Figure 2.1 A Boolean model of our typical negative autoregulatory circuit. Just as we saw in Figure 1.3, our system encapsulates a gene, transcription into mRNA, translation into protein, activation of the protein by an external factor, and transcriptional repression (blunt arrow) following DNA-protein interaction. For simplicity, this Boolean model represents translation and activation as a single process called "translation".
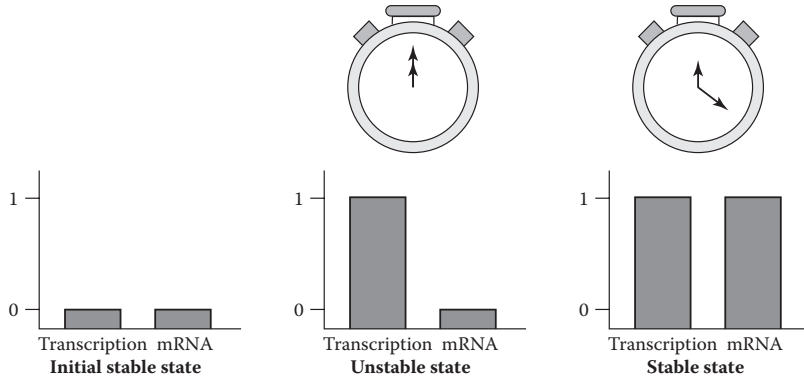
Figure 2.2 Stable and unstable states in the Boolean framework. The system is originally in a stable state, where the values of Transcription and mRNA are equal. At time = 0 (shown schematically with a stopwatch), the value of Transcription increases to 1. This state is unstable because the mRNA value is not yet equal to the Transcription value; however, after some time, the mRNA value increases to 1, and the result is a stable state.

Inputs

		Gene	Activator
		0	0
Initial conditions	mRNA 0	Trs	Trl
	Protein 0	0	0

Processes (calculated)

Figure 2.3 The state matrix for our negative autoregulatory circuit when neither gene nor protein is present in the system. The values for the variables Gene, Activator, Transcription (Trs), Translation (Trl), Protein, and mRNA are shown. This system is stable under the conditions depicted in the matrix.

Figure 2.4 An expansion of the initial state matrix of our typical negative autoregulatory circuit. This expansion depicts the change in the system when the initial conditions include the presence of protein. The updated step appears at the bottom of the figure, and the transition and stable state are highlighted by the red arrow and red box, respectively. Abbreviations are as in Figure 2.3.

Inputs

		Gene	Activator
		0	0
mRNA	0	Trs	Trl
Protein	0	0	0
	0	0	0
	1		
	1	0	0
	1		
	1	0	0
	0		

Initial conditions

Figure 2.5 Full expansion of the initial state matrix of our typical negative autoregulatory circuit. This state matrix has now been fully expanded for the input (Gene = 0, Activator = 0). Only one stable state occurs for this system. Notations and abbreviations are as in Figure 2.3.

Inputs

		Gene	Activator
		0	1
mRNA	0	Trs	Trl
Protein	0	0	0
	0	0	0
	1		
	1	0	1 —1
	1		
	1	0	1 —1
	0		

Initial conditions

2

Figure 2.6 The state matrix for our typical negative autoregulatory circuit when (Gene = 0, Activator = 1). Our circuit has only one stable state possible, regardless of the presence of activator. However, the dynamics differ from the case in which activator is absent (Figure 2.5). Notations and abbreviations are as in Figure 2.3.
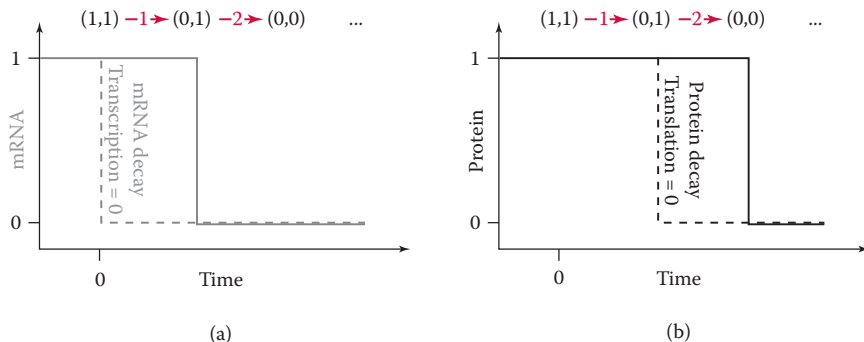
Figure 2.7 Dynamic plots of the system, with initial conditions of (mRNA = Protein = 1, Gene = 0). The arrows and numbers (mRNA, Protein) above are for direct comparison with the corresponding trajectory in Figure 2.6. (a) At time = 0, Transcription is set to 0, and after some time, the mRNA decays from the system. (b) This decay causes the value of Translation to be set to 0, and after some time, the protein is lost as well.
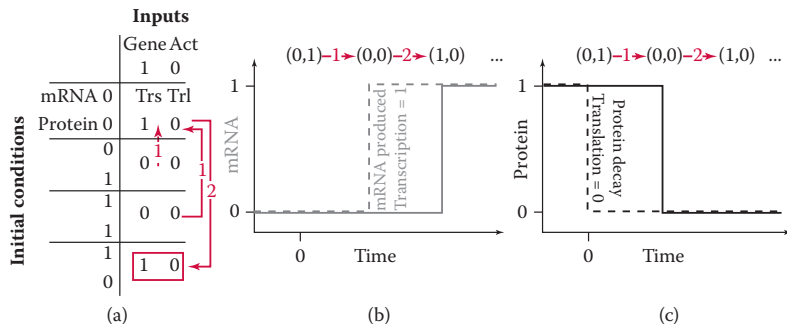
Figure 2.8 Solution to Practice Problem 2.1: the state matrix and dynamic plot for our typical negative autoregulatory circuit when (Gene = 1, Activator = 0). (a) This state matrix shows that the stable state of our system has changed compared to the stable states in Figures 2.3–2.6. Notations and abbreviations are as in Figure 2.3. (b), (c) Dynamics plots of system behavior with initial conditions of (mRNA = 0, Protein = 1).

