1 Exercise 8

Using the next reaction method, simulate and plot a single trajectory of the model in Example 6.3 with $\kappa_1 = 200$, $\kappa_2 = 10$, $d_M = 25$, $d_p = 1$, an initial condition of 1 gene, 10 mRNA, and 50 protein molecules, and a terminal time of T = 8.

This model yields the four reaction vectors:

$$\xi_1 = (0, 1, 0), \ \xi_2 = (0, 0, 1), \ \xi_3 = (0, -1, 0), \ \xi_4 = (0, 0, -1).$$

2 Exercise 11

Let

$$\xi_1 = (-1, 1, 0)$$
 and $\xi_2 = (0, -1, 1)$,

and let X_n^{θ} be a discrete time Markov chain on $\mathbb{Z}^3_{\geq 0}$ with the following transition probabilities:

$$p_{\vec{x},\vec{x}+\xi_1} = \frac{\theta xy}{\theta xy + y} \tag{1}$$

$$p_{\vec{x}, \vec{x} + \xi_2} = 1 - p_1(x, y, z), \tag{2}$$

Assume that $X_0^{\theta}=(100,5,0)$ and $\theta=0.05$. Let $f(X^{\theta})=\left(X_1^{\theta}\right)_{100}$; that is the first component of the process after 100 steps. We estimate $\frac{d}{d\theta}E\left[f(X^{\theta})\right]$ using a number of different techniques.

2.1 Finite Difference Method

In this problem, we employ a centered finite difference method using the estimator

$$\hat{\mu}_k^{\theta,h} = \frac{f(X_k^{\theta+h/2}) - f(X_k^{\theta-h/2})}{h}.$$

In an attempt to reduce the variance, we employ the common random variables technique; in which we will use the same sequence of uniform random variables when generating relizations $X_k^{\theta+h/2}$ and $X_k^{\theta-h/2}$. We took n=10,000 samples and obtained the following results for various h.

h	$\hat{\mu}^{\theta,h}$	σ^2	Confidence
0.01	-306.59	18,230.86	2.56
0.005	-304.76	36,782.56	3.76
0.001	-296.61	215,947.83	9.11
0.0005	-298.46	507,757.71	13.97

2.2 Likelihood Ratio Method

For likelihood ratio method, we took n=100,000 samples.

$\hat{Y}^{ heta}$	σ^2	Confidence
-331.29	564,0541.81	46.55

While emplying a control variate with the weight function obtained using the Likelihood Ratio method, we had a dramatic reduction in variance.

$\hat{Y}^{ heta}$	σ^2	Confidence
-302.56	190,379.28	8.55