

Report

École Polytechnique Fédérale de Lausanne, Switzerland

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1 Introduction

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2 The Model

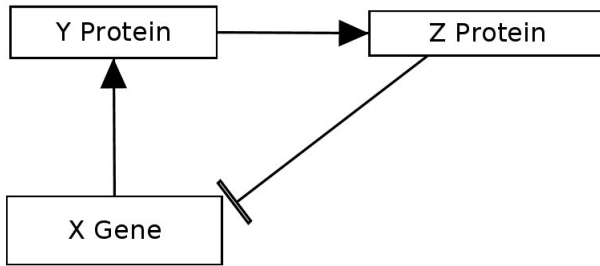


Figure 1: One-Cell Model

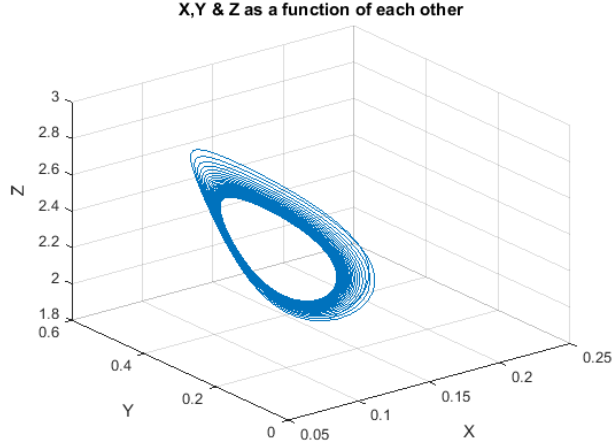
The gene X codes for protein Y which, in turn, activates transcriptional inhibitor Z . The resulting model behaves as a three-variable oscillator.

$$\frac{\delta X}{\delta t} = v_1 \frac{K_1^n}{K_1^n + Z^n} - v_2 \frac{X}{K_2 + X}$$

$$\frac{\delta Y}{\delta t} = k_3 X - v_4 \frac{Y}{K_4 + Y}$$

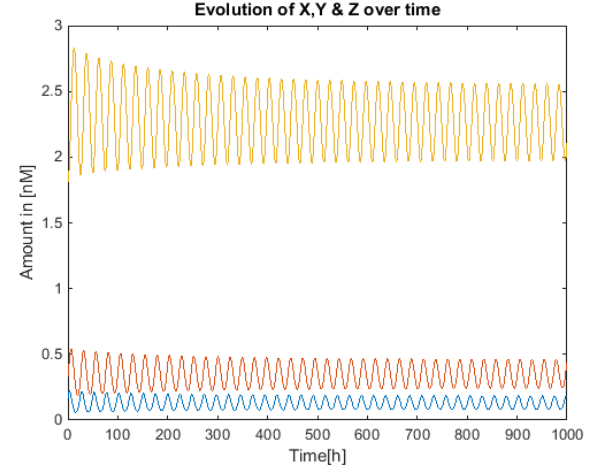
$$\frac{\delta Z}{\delta t} = k_5 Y - v_6 \frac{Z}{K_6 + Z}$$

