

# Stochastic modelling in Mathematical Biology

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# Outline

Introduction

Master Equation and Monte Carlo methods

Kinetic Chemical Reactions and the Gillespie Stochastic Simulation Algorithm

Examples

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Kinetic Chemical Reactions and the Gillespie Stochastic Simulation Algorithm

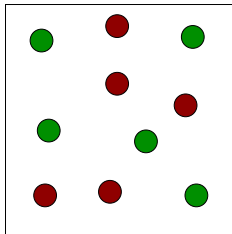
Examples

## Motivation

- There exists the general idea that randomness and noise simply add an unsystematic perturbation to a well-defined average behaviour.
- I will present several examples of systems in which noise contributes to the behaviour of the system in a non-trivial manner and it is fundamental to understanding the system.
- From these examples I will extract rules of thumb for ascertaining when randomness plays a fundamental roles.
- I will show you how to modelize some natural process in a better way than using a continuous and deterministic approach.

## The Moran Process

The Moran process, named after the Australian statistician Pat Moran, is a widely-used variant of the Wright-Fisher model and is commonly used in population genetics.



- $N$  individuals of two types.  $N$  is kept fixed.
- $n$ : number of normal individuals.  $m$ : number of mutant individuals.  $N=m+n$ .
- At each time step:
  - $n \rightarrow n + 1$  and  $m \rightarrow m - 1$  with probability rate  $W_+(n) = \frac{n}{N} \left(1 - \frac{n}{N}\right)$ .
  - $n \rightarrow n - 1$  and  $m \rightarrow m + 1$  with probability rate  $W_-(n) = \frac{n}{N} \left(1 - \frac{n}{N}\right)$ .

## The Moran Process

- Note that  $W(n+1) = W(n-1)$ , i.e.  $\mathbb{E}[\Delta n] = \mathbb{E}[n(t+\Delta t) - n(t)] = 0$ .
- This implies that with  $m = \mathbb{E}[n]$ :

$$\frac{dm}{dt} = 0 \quad (1)$$

- *The system has two absorbing states:*

$$W_+(n=0) = W_-(n=0) = 0 \text{ and}$$

$$W_+(n=N) = W_-(n=N) = 0$$

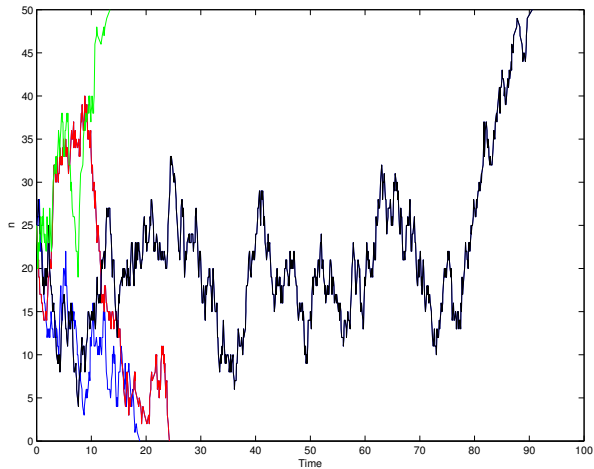
- This means that

$$\lim_{t \rightarrow \infty} P(n(t) = 0 \cup n(t) = N) = 1 \quad (2)$$

- This behaviour is not at all captured by the deterministic equation, which predicts that the population will stay constant.

## The Moran Process

### Simulation results:



## Logistic growth

- The logistic equation,

$$\frac{dm}{dt} = m \left( 1 - \frac{m}{K} \right), \quad (3)$$

has two steady states:  $m = 0$  **unstable** and  $m = K$  **stable**, i.e. regardless of the value of  $K$  and for any initial condition such that  $m(t = 0) > 0$ ,  $m(t)$  will asymptotically approach  $K$ .

