Stochastic modeling of biochemical and genetic networks (adapting notes from my student Brian Ingalls)

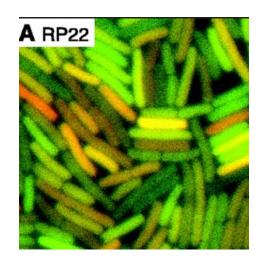
Variability in biology

 Development: genetically identical but phenotypically different

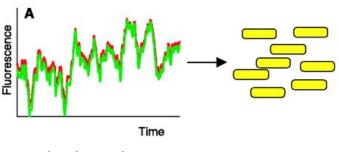




 Gene expression: genetically identical but phenotypically different

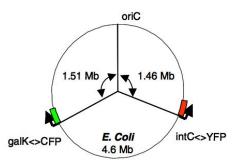


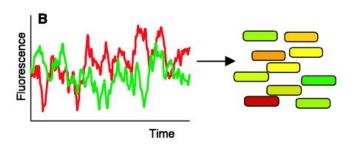
Intrinsic and Extrinsic noise Elowitz *et. al,* Science, 2002



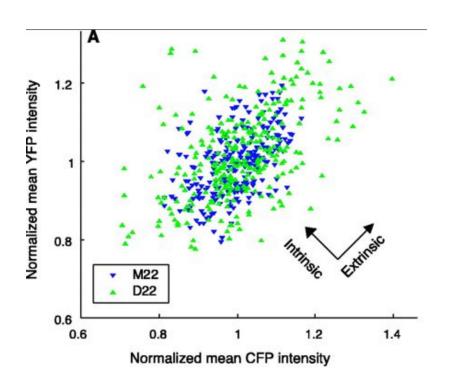
Extrinsic noise

Experimental design:
2 reporter genes in
`equivalent' positions in the
genome





Intrinsic and extrinsic noise

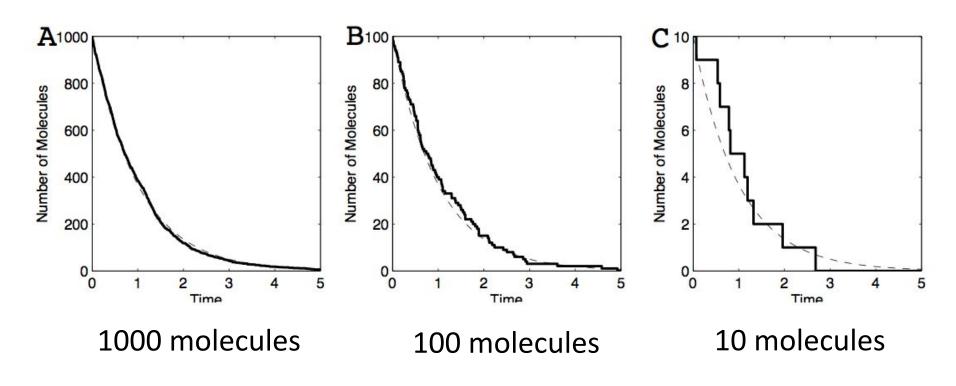


Results

Variability in Molecular Biology

- All reaction events are driven by thermal agitation ('noise')
- Over large numbers of events, 'noise' is averaged out
- Variability can be a nuisance, or can be useful (e.g. persistence)
- At the cellular level, we distinguish
 - intrinsic noise (thermal agitation)
 - extrinsic noise (variability in localization, environmental factors)

Deterministic behaviour vs. random (stochastic) behaviour



$$A \rightarrow$$

A discrete modeling framework

- Spatial homogeneity assumed
- System State: number of molecules of each species, collected in vector N
- Reaction k characterized by
 - stoichiometry vector s_k
 - reaction propensity a_k