$$v_1$$



A/A11.png

(a) Trajectories

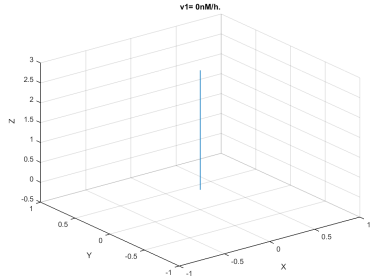


A/A12.png

(b) Frequency spectrum

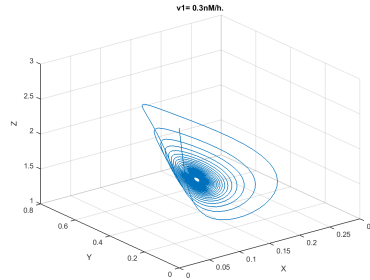
Figure 2: With nice initial conditions

A/LotsofthesameA/A-AA0.png



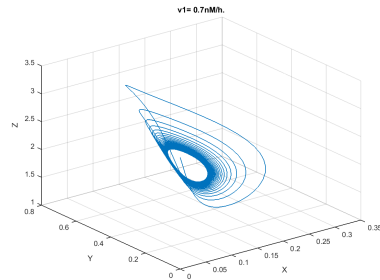
(a) $v_1 = 0$ nM/h

A/LotsofthesameA/A-AA3.png



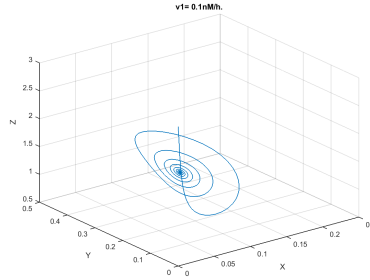
(d) $v_1 = 3$ nM/h

A/LotsofthesameA/A-AA7.png



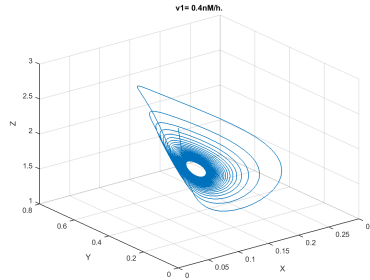
(g) $v_1 = 8$ nM/h

A/LotsofthesameA/A-AA1.png



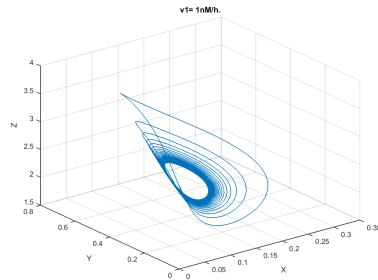
(b) $v_1 = 1$ nM/h

A/LotsofthesameA/A-AA4.png



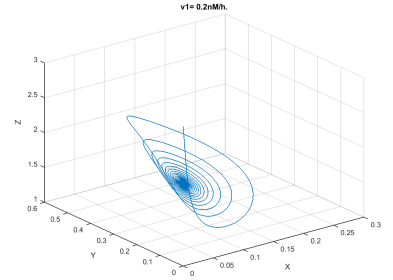
(e) $v_1 = 4$ nM/h

A/LotsofthesameA/A-AA10.png



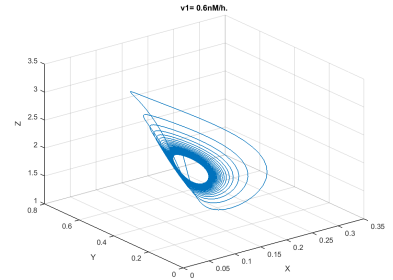
(h) $v_1 = 10$ nM/h

A/LotsofthesameA/A-AA2.png



(c) $v_1 = 2$ nM/h

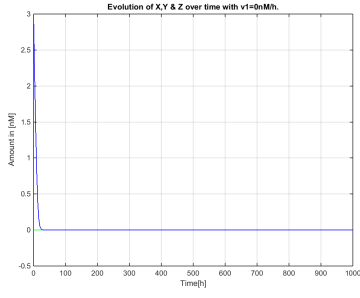
A/LotsofthesameA/A-AA6.png



(f) $v_1 = 6$ nM/h

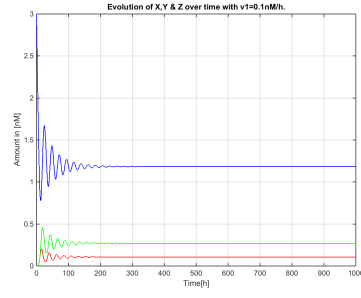
