Table 1| Viral Infection Network

Opened Network	Kinetic Constants
DNA + Protein --> 0 DNA --> RNA + DNA RNA --> 0 RNA --> DNA + RNA RNA --> Protein + RNA Protein --> 0	k_1 = 1.0378 k_2 = 3 k_3 = 1 k_4 = 10 k_5 = 110 k_6 = 200
Reference: J. Goutsias, 2005, doi: 10.1063/1.1889434	

The original network has three components and six reactions, that is already opened up. From the opened network steady state mass balances for DNA (D), RNA (R), and the Protein (P) are derived.

$$\frac{dD}{dt} = 0 = -k_1 DP + k_4 R \tag{1}$$

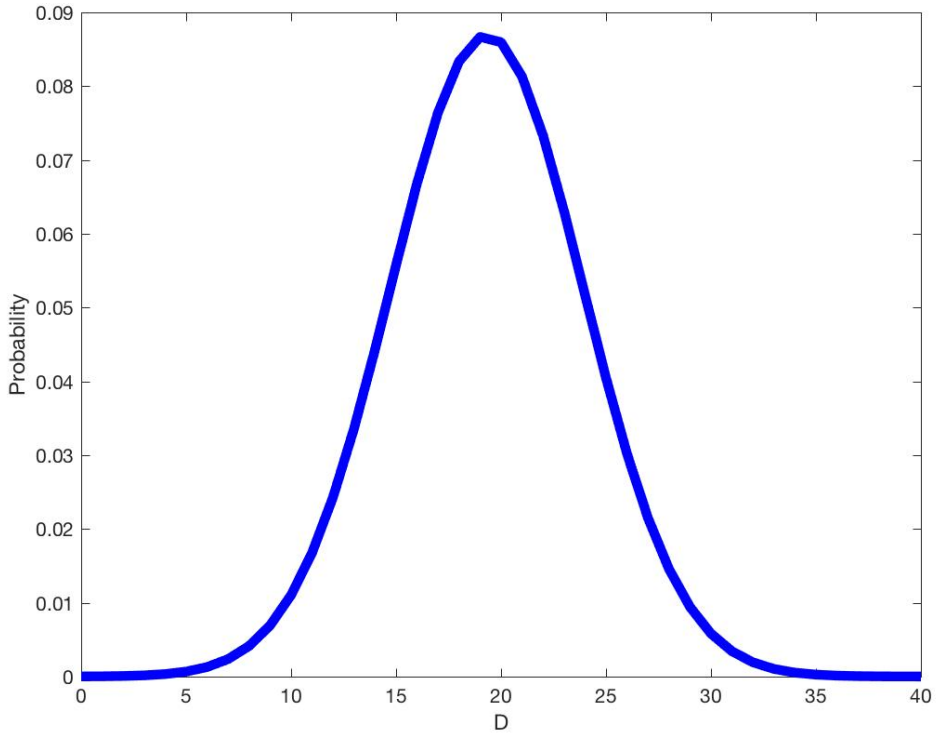
$$\frac{dR}{dt} = 0 = k_2 D - k_3 R \tag{2}$$

