

Module 3: Introduction to Stoichiometry and Propensity Functions

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Motivation





Intensity signals of nascent protein display fluctuations over time due to underlying transcription dynamics

Motivation: What are models good for?



Outline

Reaction

 Reaction Propensity

 Law of Mass Action Putting it all

Together

Final Notes
Example 1
Example 2

Example 3Example 4

 Mechanistic Model

Motivation & Intro

Stoichiometry

What are dynamic models useful for in biological processes?

- 1. Mechanistic underpinning of real data
- 2. Predictive power in new circumstances
- 3. Biophysical based analysis



Many biological data can be explained by using deterministic or stochastic formulations of chemical reactions using the law of mass action!

Motivation



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What changes in a dynamic chemical system?

- Reactions have a <u>propensity</u> to cause a change in species count according to the <u>stoichiometry</u> of the system
- 2. The *propensity* to react changes depending on the instantaneous state of the system
- 3. The *stoichiometry* of a reaction tell us how each reaction changes on the number of species in the system

What is a '**model**'?

A model is a combination of both <u>stoichiometry, and propensity which can</u> <u>be used to capture the dynamics of a biological system</u>

Model time dynamics can be analyzed using differential equations, stochastic simulation algorithms and chemical master equations

Motivation:



 Outline Motivation & Intro Mechanistic Model Reaction Stoichiometry Reaction Propensity Law of Mass Action Putting it all Together Final Notes Example 1 Example 2 Example 3 Example 4 	Different levels of model detail give arise to different levels of accuracy and complexity				
			Deterministic Analysis	Stochastic Analysis	
	Less Detail	Mixed Models	Ordinary Differential Equation	Chemical Master Equation Stochastic Simulation Alg.	
	Mid Detail	Compartmental Models	System of Ordinary Differential Equations	Chemical Master Equation Stochastic Simulation Alg.	
	More Detail	Spatial Models	Partial Differential Equations	Reaction-Diffusion Master Equation	

- Mixed models assume the the space where the chemical reactions occur are well mixed ۲
- Compartmental models break down the space into a set of compartments ۲
- Spatial models assume that each point in space has an associated local concentration ۲

Motivation:





Mixed Model: One value for concentration everywhere Compartmental Model: Different compartments share the same concentration Spatial Model: Every point in space has its own concentration

Intro- Deterministic vs Stochastic Models



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Ordinary Differential Equations (ODE's) are used to solve a model.

ODE modeling methods for chemical reactions do not work well to model noise

$$\frac{lx}{lt} = k - \gamma x$$
$$\frac{lx}{dt} = ????$$

Where **ODEs** can be misleading:

- Molecule counts aren't continuous, especially for small volumes like cells
- Real systems exhibit fluctuations

Learning Objectives

Learning objectives for this lecture:

- Learn to define propensity functions and stoichiometry vectors for chemical reactions
- Learn how to use the law of mass action to estimate propensity functions

Making chemical reaction sets out of mechanistic mo uq-bio

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Example: Model for membrane dimerization



- 1. Monomers are brought to the cell membrane
- 2. Monomers can dimerize into dimers
- 3. Dimers become phosphorylated and become active dimers



How would you model this using Spatial, Compartmental, or well-mixed? How would you model this using deterministic vs stochastic assumptions?

Making chemical reactions out of models

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Break down the system into five reactions



 $\emptyset \to x_1$ $x_1 \to \emptyset$ $x_1 + x_1 \rightarrow x_2$ $\begin{array}{c} x_2 \to x_3 \\ x_3 \to \emptyset \end{array}$

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Reaction Stoichiometry



The stoichiometry matrix shows the net change in molecule count after each Outline Motivation & Intro reaction Mechanistic Model Reaction Stoichiometry **Steps to Defining Stoichiometry Vectors:** $\emptyset \rightarrow x_1$ Reaction Identify the number of unique species (N=3) Propensity $x_1 \rightarrow \emptyset$ Law of Mass Identify the number of reactions (M=5) Action The stoichiometry vector of a reaction is the *net change* of each species $x_1 + x_1 \rightarrow x_2$ Putting it all Stoichiometry matrix is a bundle of all the vectors Together Final Notes $x_2 \rightarrow x_3$ There are M stoichiometry vectors, and each is a Nx1 vector. Example 1 $x_3 \rightarrow \emptyset$ Example 2 The stoichiometry of a reaction system can be represented as a NxM matrix: Example 3 $S = [s_1, s_2, ..., s_M]$ Example 4 Write the Stoichiometry matrix for the chemical reaction set above.

