

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 |

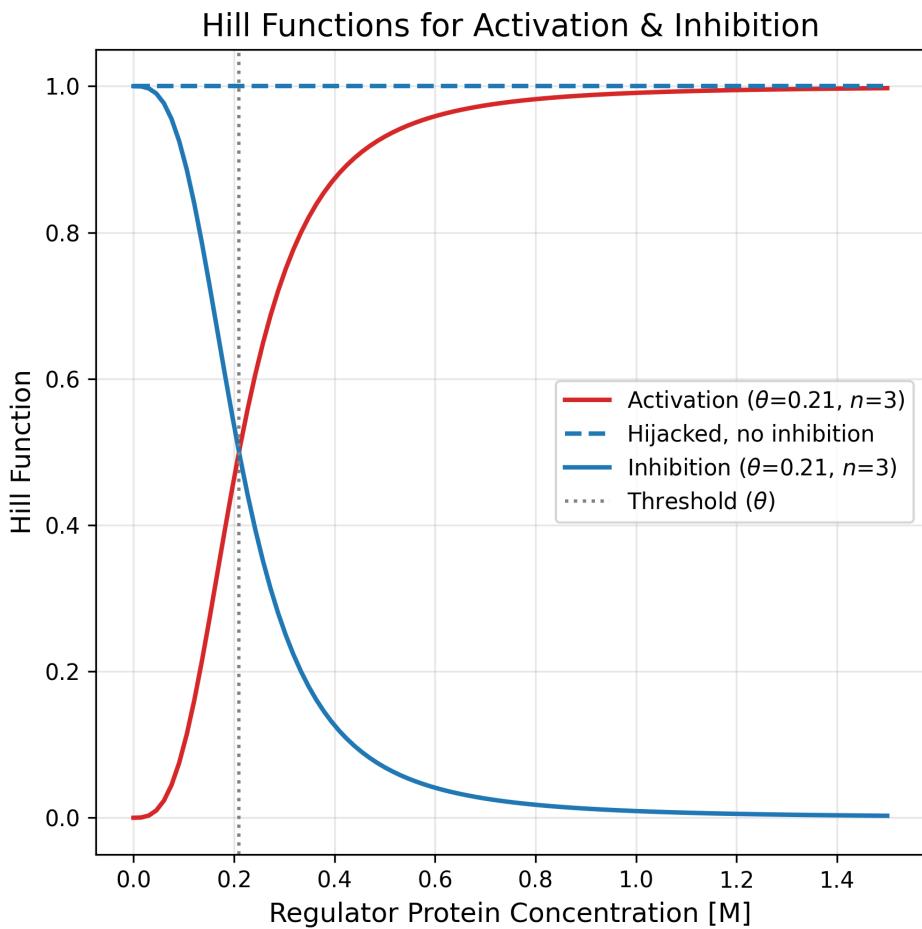


Figure 1: Activation and Inhibition Hill Functions

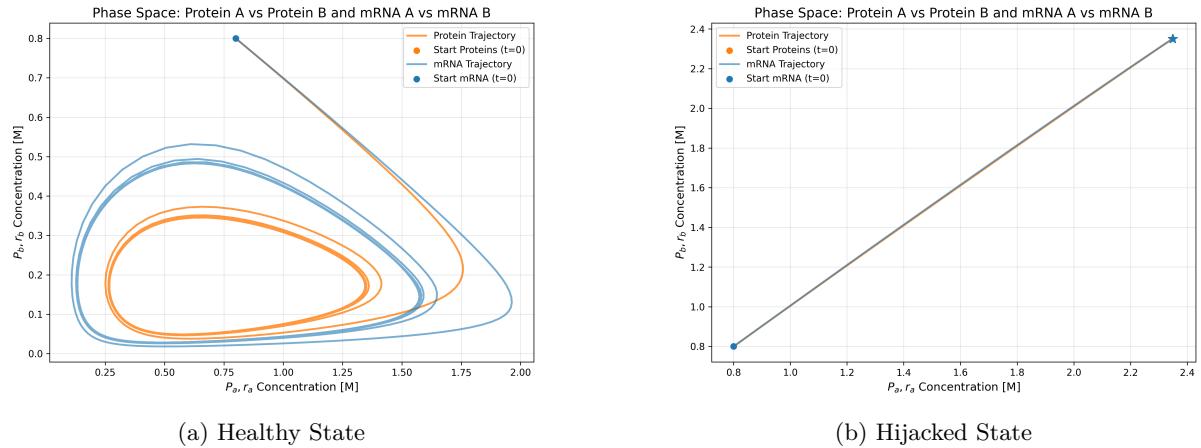


Figure 2: Phase Portrait of Proteins and mRNAs concentrations for Patient Alpha