- Consider now a continuous-time Markov process  $n_t$  whose dynamics are given by the following transition rate:
  - $n \rightarrow n + 1$  with probability rate  $n$ .
  - $n \rightarrow n - 1$  with probability rate  $\frac{n(n-1)}{2} \frac{1}{K}$ .
- This stochastic process has a unique absorbing state:  $n = 0$ , and therefore we expect the stochastic dynamics to show strong discrepancies with Equation (3) when randomness is dominant.

## Logistic growth

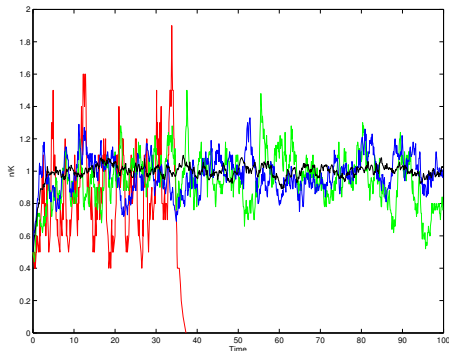


Figure: Red line  $K = 10$ , green  $K = 50$ , blue  $K = 100$ , black  $K = 1000$

We observe that for small  $K$  fluctuations dominate the behaviour of the system. Extinctions are common for small  $K$ , in contradiction to the behaviour predicted by the logistic equation Eq. (3), and become rarer as  $K$  is allowed to increase.

## Steady states vs Absorbing states

- The definition of equilibrium states in stochastic systems is a bit technical and there are several definitions of equilibrium.
- Consider again the stochastic logistic growth, i.e. a process  $n_t$  such that:
  - $n \rightarrow n + 1$  with probability rate  $W_+(n) = n$
  - $n \rightarrow n - 1$  with probability rate  $W_-(n) = \frac{n(n-1)}{2} \frac{1}{K}$
- Consider a state of system,  $n_s$ , is, roughly speaking, a state of the process such that  $W_+(n_s) = W_-(n_s)$ .
  - $W_+(n_s)$  is the number of births within a population of  $n_s$  individuals
  - Likewise,  $W_-(n_s)$  is the number of deaths within a population  $n_s$  individuals
  - So an steady state of our population dynamics is reached when  $n_t = n_s$ , since death rate is balanced by birth rate and therefore the population stays roughly constant
- $n_s = K$  which coincides with the deterministic stable fixed point.
- Note that  $W_+(n) - W_-(n) > 0$  if  $n < n_s$  and  $W_+(n) - W_-(n) < 0$  if  $n > n_s$

## Steady stats vs Absorbing states

- An absorbing state,  $n_0$ , is characterised by  $W_i(n_0) = 0$  i.e. once the system has reached the absorbing state, it cannot leave anymore.
- Consider again, the stochastic logistic growth rate, we have:
  - Steady states are in general not absorbing states.
  - $W_+(n_s) \neq 0$  and  $W_-(n_s) \neq 0$ .
  - If  $n = 0$  then  $W_+(0) = W_-(0) = 0$  therefore  $n = 0$  is an absorbing state.
- $n_s$  belongs to the set of accessible states of  $n = 0$ , that means there is at least one consecutive set of transition that connects  $n_s$  and  $n_0$ . For Example:  
 $K \rightarrow K - 1 \rightarrow K - 2 \rightarrow \dots \rightarrow 1 \rightarrow 0$ .
- However, if  $K \gg 1$  the probability of such a chain of events is vanishingly small.

## Summary

- $n_s$  is an steady state in the sense that births and deaths are balanced. Moreover,  $W_+(n) - W_-(n) > 0$  if  $n < n_s$  and  $W_+(n) - W_-(n) < 0$  if  $n > n_s$ . This is essentially equivalent to what happens in the deterministic logistic growth model.
- However,  $n_s$  is not an absorbing state of the stochastic dynamics. The only absorbing state is  $n = 0$ .
- Stochastic extinctions are relatively rare provided  $K$  is big. If this is the case, the deterministic system provides a reasonable approximation to the behaviour of the model.
- If, on the contrary,  $K$  is small stochastic extinctions are relatively common and the deterministic description is not an accurate one
- We have seen several examples of stochastic systems in which noise and randomness are the dominating factors. Their behaviours are not captured by their deterministic counterparts.
- In general, we should expect non-trivial random effects for small populations or dynamics with absorbing states.