Reaction Stoichiometry

Example 4



The stoichiometry matrix shows the net change in molecule count after each Outline Motivation & Intro reaction Mechanistic Model Reaction Stoichiometry **Steps to Defining Stoichiometry Vectors:** $\emptyset \rightarrow x_1$ Reaction Identify the number of unique species (N=3) Propensity $x_1 \rightarrow \emptyset$ Law of Mass Identify the number of reactions (M=5) Action The stoichiometry vector of a reaction is the *net change* of each species $x_1 + x_1 \rightarrow x_2$ Putting it all Stoichiometry matrix is a bundle of all the vectors Together Final Notes $x_2 \rightarrow x_3$ There are M stoichiometry vectors, and each is a Nx1 vector. Example 1 $x_3 \rightarrow \emptyset$ Example 2 The stoichiometry of a reaction system can be represented as a NxM matrix: Example 3

 $\boldsymbol{S} = [s_1, s_2, \dots, s_M]$

Write the Stoichiometry matrix for the chemical reaction set above.

 $s_{1} = [1, 0, 0]^{T}$ $s_{2} = [-1, 0, 0]^{T}$ $s_{3} = [-2, 1, 0]^{T}$ $s_{4} = [0, -1, 1]^{T}$ $s_{5} = [0, 0, -1]^{T}$

$$S = \begin{bmatrix} 1 & -1 & -2 & 0 & 0 \\ 0 & 0 & 1 & -1 & 0 \\ 0 & 0 & 0 & 1 & -1 \end{bmatrix}$$

Reaction Rates and Propensity Functions



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Reaction rates are functions of the state $w_{\mu}(x_{1,x_{2,...}})$ that describes the instantaneous speed of chemical reaction.

- For deterministic models $\mathbf{w}_{\mu}dt$ is the amount that the μ^{th} reaction occurs in a time step dt
- $\mathbf{w}_{\mu}dt$ is the probability that the μ^{th} reaction will occur in a time step of length dt.
- Reaction rate and propensities are usually dependent on the current state (x1,x2,...) of the system (e.g., law of mass action).
- Reaction rates and Propensities are always positive



Reaction rates and propensities depend on the current state

Law of Mass Action



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The law of mass action states that the rate of a chemical reaction is proportional to the number of unique combinations by which reactants can combine to form the products:

$$w_m \propto \prod_{n=1}^{N} (x_n \text{ choose } R_{nm})$$
 $w_m = k \prod_{n=1}^{N} (x_n \text{ choose } R_{nm})$

where R_{nm} is the number of *reactant* molecules of species *n* needed for the *m*th reaction and k arbitrary

n!	Reaction	x_n choose k	Propensity equation
$n \ choose \ m = \frac{1}{m! \ (n-m)!}$	$r_1: x_1 \to x_2$	x_1 choose $1 = x_1$	kx_1
•	$r_2: x_1 + x_1 \to x_2$	$(x_1 \ choose \ 2) = x_1(x_1 - 1)/2$	$kx_1(x_1 - 1)/2$
• •	$r_3: 2x_1 + x_2 \to x_3$	$(x_1 choose 2)(x_2 choose 1)$	$kx_1(x_1 - 1)(x_2)/2$
•	$r_4: \emptyset \to x_1$	$(x_1 \ choose \ 0) = 1$	k

- When x is large, x(x-1) is approximately equal to x^2 . This is the common form of mass action for ODE analyses.
- When x is small (integer copy numbers), the effect of finite molecule counts is far more important.
- k is an arbitrary proportionality coefficient in many applications, the integer in the denominator of the combinatorial is lumped into this constant.
- Propensity functions depend only on the *reactants* the products are irrelevant.

Reaction Propensity

 $\emptyset \rightarrow x_1$

 $x_1 \to \emptyset$

 $x_1 + x_1 \rightarrow x_2$

 $x_2 \rightarrow x_3$

 $x_3 \rightarrow \emptyset$



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Propensity is a function of state and time which describes the instantaneous rate of reaction of chemical reactions

Each reaction has its own propensity to react. The **propensity vector (W)** describes the propensity of each reaction in a vector:

$$w_1 = \dots$$

 $w_2 = \dots$
 $w_m = \dots$

Use the Law of Mass action to write the propensity of the above reactions.

