Report

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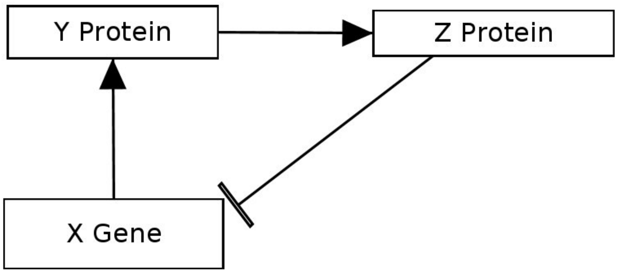
1 Introduction

Introduction to the article goes here Introduction to the article goes here

2 The Model

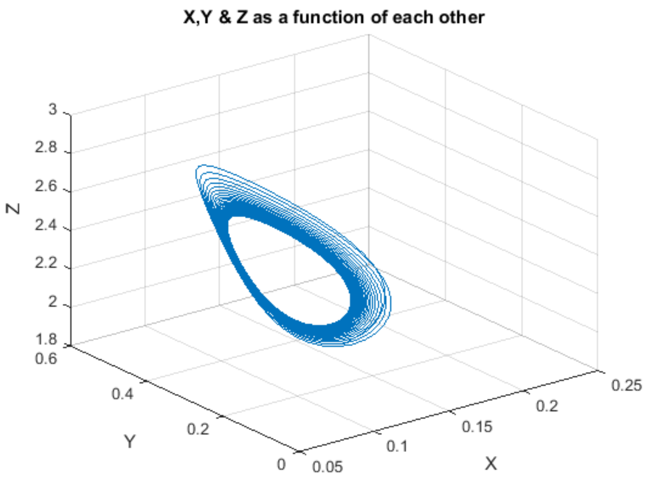


(a) One-Cell Model
The gene X codes for protein Y which, in turn, activates transcriptional inhibitor Z. The resulting model behaves as a three-variable oscillator.

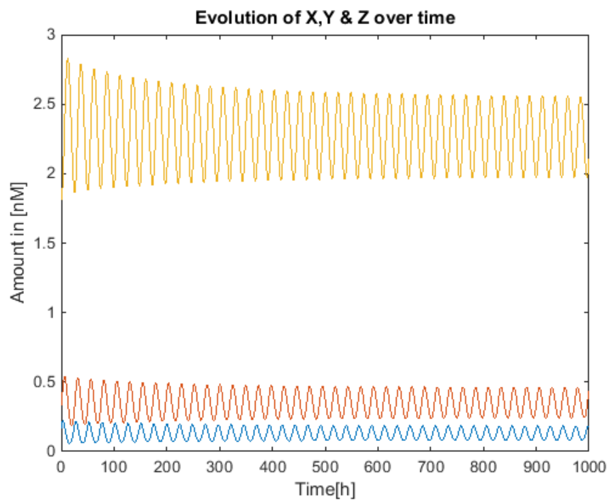
$$\frac{\delta X}{\delta t} = v_1 \frac{K_1^n}{K_1^n + Z^n} - v_2 \frac{X}{K_2 + X}$$
$$\frac{\delta Y}{\delta t} = k_3 X - v_4 \frac{Y}{K_4 + Y}$$
$$\frac{\delta Z}{\delta t} = k_5 Y - v_6 \frac{Z}{K_6 + Z}$$