Example

$$R_1: A+B \xrightarrow{k_1} C$$

$$R_2: C \xrightarrow{\kappa_2}$$

State:

$$\mathbf{N} = \left[egin{array}{c} N_A \ N_B \ N_C \end{array}
ight]$$

Stoichiometry:

$$\mathbf{s}_1 = \begin{bmatrix} -1 \\ -1 \\ 1 \end{bmatrix} \quad \begin{array}{l} \leftarrow A \\ \leftarrow B \\ \leftarrow C \end{array}$$

$$\mathbf{s}_2 = \left[\begin{array}{c} 0 \\ 0 \\ -1 \end{array} \right] \quad \begin{array}{c} \leftarrow A \\ \leftarrow B \\ \leftarrow C \end{array}$$

Propensity:

$$a_1(\mathbf{N}) = k_1 N_A N_B$$

$$a_2(\mathbf{N}) = k_2 N_C$$

A technical complication

for a homodimer type of reaction such as

$$A + A \rightarrow B$$

we cannot write $k * A^2$, because the reaction cannot take place is A = 1!

the correct formula has: k * A (A-1)/2 i.e. we need to consider all possible pairs

when numbers are large, $A-1 \approx A$ and the 2 can be absorbed; hence we don't worry about this

see my notes for more, including effects of volume (also not trivial)

Example

$$R_1: A+B \xrightarrow{k_1} C$$

$$R_2: C \xrightarrow{\kappa_2}$$

Stoichiometry:

$$\mathbf{s}_1 = \begin{bmatrix} -1 \\ -1 \\ 1 \end{bmatrix} \quad \begin{array}{l} \leftarrow A \\ \leftarrow B \\ \leftarrow C \end{array}$$

$$\mathbf{s}_2 = \begin{bmatrix} 0 \\ 0 \\ -1 \end{bmatrix} \quad \begin{array}{l} \leftarrow A \\ \leftarrow B \\ \leftarrow C \end{array}$$

State:

$$\mathbf{N} = \left[egin{array}{c} N_A \ N_B \ N_C \end{array}
ight] = \left[egin{array}{c} 11 \ 6 \ 3 \end{array}
ight]$$

Reaction 1 fires:

$$\mathbf{N} \to \mathbf{N} + \mathbf{s}_1 = \left| \begin{array}{c|c} 11 \\ 6 \\ 3 \end{array} \right| + \left| \begin{array}{c|c} -1 \\ -1 \\ 1 \end{array} \right| = \left| \begin{array}{c} 10 \\ 5 \\ 4 \end{array} \right|$$

Stochastic Dynamic Model: stochastic process

- Cannot confidently characterize state of the system at time t (as in N=N(t))
- Instead, describe *probability* of the state taking a particular value at time t:

$$P(\mathbf{N},t)=$$
 Probability that the system is in state **N** at time t

e.g.
$$P\left(\begin{bmatrix} 1\\0\\1\end{bmatrix},2\right) = 0.03$$

Stochastic dynamic model

- Assumption: there is a small time-increment dt such that
- at most one reaction can occur during any time interval of length dt
- probability that reaction R_k occurs in a time interval [t, t+dt] is $a_k(\mathbf{N}(t)) dt$
- probability that no reactions occur during a time interval [t, t+dt] is therefore:

$$1-\sum_k a_k(\mathbf{N}(t))dt$$
 Sum over all reactions, assumed independent

(actually, even if two reactions occur, it won't make any difference, because we'll get terms (dt)² that will go to zero when forming the ODE next)

$$P(\mathbf{N}, t + dt) = P(\mathbf{N}, t) \cdot \left(1 - \sum_{k} a_k(\mathbf{N}) dt\right)$$
probability of no reactions firing

+
$$\sum_{k} \underbrace{P(\mathbf{N} - \mathbf{s}_k, t) a_k(\mathbf{N} - \mathbf{s}_k) dt}_{\text{probability of reaction } R_k \text{ occurring while in state } \mathbf{N} - \mathbf{s}_k$$

Example: single species A

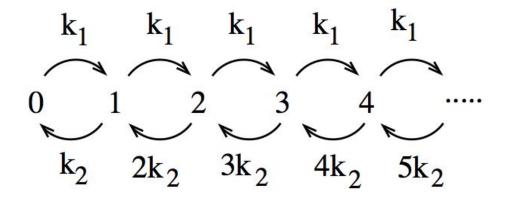
State:
$$N = N_A$$

Reactions:
$$R_1: \xrightarrow{k_1} A \qquad R_2: A \xrightarrow{k_2}$$

– stoichiometry
$$s_1 = [1]$$
 $s_2 = [-1]$

- propensity
$$a_1=k_1$$
 $a_2=k_2N_A$

Example: state transitions:



Probability balance:

$$P(0, t + dt) = P(0, t) [1 - k_1 dt] + P(1, t) \cdot k_2 dt$$

$$P(1, t + dt) = P(1, t) [1 - (k_1 + k_2) dt] + P(0, t) \cdot k_1 dt + P(2, t) \cdot 2k_2 dt$$

Example: state transitions:

Probability balance:

$$\begin{array}{lcl} P(0,t+dt) & = & P(0,t)\left[1-k_1dt\right] + P(1,t)\cdot k_2\,dt \\ P(1,t+dt) & = & P(1,t)\left[1-(k_1+k_2)dt\right] + P(0,t)\cdot k_1\,dt + P(2,t)\cdot 2k_2\,dt \\ P(2,t+dt) & = & P(2,t)\left[1-(k_1+2k_2)dt\right] + P(1,t)\cdot k_1\,dt + P(3,t)\cdot 3k_2\,dt \\ P(3,t+dt) & = & P(3,t)\left[1-(k_1+3k_2)dt\right] + P(2,t)\cdot k_1\,dt + P(4,t)\cdot 4k_2\,dt \\ & \vdots \\ P(N,t+dt) & = & P(N,t)\left[1-(k_1+Nk_2)dt\right] + P(N-1,t)\cdot k_1\,dt + P(N+1,t)\cdot (N+1)k_2\,dt \\ & \vdots \end{array}$$

Differential equation for probability distribution:

Probability balance:

$$P(\mathbf{N}, t + dt) = P(\mathbf{N}, t) \cdot \underbrace{\left(1 - \sum_{k} a_k(\mathbf{N}) dt\right)}_{\text{probability of no reactions firing}} + \sum_{k} \underbrace{P(\mathbf{N} - \mathbf{s}_k, t) \, a_k(\mathbf{N} - \mathbf{s}_k) \, dt.}_{\text{probability of reaction } R_k \text{ occurring while in state } \mathbf{N} - \mathbf{s}_k}$$

Subtracting $P(\mathbf{N},t)$ from both sides:

$$P(\mathbf{N}, t + dt) - P(\mathbf{N}, t) = -P(\mathbf{N}, t) \left(\sum_{k} a_k(\mathbf{N}) dt \right) + \sum_{k} P(\mathbf{N} - \mathbf{s}_k, t) a_k(\mathbf{N} - \mathbf{s}_k) dt$$

Dividing by *dt*:

$$\frac{P(\mathbf{N}, t + dt) - P(\mathbf{N}, t)}{dt} = -P(\mathbf{N}, t) \left(\sum_{k} a_k(\mathbf{N}) \right) + \sum_{k} P(\mathbf{N} - \mathbf{s}_k, t) a_k(\mathbf{N} - \mathbf{s}_k)$$

Limit as *dt* tends to zero:

$$\frac{d}{dt}P(\mathbf{N},t) = -P(\mathbf{N},t)\left(\sum_{k}a_{k}(\mathbf{N})\right) + \sum_{k}P(\mathbf{N}-\mathbf{s}_{k},t)a_{k}(\mathbf{N}-\mathbf{s}_{k})$$

Differential equation for probability distribution:

$$\frac{d}{dt}P(\mathbf{N},t) = -P(\mathbf{N},t)\left(\sum_{k} a_{k}(\mathbf{N})\right) + \sum_{k} P(\mathbf{N} - \mathbf{s}_{k},t)a_{k}(\mathbf{N} - \mathbf{s}_{k})$$

$$= \sum_{k} \left(\underbrace{-P(\mathbf{N},t)a_{k}(\mathbf{N})}_{\text{flow out of state } \mathbf{N}} + \underbrace{P(\mathbf{N} - \mathbf{s}_{k},t)a_{k}(\mathbf{N} - \mathbf{s}_{k})}_{\text{flow into state } \mathbf{N}}\right)$$