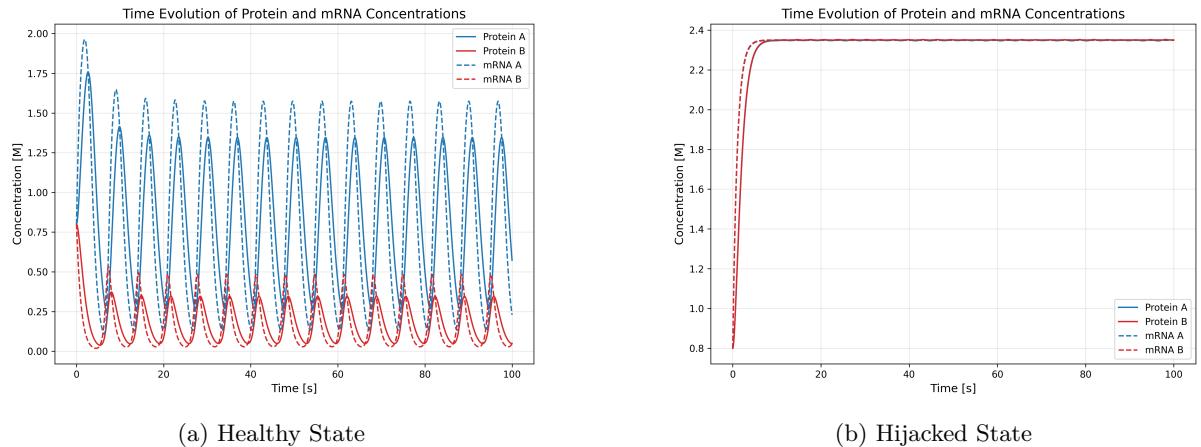


Figure 3: Concentration of Proteins and mRNAs overtime for Patient Alpha

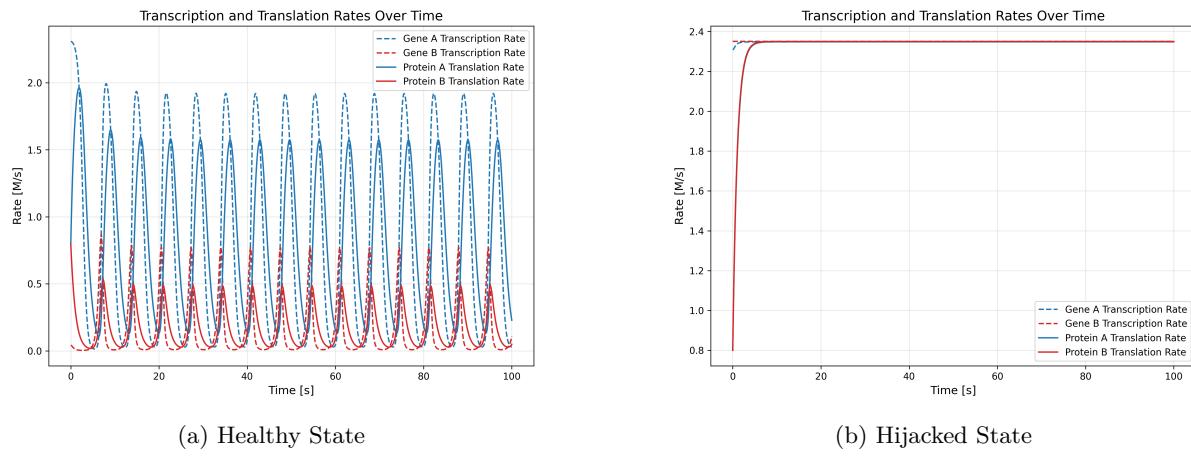


Figure 4: Translation and Transcription Rates overtime for Patient Alpha