(b)

v_1	this is
v_2	
k_3	
v_4	
k_5	
v_6	

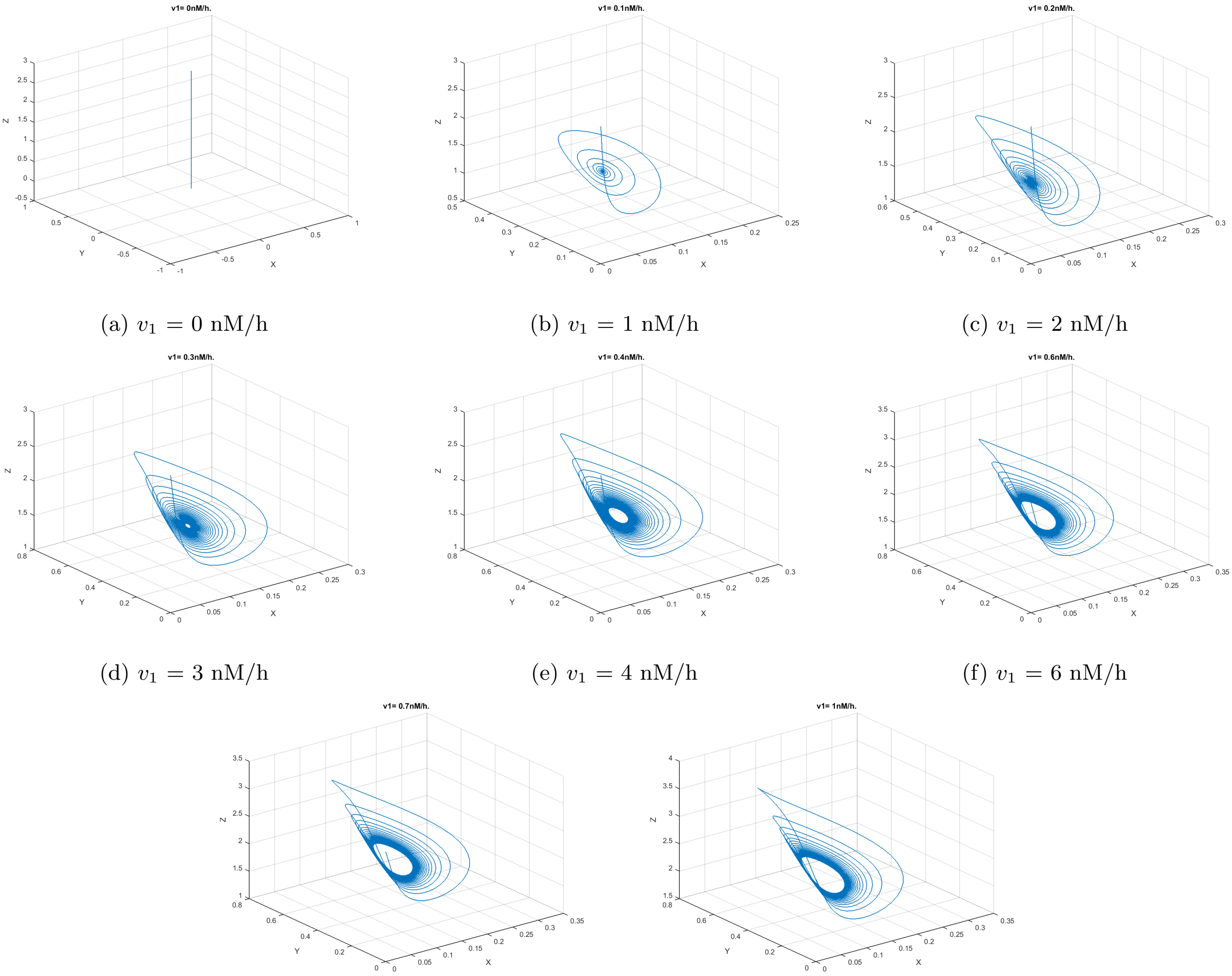


(a) Trajectories
The limit cycle is reached as the variations of $X(t)$, $Y(t)$ and $Z(t)$ become fixed : The trajectories converge, non-lineary (the distance between similar trajectories aren't regular) towards an ellipse (where the blue stripes accumulate)



(b) Frequency spectrum
The amplitude of the three variations stabilize after a few hundred hours. The signal are not in phase but have the same, regular, frequencies.