The Chemical Master Equation (CME)

The Chemical Master Equation

Example system:
$$\stackrel{k_1}{\rightarrow} A \stackrel{k_2}{\rightarrow}$$

Master equation:

$$\frac{d}{dt}P(0,t) = -P(0,t) k_1 + P(1,t) k_2$$

$$\frac{d}{dt}P(1,t) = -P(1,t) (k_1 + k_2) + P(0,t)k_1 + P(2,t) 2k_2$$

$$\frac{d}{dt}P(2,t) = -P(2,t) (k_1 + 2k_2) + P(1,t)k_1 + P(3,t) 3k_2$$

$$\vdots$$

$$\frac{d}{dt}P(N,t) = -P(N,t) (k_1 + Nk_2) + P(N-1,t) k_1 + P(N+1,t) (N+1)k_2$$

$$\vdots$$

The master equation is a system of (typically infinitely many) differential equations

Network:
$$R_1: A \xrightarrow{k_1} B \qquad R_2: B \xrightarrow{k_2} A$$

State:
$$\mathbf{N} = (N_A, N_B)$$

Two molecules:
$$\mathbf{N} = (2,0), (1,1), (0,2)$$

Master equation:

$$\frac{d}{dt}P((2,0),t) = -P((2,0),t) 2k_1 + P((1,1),t) k_2$$

$$\frac{d}{dt}P((1,1),t) = -P((1,1),t) k_2 - P((1,1),t) k_1 + P((2,0),t) 2k_1 + P((0,2),t) 2k_2$$

$$\frac{d}{dt}P((0,2),t) = -P((0,2),t) 2k_2 + P((1,1),t) k_1$$

Network:

$$R_1: A \xrightarrow{k_1} B \qquad R_2: B \xrightarrow{k_2} A$$

Master equation:

$$\frac{d}{dt}P((2,0),t) = -P((2,0),t) 2k_1 + P((1,1),t) k_2$$

$$\frac{d}{dt}P((1,1),t) = -P((1,1),t) k_2 - P((1,1),t) k_1 + P((2,0),t) 2k_1 + P((0,2),t) 2k_2$$

$$\frac{d}{dt}P((0,2),t) = -P((0,2),t) 2k_2 + P((1,1),t) k_1$$

$$0 = -P^{ss}(2,0) 2k_1 + P^{ss}(1,1) k_2$$
Steady state:
$$0 = -P^{ss}(1,1) k_2 - P^{ss}(1,1) k_1 + P^{ss}(2,0) 2k_1 + P^{ss}(0,2) 2k_2$$

$$0 = -P^{ss}(0,2) 2k_2 + P^{ss}(1,1) k_1$$

$$P^{ss}(2,0) = \frac{k_2^2}{(k_1 + k_2)^2}, \qquad P^{ss}(1,1) = \frac{2k_1k_2}{(k_1 + k_2)^2}, \qquad P^{ss}(0,2) = \frac{k_1^2}{(k_1 + k_2)^2}$$

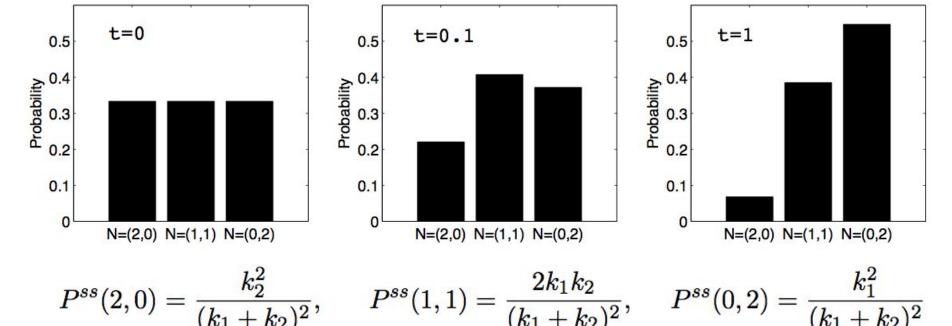
can prove binomial - in fact, can write ss distro in "closed form" for WR deficiency zero networks!