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 |

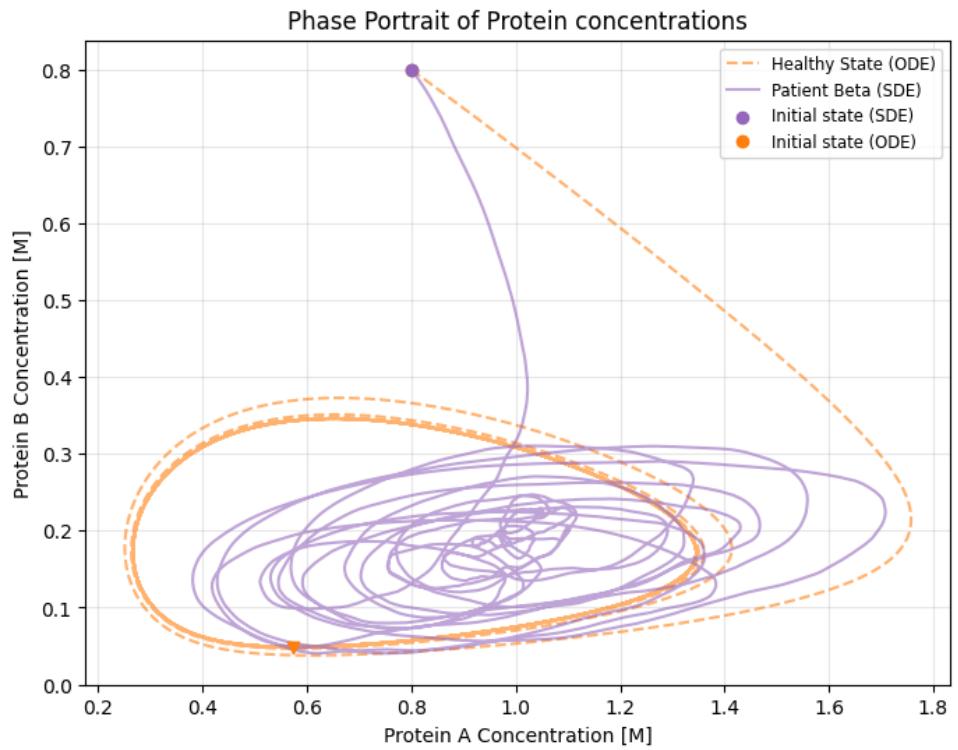


Figure 5: Phase Portrait of the Protein concentrations of Patient Beta

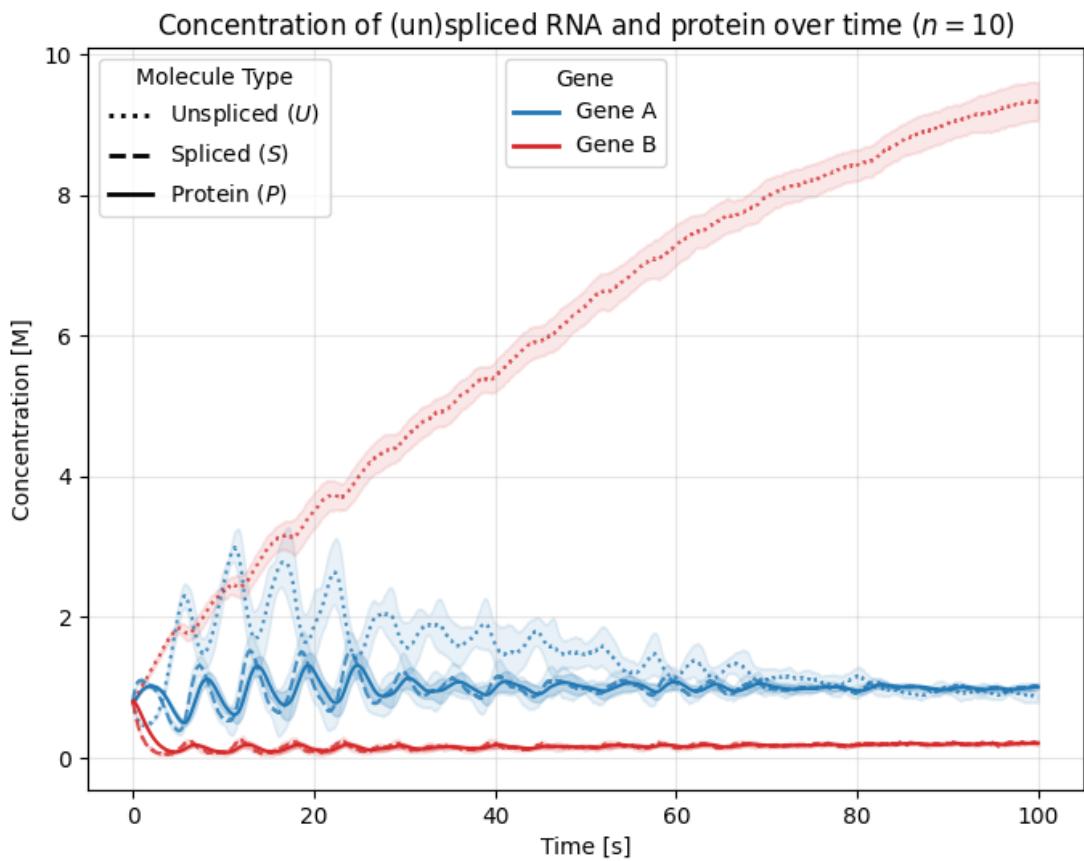


Figure 6: Comparison of the (average) concentration