$$\frac{dP}{dt} = 0 = -k_1 DP + k_5 R - k_6 P \tag{3}$$

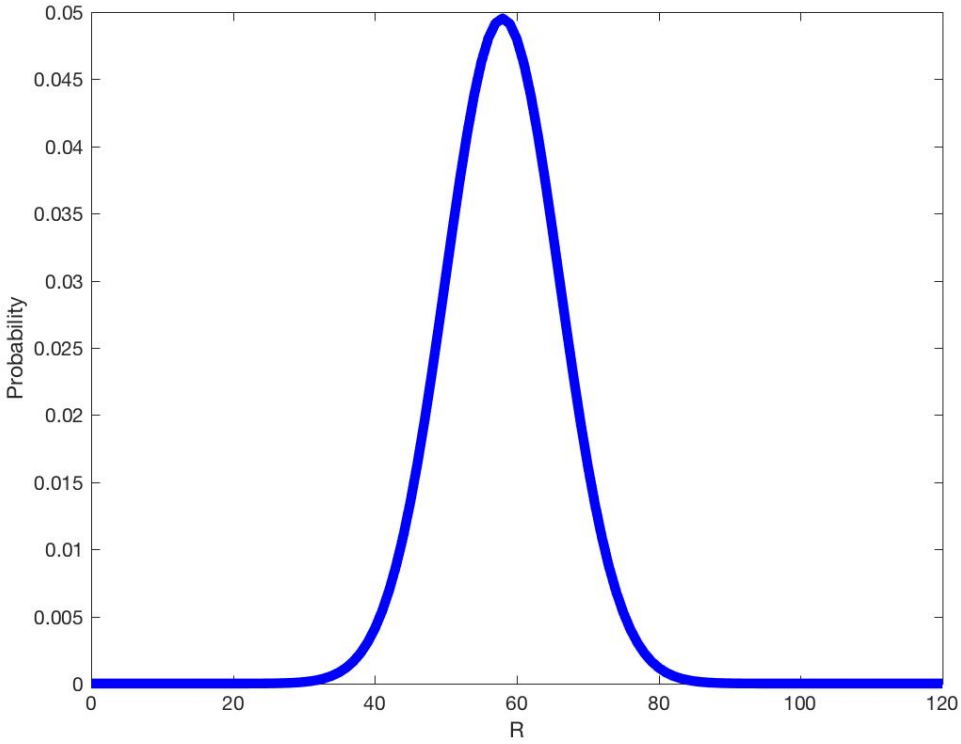
From the steady state balances there are three equations and nine unknowns, this leaves six variables to be specified. The kinetic constants, k_1, k_2, k_3, k_4, k_5, and k_6 are specified as 1.0378, 3, 1, 10, 110, and 200 respectively. To run the simulation the minimum value for all components is set to zero, and the maximum values for DNA, RNA, and the Protein are set to 40, 120, 60. The maximum number of moments is set to 2, and all of the initial guesses for the Lagrange Multipliers are set to zero. Table 2 summarizes the parameters required for the simulation, and Figure 1 displays the results.

Table 2| Simulation Parameters

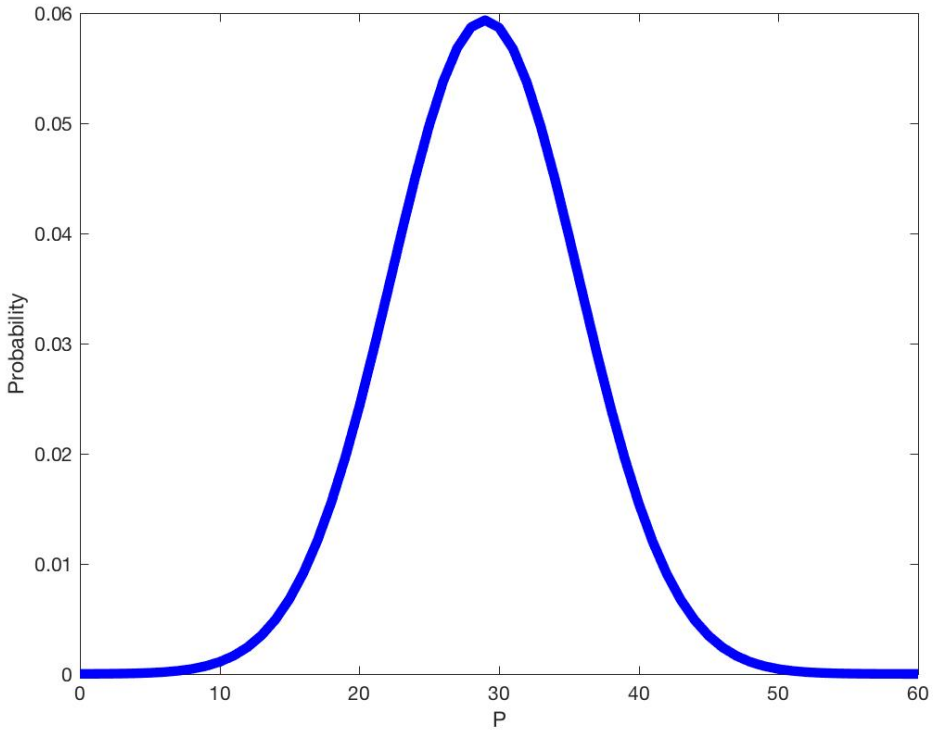
Minimum Values (D, R, P)	Maximum Value (D)	Maximum Value (R)	Maximum Value (P)	Maximum Number of Moments	LaGrange Multipliers (Initial Guess)
0	40	120	60	2	0


Probability
D
0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
0
5
10
15
20
25
30
35
40

(A)


Probability
R
0.05
0.045
0.04
0.035
0.03
0.025
0.02
0.015
0.01
0.005
0
0
20
40
60
80
100
120

(B)



(C)

Figure 1| Results from Simulation. A) Component D **B)** Component R **C)** Component P