Network:

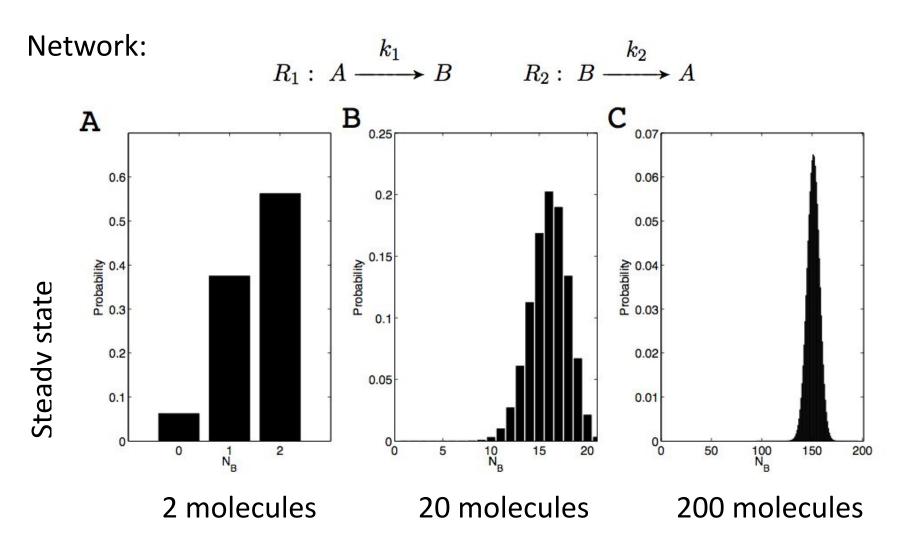
$$R_1: A \xrightarrow{k_1} B$$

$$R_1: A \xrightarrow{k_1} B \qquad R_2: B \xrightarrow{k_2} A$$

Dynamics: two molecules $(k_1 = 3, k_2 = 1)$



 $E(B) = 0.P^{ss}(2,0) + 1.P^{ss}(0,1) + 2.P^{ss}(0,2) = 2 N k_1 / (k_1 + k_2) = \frac{3}{4}N = 1.5 \text{ when } N = 2$ which is what we get from the ODE by setting $k_1 * A = k_2 * B$ and A=N-B so in this case (generally true for 0th and first order reactions), mean of stochastic = deterministic (and also for transients, not just ss)



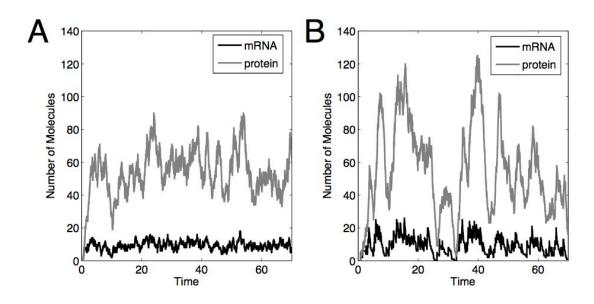
 $\sqrt[3]{4}$ N = $\sqrt[3]{4}$ 200 = 150, note how distribution peaks at 150 in case of large # molecules!

Master equation

- Approaches the deterministic (differential equation) description at large molecule numbers
- Difficult to analyse. Approximation approaches:
 - moment closure / "fluctuation-dissipation"
 - chemical Langevin equation (stochastic differential equation)
 - various finite-dimensional truncations
- Alternative approach: simulation of an ensemble of sample paths

Gillespie's Stochastic Simulation Algorithm

- Monte Carlo (probabilistic approach)
- Generates individual sample paths
- Sample statistics from an *ensemble* of sample paths indicate probability distribution.