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## The Master Equation

- The Master Equation is our fundamental mathematical description of an stochastic process and the starting point for any attempt to analyse a particular model.
- It is obtained as a probability balance for all the events that can occur during the time interval  $(t, t + \Delta t)$ .
- Mathematically, it is a set of ordinary differential equations for the probability distribution  $P(n, t)$  i.e. the probability that the number of individuals in the population at time  $t$  to be  $n$ .

## The Master Equation II

### Example: Birth and death process

- Birth  $n \rightarrow n + 1$  with probability rate  $W_+(n) = \lambda n$ . Death:  $n \rightarrow n - 1$  with probability rate  $W_-(n) = \sigma n$ .
- Probability balance:  

$$P(n, t + \Delta t) = \lambda(n - 1)\Delta t P(n - 1, t) + \sigma(n + 1)\Delta t P(n + 1, t) + (1 - (\lambda n \Delta t + \sigma n \Delta t))P(n, t).$$
- When  $\Delta t \rightarrow 0$ :

$$\frac{dP(n, t)}{dt} = \lambda(n - 1)P(n - 1, t) + \sigma(n + 1)P(n + 1, t) - (\lambda n + \sigma n)P(n, t)$$

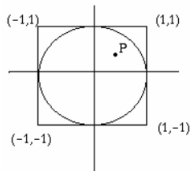
- **Big Problem:** In general is not possible to get the analytical solution of the Master Equation, even a numerical solution of the Master Equation can be very hard.

## Monte Carlo Simulations

- The first thoughts and attempts made to practice the Monte Carlo Method were suggested by a question which occurred in 1946 to Stanislaw Ulam was convalescing from an illness and playing solitaires. The question was what are the chances that a Canfield solitaire laid out with 52 cards will come out successfully?
- After spending a lot of time trying to estimate them by pure combinatorial calculations, he wondered whether a more practical method than "abstract thinking" might not be to lay it out say one hundred times and simply observe and count the number of successful plays.
- In 1950s Stanislaw Ulam and John von Neumann started a research in this topic founded by The RAND Corporation and the U.S. Air Force.
- Uses of Monte Carlo methods require large amounts of random numbers, and it was their use that spurred the development of pseudorandom number generators.

## Monte Carlo Simulations

- There is no consensus on how Monte Carlo method should be defined.
- Example: Approximate the value of  $\pi$ 
  - Consider a random point  $P$  in the unit square, which is the probability that  $P$  is in the unit circle?



- The probability has to be the quotient of the areas, that is  $\frac{\pi}{4}$ .
  - a Set  $Ok = 0$
  - b Generate two random numbers  $x, y \in [-1, 1]$  if  $x^2 + y^2 < 1$ , then  $Ok = Ok + 1$
  - c Repeat it  $N$  times. When  $N \rightarrow \infty$ , then  $\frac{Ok}{N} \rightarrow \frac{\pi}{4}$

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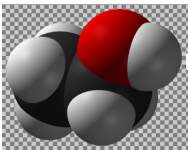
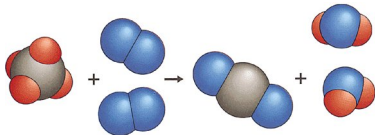
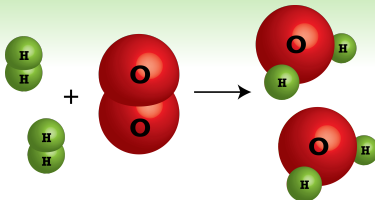
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## A Chemical Reacting System

- Molecules of  $N$  chemical species  $S_1, \dots, S_N$ 
  - Inside some volume  $\Omega$ , at some temperature  $T$ .
- Interacting through  $M$  elemental reaction channels  $R_1, \dots, R_M$ .
- $R_j$  is assumed to describe a single instantaneous physical event which changes the population of at least one species.