of protein over time from ODE versus 10 SDEVelo simulations with 95% confidence interval

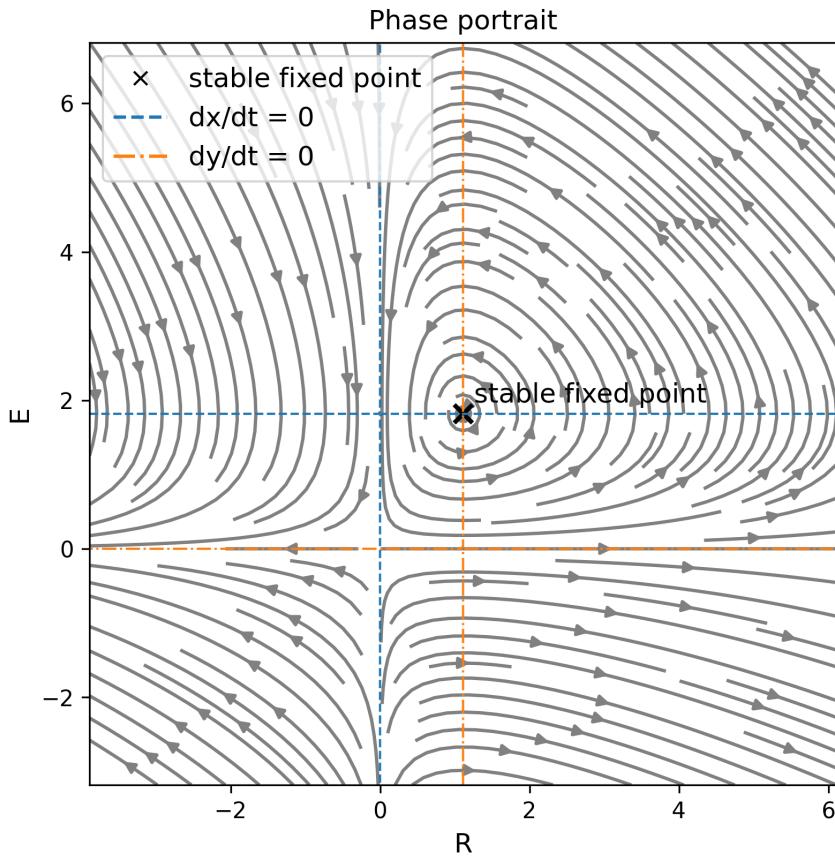


Figure 7: Stream plot with equilibrium point and nullclines for interaction between metabolite R , and growth-promoting enzyme E