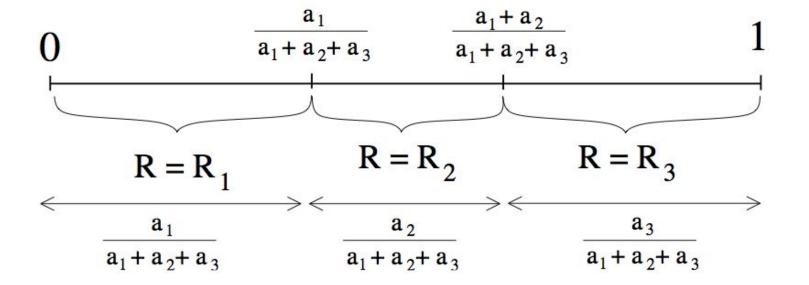
Stochastic Simulation Algorithm

- Depends on the properties of two random variables: variables characterized by probability distributions.
 - time until next reaction event T
 - which reaction occurs next R

Determining the next reaction

• Example: Reactions R_1 , R_2 , R_3 , propensities a_1 , a_2 , a_3

$$P(R=R_1) = rac{a_1}{a_1 + a_2 + a_3} \ P(R=R_2) = rac{a_3}{a_1 + a_2 + a_3}$$



Determining the next reaction

• Example: Reactions R₁, R₂, R₃, propensities a₁, a₂, a₃

Sampling algorithm: *u* drawn from a uniform distribution over [0,1]

$$\begin{array}{lll} \text{if} & 0 \leq & u & \leq \frac{a_1}{a_1 + a_2 + a_3}, & \text{then we set } R = R_1 \\ \\ \text{if} & \frac{a_1}{a_1 + a_2 + a_3} < & u & \leq \frac{a_1 + a_2}{a_1 + a_2 + a_3}, & \text{then we set } R = R_2 \\ \\ \text{if} & \frac{a_1 + a_2}{a_1 + a_2 + a_3} < & u & \leq \frac{a_1 + a_2 + a_3}{a_1 + a_2 + a_3} = 1, & \text{then we set } R = R_3. \end{array}$$

Determining the time to the next reaction

- T can shown to be an exponential random variable
- Cumulative distribution function:

$$P(0 \le T \le t) = 1 - e^{-at}$$

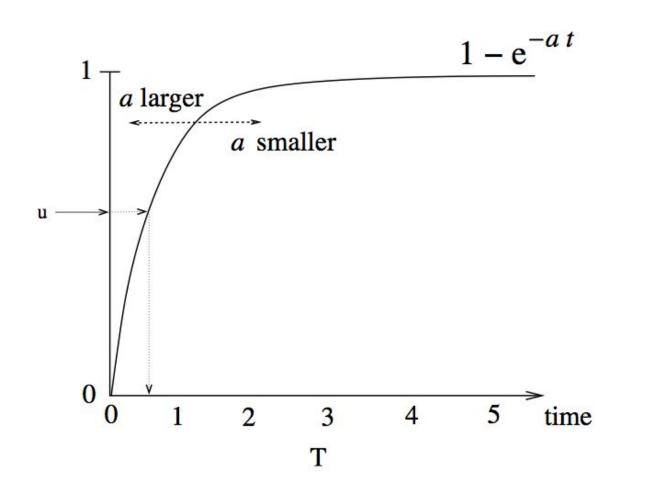
where a is the sum of the propensities:

$$a = a_1 + a_2 + a_3$$

(think of Poisson random arrivals)

Time to the next reaction

Sampling algorithm: *u* drawn from a uniform distribution over [0,1]