## Deterministic vs Stochastic

The time-evolution of chemical systems has traditionally been analyzed using continuous, deterministic mathematics (ODEs, PDEs).

But in fact, chemical systems evolve

- Discretely, because molecules come in integer numbers
- Stochastically, for several reasons:
  - Even if all the molecules moved according to deterministic Newtonian mechanics, the system is so sensitive to initial conditions that its behaviour will be random.
  - Chemical systems of practical interest are NEVER isolated. The reason why a system is at a temperature  $T$  is because it is having random exchanges of energy with its environment.
  - All unimolecular reactions  $S \rightarrow \text{anything}$  are inherently stochastic.

## Deterministic vs Stochastic

For the simplest chemical reaction:  $S \rightarrow \emptyset$

- Traditional wisdom asserts that  $X(t) \equiv$  the number of  $S$  molecules in the system at time  $t$ , evolves according to the ODE

$$\frac{dX(t)}{dt} = -cX(t). \quad (4)$$

- But **physics**  $\implies$  the  $S$  molecules react independently of each other.
- The problem: There is no plausible physical mechanism that could give rise to such exquisitely coordinated deterministic behavior!
- The most reasonable mechanism for  $S \rightarrow \emptyset$  is that the lifetimes of the individual  $S$  molecules are i.i.d. random variables. In that case (4) might describe how the average  $S$  population evolves in time:

$$\frac{dX_{avg}(t)}{dt} = -cX_{avg}(t). \quad (5)$$

- If the average  $S$  population evolves according to (5), then the lifetime of each  $S$  molecule must be an exponential random variable with mean  $\frac{1}{c}$ , or equivalently,

$$c \cdot dt = \text{Prob}\{\text{a given } S\text{-molecule will die in the next } dt\}$$

## Proof of this result:

- With  $x_0$  molecules at time 0, the ODE (5) implies

$$X_{avg}(t) = x_0 e^{-ct} \quad (t > 0)$$

- Let  $f(t)$  denote the cdf of the molecule lifetime. Then for any  $t > 0$ ,  $(1 - f(t))$  = the probability that any particular one of the  $x_0$  molecules at time 0 will still be alive at time  $t$ .
- So the probability that exactly  $x$  molecules will be alive at this  $t$  time is:

$$(1 - f(t))^x (f(t))^{x_0 - x} \frac{x_0!}{x!(x_0 - x)!}.$$

- From these expressions we obtain  $f(t) = 1 - e^{-ct}$ . This is the cdf of the exponential random variable with mean  $\frac{1}{c}$ .
- The corresponding pdf  $p(t) \equiv df(t)/dt = ce^{-ct}$  is such that  $p(t)dt = \text{Prob}\{\text{the molecule will die in } [t, t + dt)\}$ . Thus,  $p(0)dt = c dt$ . **QED**

This has some implications:

- The deterministic equation  $\frac{dX}{dt} = -cX$  for  $S \rightarrow \emptyset$  makes no sense physically unless there is an underlying stochastic dynamics for the  $S$  molecules.
- And not just any stochastic dynamics, but a stochastic dynamics of a very particular kind: Each  $S$  molecule must disappear in the next  $dt$  with probability  $c \cdot dt$ .
- If the  $S$  molecules don't behave in that way, then the equation  $\frac{dX}{dt} = -cX$  will not correctly describe the reaction  $S \rightarrow \emptyset$ .
- No fundamental physical theory of chemical kinetics can be premised on a traditional ODE like  $\frac{dX}{dt} = -cX$ . Such an ODE can be, at best, a consequence of a more fundamental theory, and perhaps only an approximate consequence.

A tractable discrete-stochastic mathematical description of chemically reacting systems is possible if successive reactive collisions between molecules tend to be separated in time by very many non-reactive collisions.

