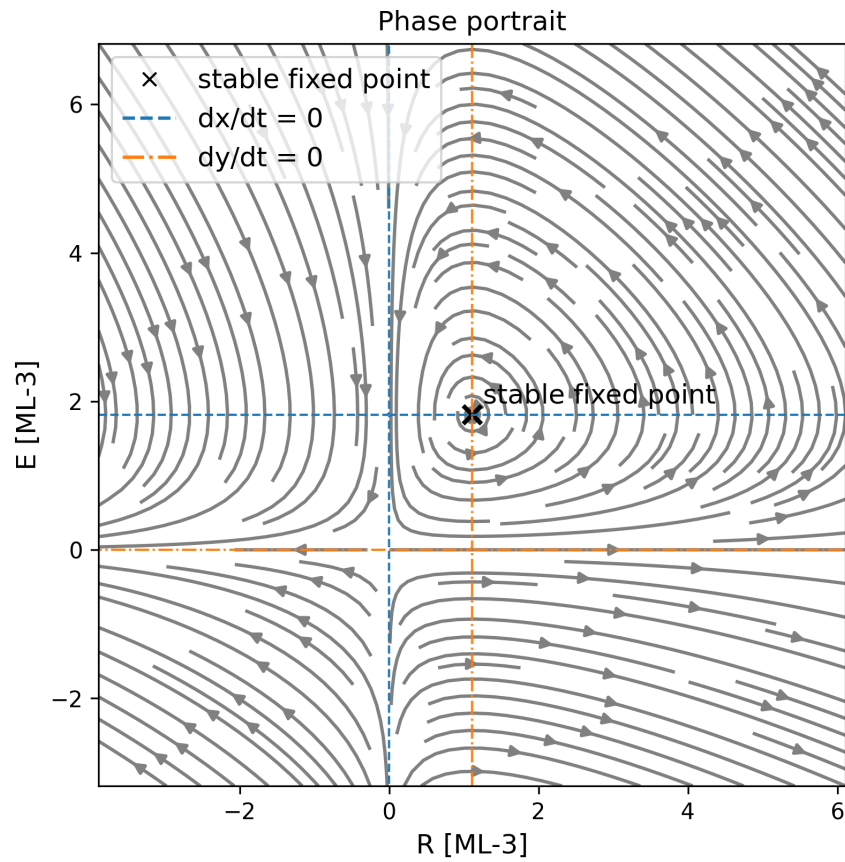
Figure 7: Stream plot with equilibrium point and nullclines for interaction between metabolite R, and growth-promoting enzyme E