Figure 2:
Trajectories of $X(t)$, $Y(t)$ and $Z(t)$ when using initial conditions : $X_0 =$, $Y_0 =$, $Z_0 =$
We observe on both graphs that $Z(t)$ has the bigger amplitude of variation whereas $X(t)$ and $Y(t)$ have small amplitudes. Additionaly, the convergence towards a single loop in (a) indicate that the frequencies of the signals are equal; this is illustrated as well in (b)



(a) $v_1 = 0$ nM/h

(b) $v_1 = 1$ nM/h

(c) $v_1 = 2$ nM/h

(d) $v_1 = 3$ nM/h

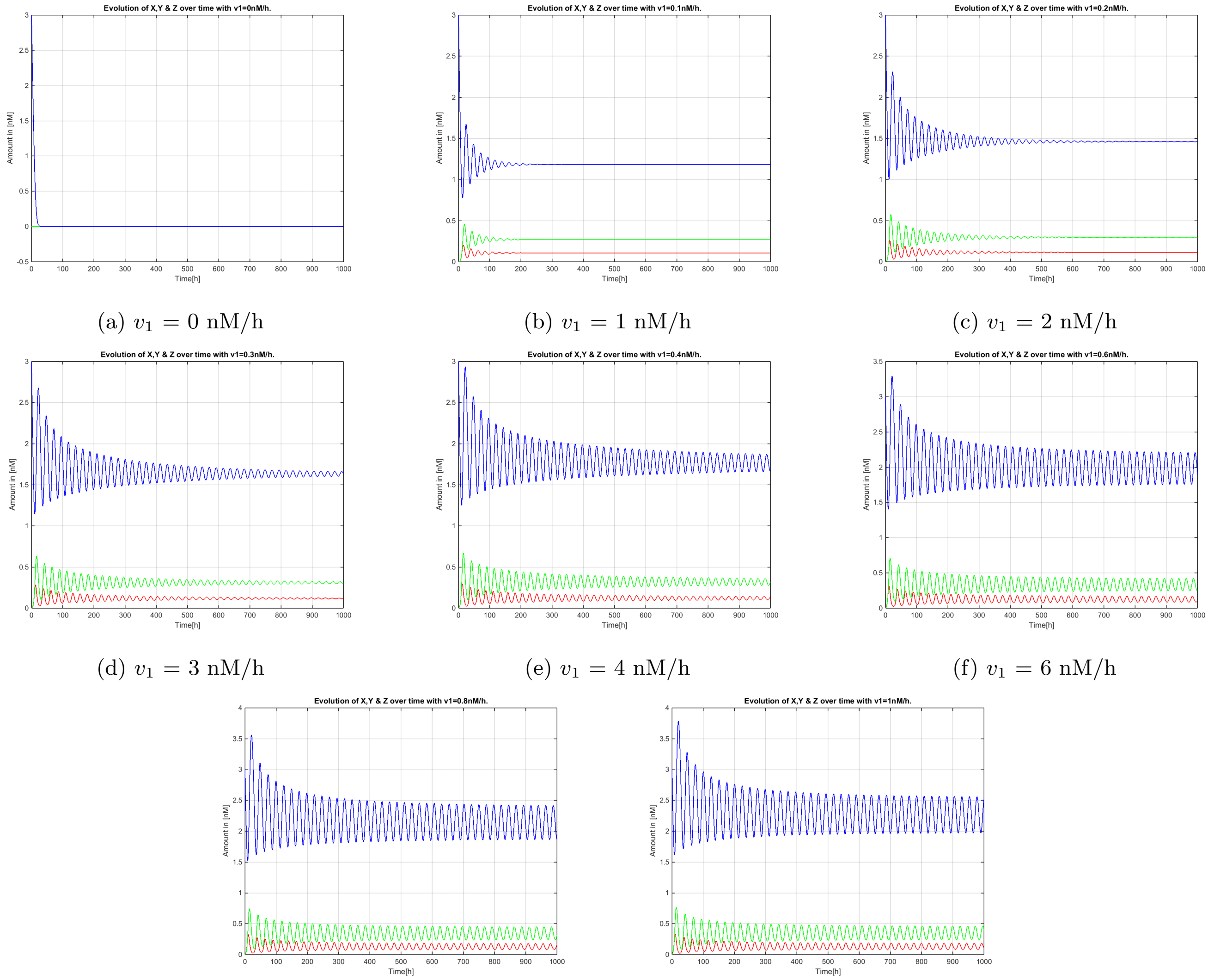
(e) $v_1 = 4$ nM/h

(f) $v_1 = 6$ nM/h