Figure 3: With nice initial conditions

A/LotsofthesameA/A-A0.png



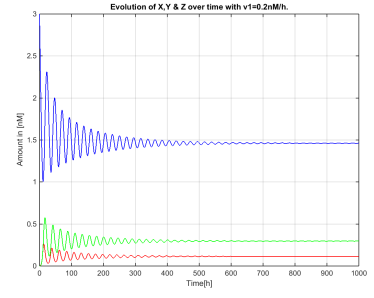
(a) $v_1 = 0$ nM/h

A/LotsofthesameA/A-A1.png



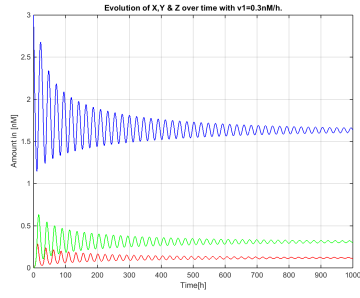
(b) $v_1 = 1$ nM/h

A/LotsofthesameA/A-A2.png



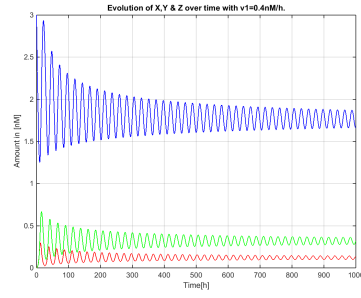
(c) $v_1 = 2$ nM/h

A/LotsofthesameA/A-A3.png



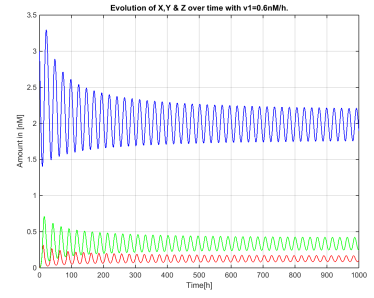
(d) $v_1 = 3$ nM/h

A/LotsofthesameA/A-A4.png



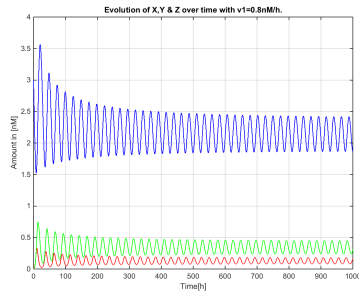
(e) $v_1 = 4$ nM/h

A/LotsofthesameA/A-A6.png



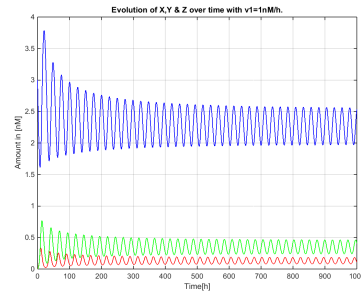
(f) $v_1 = 6$ nM/h

A/LotsofthesameA/A-A8.png



(g) $v_1 = 8$ nM/h

A/LotsofthesameA/A-A10.png



(h) $v_1 = 10$ nM/h

Figure 4: With nice initial conditions

A/A2.png

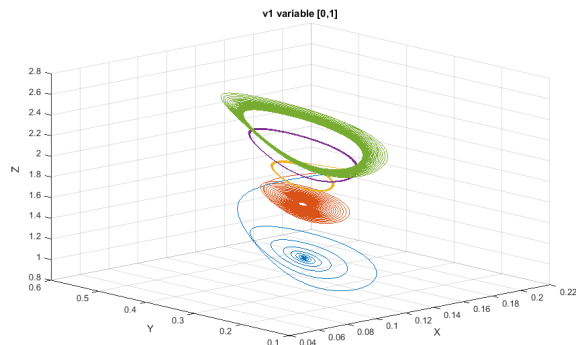


Figure 5: $v_1 = 0.1/0.3/0.5/0.7/0.9$ nM/h

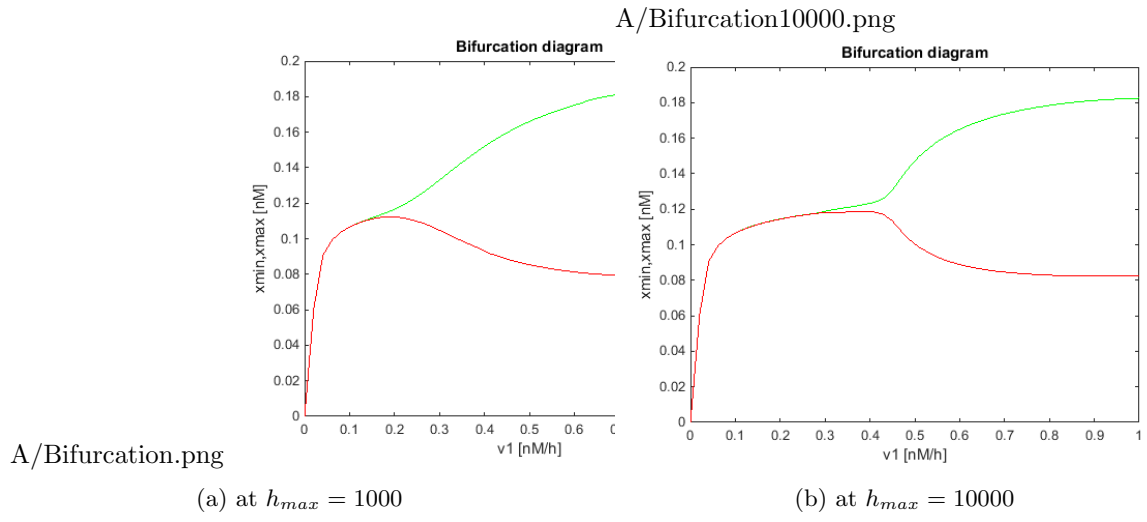


Figure 6: Bifurcation Diagram
 plotted at time intervals : $[9/10; 1]$ of h_{max}