- In that case, the many non-reactive collisions tend to randomize
  - the velocities of the molecules (Maxwell-Boltzmann distribution),
  - the positions of the molecules (randomly uniform inside  $\Omega$  ).
- Then, instead of having to describe the systems state by giving the position, velocity and species of every molecule in  $\Omega$  , we can get away with specifying the much lower dimensional vector function.

$$X(t) = (X_1(t), \dots, X_N(t)),$$

provided its  $i^{th}$  component,

$X_i(t)$  the number of  $S_i$  molecules in  $\Omega$  at time  $t$  ,  
is treated as a random variable.

Each reaction channel  $R_j$  can then be characterized by **two entities**:

- Its **propensity function**  $a_j(x)$ : If the system is currently in state  $x$ ,

$a_j(x) \cdot dt :=$  probability that one  $R_j$  event will occur in the next  $dt$ .

The existence and form of  $a_j(x)$  must come from molecular physics.

- Its **state change vector**  $v_j \equiv (v_{1j}, \dots, v_{Nj})$ :

$v_{i,j}$  = the change in  $X_i$  caused by one  $R_j$  event.

$R_j$  induces the state change  $x \rightarrow x + v_j$ .

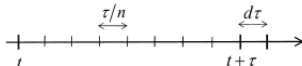
- Examples:

- $S_1 \rightarrow S_2$ :  $v_j = (-1, 1, 0, \dots, 0)$ ;  $a_j(x)dt = (c_j dt)x_1 \implies a_j(x) = c_j x_1$
- $S_1 + S_2 \rightarrow 2S_2$ : same  $v_j$ ;  $a_j(x)dt = (c_j dt)x_1 x_2 \implies a_j(x) = c_j x_1 x_2$

## The Gillespie stochastic simulation algorithm (SSA)

A procedure for constructing sample paths or realizations of  $X(t)$ :

- Idea: Generate properly distributed random numbers for
  - the time  $\tau$  to the next reaction
  - the index  $j$  of that reaction
- $p(\tau, j|x, t) \cdot d\tau \equiv$  probability, given  $X(t) = x$ , that the next reaction will occur in  $[t + \tau, t + \tau + d\tau)$ , and will be  $R_j$ .



$$\sum_{k=1}^M a_k(x) \equiv a_0(x)$$

$$p(\tau, j|x, t)d\tau = \left(1 - a_0(x)\frac{\tau}{n}\right)^n a_j(x)d\tau \rightarrow e^{-a_0(x)\tau} a_j(x)d\tau$$

- Therefore,  $p(\tau, j|x, t)d\tau = e^{-a_0(x)\tau} a_j(x)d\tau = a_0(x)e^{-a_0(x)\tau} \cdot \frac{a_j(x)}{a_0(x)} d\tau$ 

$$\implies$$
  - $\tau$  is the exponential r.v. with mean  $\frac{1}{a_0(x)}$ .
  - $j$  is the integer r.v. with probability mass  $\frac{a_j(x)}{a_0(x)}$ .
  - $\tau$  and  $j$  are statistically independent.

## The Gillespie stochastic simulation algorithm (SSA)

The following scheme is a Method of implementing the SSA

- 1 In state  $x$  at time  $t$ , evaluate  $a_1(x), \dots, a_M(x)$  and  $a_0(x) = \sum_{k=1}^M a_k(x)$ .
- 2 generate  $r_1$  and  $r_2$  random numbers in  $[0, 1]$ , and compute  $\tau$  and  $j$  according to
  - $\tau = \frac{1}{a_0(x)} \ln \left( \frac{1}{1 - r_1} \right)$ ,
  - $j = \text{the smallest integer satisfying } \sum_{k=1}^j a_k(x) > r_2 a_0(x)$ .
- 3  $t = t + \tau$  and  $x = x + v_j$
- 4 Record  $(x, t)$ . Go to 1 or end the simulation.