(g) $v_1 = 8$ nM/h

(h) $v_1 = 10$ nM/h

Figure 3: With nice initial conditions



(a) $v_1 = 0$ nM/h

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(e) $v_1 = 4$ nM/h

(f) $v_1 = 6$ nM/h

(g) $v_1 = 8$ nM/h

(h) $v_1 = 10$ nM/h

Figure 4: With nice initial conditions

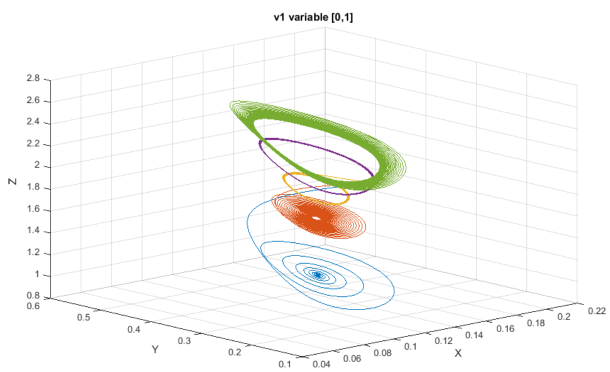
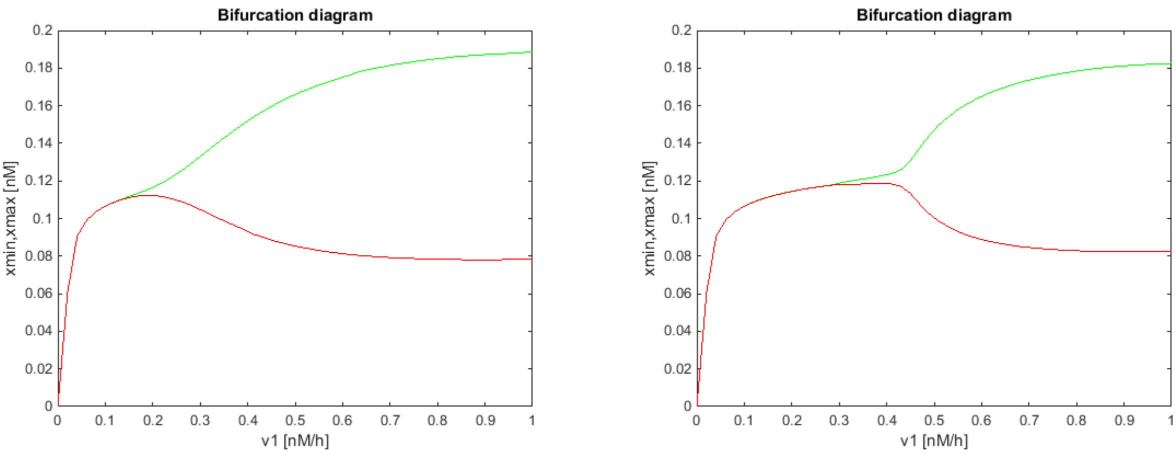


Figure 5: $v_1 = 0.1/0.3/0.5/0.7/0.9$ nM/h



(a) at $h_{max} = 1000$

(b) at $h_{max} = 10000$

Figure 6: Bifurcation Diagram
plotted at time intervals : $[9/10; 1]$ of h_{max}