Inputs

		Gene	Act	Gene	Act	Gene	Act	Gene	Act
		0	0	0	1	1	0	1	1
mRNA	0	Trs	Trl	Trs	Trl	Trs	Trl	Trs	Trl
Protein	0	0	0	0	0	1	0	1	0
	0 / 1	0	0	0	0	0	0	0	0
	1 / 1	0	0	0	1	0	0	0	1
	1 / 0	0	0	0	1	1	0	1	1

(left axis label) Initial conditions

Start: add Act

Figure 2.9 The complete state matrix for our typical negative autoregulatory circuit, including the case in which (Gene = 1, Activator = 1). This solution to Practice Problem 2.2 reveals that, under these conditions, our circuit has no stable state. The trajectory specific to (Gene = 1, Activator = 1) is highlighted in red; abbreviations are as in Figure 2.3.
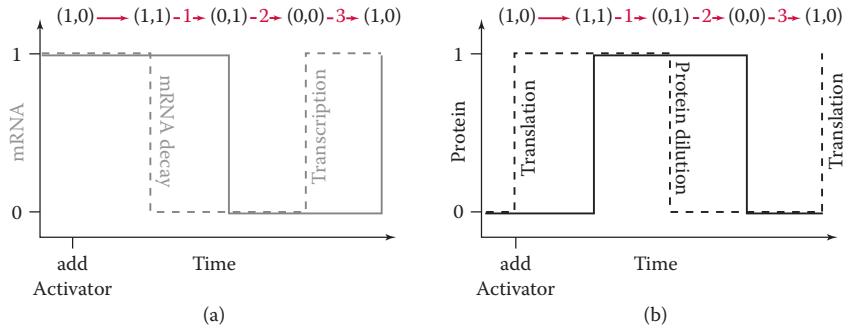
002x009.eps

Figure 2.10 The dynamics over time for the (a) mRNA and (b) Protein variables from Figure 2.9. The corresponding transitions in the state matrix appear at the top. mRNA decay and protein dilution are inferred in the absence of transcription (gray dashed line) and translation (black dashed line), respectively.
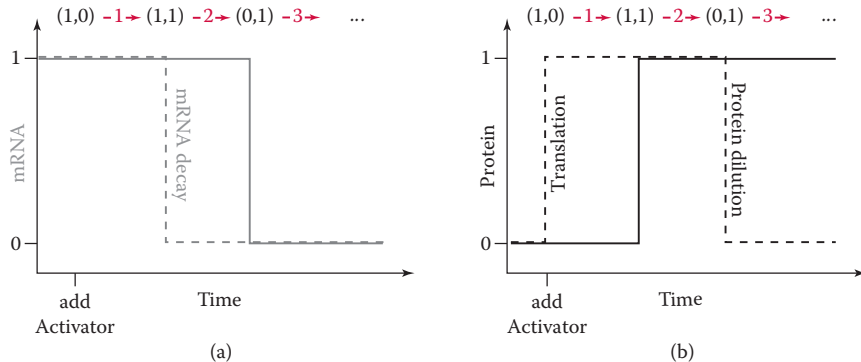
Figure 2.11 Adding the timescale information to the dynamics over time shown in Figure 2.10. Notice the loss of cyclical behavior within a few *E. coli* generations. Symbols and notation are as in Figure 2.10.

002x011.eps