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## Examples

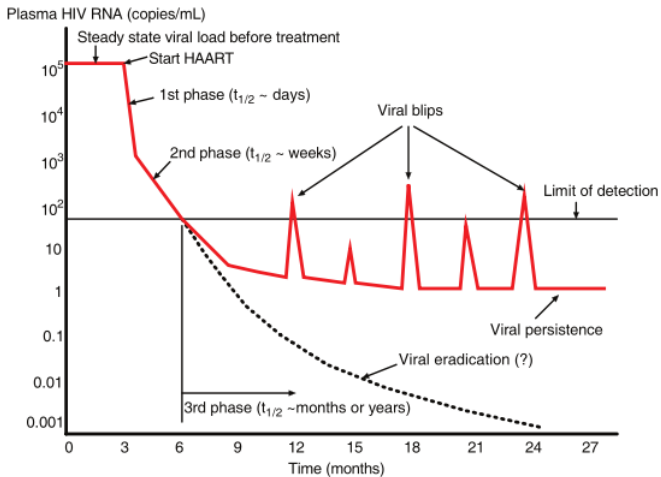
This kind of models can be used in a lot of situations:

- Chemistry, modelling chemical reactions.
- Ecology, for instance in prey predator systems:
  - Wolves and rabbits.
  - Bougainvillea (Brazilian plant) and Lepidoptera (bug).
- Biological and medical problems:
  - Mutant invasions.
  - Populations of cells and virus.

## HIV-1

- An HIV-1 infected person without any treatment has between  $10^5$  and  $10^6$  copies of virus per milliliter of blood.
- Following initiation of highly active antiretroviral therapy (HAART) the plasma viral load declines fast. After several months of treatment, most patients attain a level of plasma HIV-1 RNA below the detection limit (50 copies/mL).
- This does not imply that viral replication has been completely suppressed by therapy.
- Even in patients with “undetectable” plasma viral loads for many years, a low level of virus can be detected in plasma by supersensitive assays.
- An explanation is that HIV-1 establishes a state of latent infection in resting memory  $CD4^+$  T cells, and virus is released when these cells encounter their relevant antigens and are activated.
- Observation of transient episodes of viremia (“blips”) above the detection limit.

## Summary



Rong L, Perelson AS (2009) Modeling HIV persistence, the latent reservoir, and Viral Blips in HIV-infected Patients on Potent Therapy. *J Theor Biol* 260: 308-31

## Experimental results

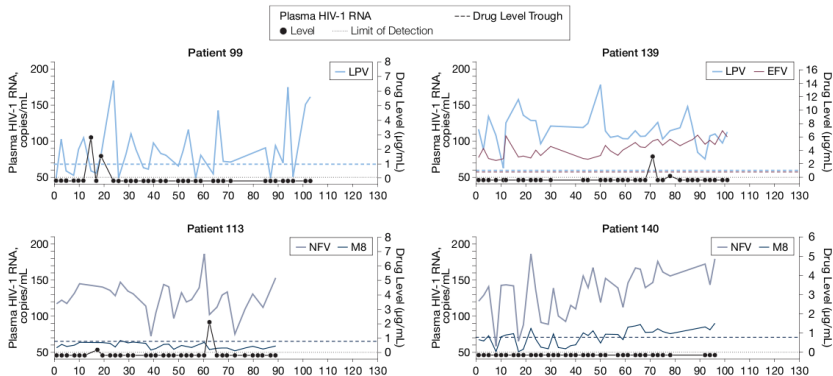
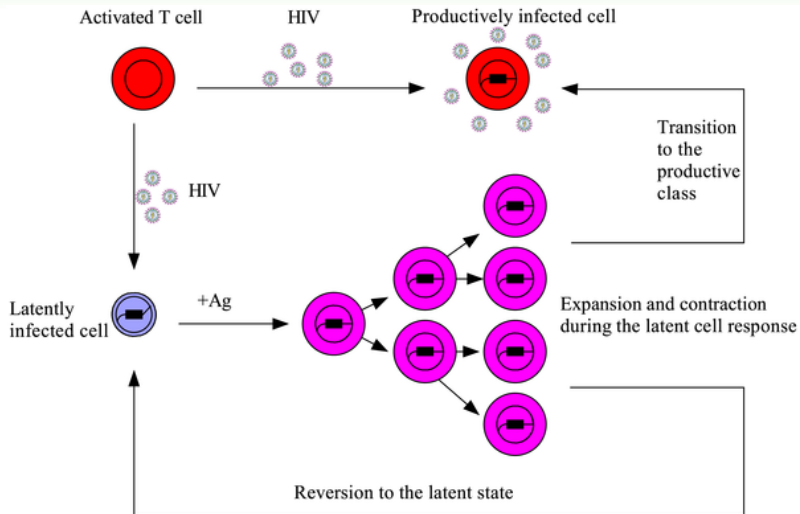