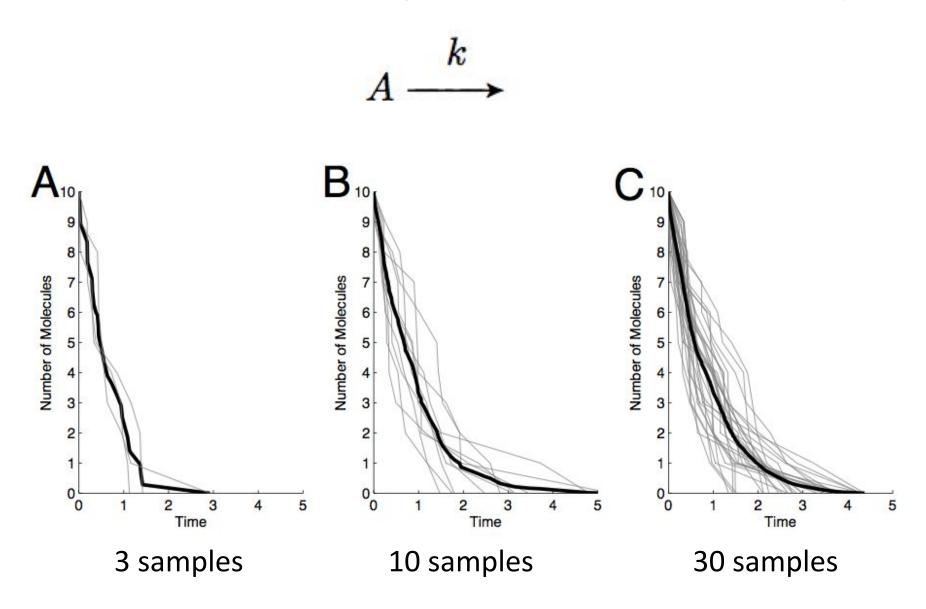


Stochastic Simulation Algorithm

Stochastic Simulation Algorithm (SSA)

- 1. Set the initial state N. Initialize time t to zero.
- 2. Calculate the reaction propensities $a_k(\mathbf{N})$.
- 3. Draw a sample R_k from the random variable R (Figure 7.43).
- 4. Draw a sample τ from the random variable T (Figure 7.44).
- 5. Increment the simulation time $t \to t + \tau$ to account for the elapsed time.
- 6. Update the state vector $\mathbf{N} \to \mathbf{N} + \mathbf{s}_k$ to reflect the fact that reaction R_k has occurred.
- 7. Return to step 2.

Ensemble average: constitutive decay



Bursty transcription

Gene expression:

 $R_1: (transcription) \longrightarrow M$ propensity: k_r

 $R_2: (translation) \longrightarrow P$ propensity: $k_p N_M$

 $R_3: (\text{degradation}) \qquad M \longrightarrow \qquad \text{propensity: } \delta_r N_M$

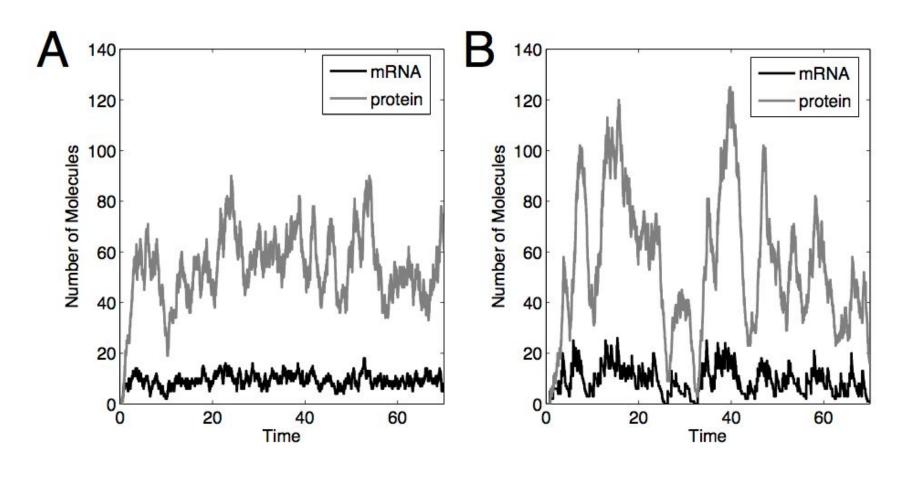
 $R_4: (\text{degradation}) \qquad P \longrightarrow \qquad \text{propensity: } \delta_p N_P$

Bursty transcription:

 \tilde{R}_1 : (bursty transcription) $\longrightarrow 5M$ propensity: $\frac{k_r}{5}$

ODE system is the same. But stochastically they behave very differently!

Bursty transcription far noisier!



"standard" transcription

bursty transcription