Figure: Experimental results from Nettles et. al

Nettles TE, Kieffer TL, Kwon P, Monie D, Han Y, et al. (2005) Intermittent HIV-1 viremia (Blips) and drug resistance in patients receiving HAART. JAMA 293: 817-829.

## Mathematical Model



## Simulations

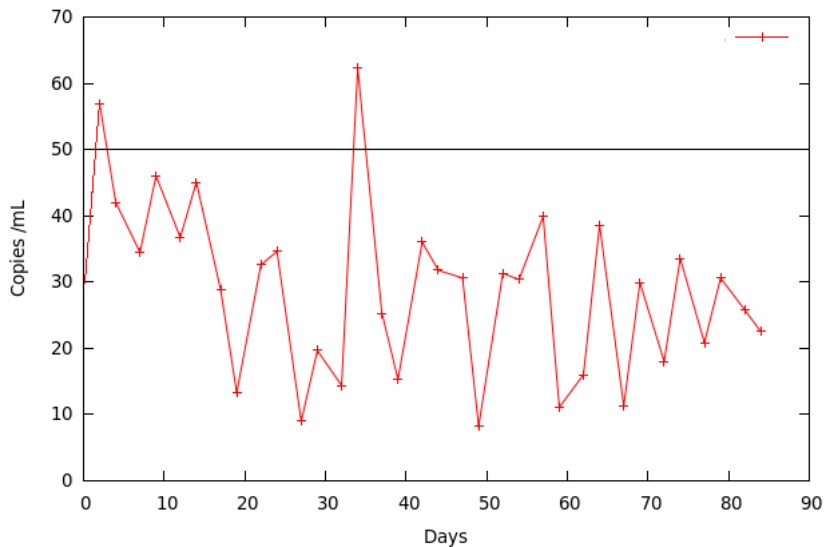


Figure: Gillespie Simulations of our system.

## Simulations

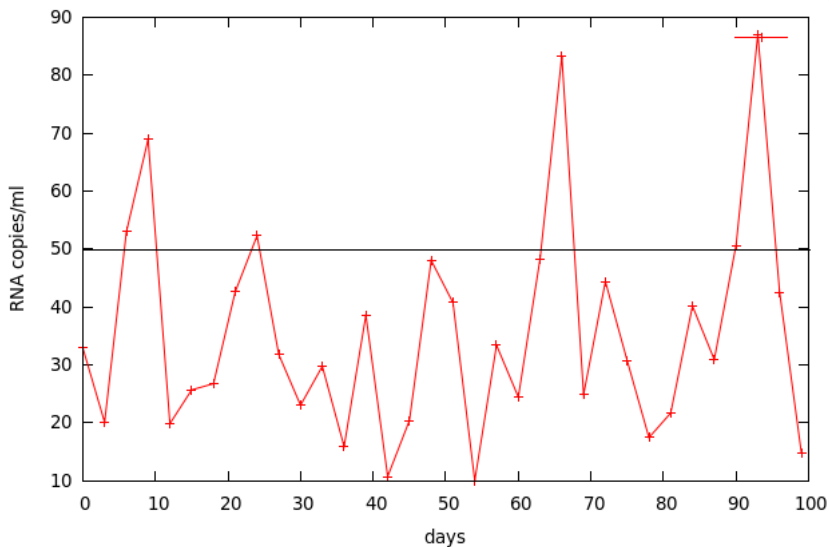


Figure: Gillespie Simulations of our system.

THANK YOU

FOR YOUR ATTENTION!!