Reaction Propensity

 $\emptyset \rightarrow x_1$

 $x_1 \to \emptyset$

 $x_1 + x_1 \rightarrow x_2$

 $x_2 \rightarrow x_3$

 $x_3 \rightarrow \emptyset$



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$$w_1 = \dots$$

 $w_2 = \dots$
 $w_m = \dots$

Use the Law of Mass action to write the propensity of the above reactions.

$$\begin{array}{l} w_1(x,t) = k_1 \\ w_2(x,t) = k_2 x_1 \\ w_3(x,t) = k_3(x_1)(x_1 - 1)/2 \\ w_4(x,t) = k_4 x_2 \\ w_5(x,t) = k_5 x_3 \end{array} \quad W(x,t) = \begin{bmatrix} k_1 \\ k_2 x_1 \\ k_3(x_1)(x_1 - 1)/2 \\ k_4 x_2 \\ k_5 x_3 \end{bmatrix} \quad \text{or } W'(x,t) = \begin{bmatrix} k_1 \\ k_2 x_1 \\ k_2 x_1 \\ k_3(x_1)(x_1 - 1)/2 \\ k_4 x_2 \\ k_5 x_3 \end{bmatrix}$$

Putting it all together



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The "mean field" ODE description for the instantaneous rate of change of the average system is given by: dx

$$\frac{dx}{dt} = S W(x,t)$$

 $S = \begin{bmatrix} 1 & -1 & -2 & 0 & 0 \\ 0 & 0 & 1 & -1 & 0 \\ 0 & 0 & 0 & 1 & -1 \end{bmatrix} \qquad \qquad W(x,t) = \begin{bmatrix} k_1 \\ k_2 x_1 \\ k'_3(x_1)(x_1 - 1) \\ k_4 x_2 \\ k_5 x_3 \end{bmatrix}$

Write the equation for $\frac{dx}{dt}$ given the S and W defined above.

$$\frac{dx_1}{dt} =$$
$$\frac{dx_2}{dt} =$$
$$\frac{dx_3}{dt} =$$

Putting it all together



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Write the equation for $\frac{dx}{dt}$ given the S and W defined above.

$$\frac{dx_1}{dt} = k_1 - k_2 x_1 - 2k'_3 x_1 (x_1 - 1)$$
$$\frac{dx_2}{dt} = k'_3 x_1 (x_1 - 1) - k_4 x_2$$
$$\frac{dx_3}{dt} = k_4 x_2 - k_5 x_3$$

$$\frac{d\mathbf{x}}{dt} = \begin{bmatrix} k_1 - k_2 x_1 - 2k'_3 x_1 (x_1 - 1) \\ k'_3 x_1 (x_1 - 1) - k_4 x_2 \\ k_4 x_2 - k_5 x_3 \end{bmatrix}$$

Putting it all together



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The ODE description for the instantaneous rate of change of the entire system is given by: $\frac{dx}{dt} = S W(x, t)$

 $S = \begin{bmatrix} 1 & -1 & -2 & 0 & 0 \\ 0 & 0 & 1 & -1 & 0 \\ 0 & 0 & 0 & 1 & -1 \end{bmatrix}$



time

 $\frac{dx}{dt}$ can be integrated numerically to solve for the ODE solution of the model.

scipy.integrate.odeint

$$W'(x,t) = \begin{bmatrix} k_1 \\ k_2 x_1 \\ k'_3(x_1)(x_1 - 1) \\ k_4 x_2 \\ k_5 x_3 \end{bmatrix}$$

Final Notes: Reaction Stoichiometry



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$\mathbf{s}_1 = [1, 0]^T$	
$egin{array}{lll} \mathcal{S}_1 & ightarrow \mathcal{S}_1 + \mathcal{S}_1 \ \mathcal{S}_2 & ightarrow \mathcal{S}_2 + \mathcal{S}_1 \ \emptyset ightarrow \mathcal{S}_1 \end{array}$	
$\mathbf{s}_2 = [-1, 0]^T$]
${\mathcal S}_1 + {\mathcal S}_1 o {\mathcal S}_1$	

 $\mathcal{S}_1 + \mathcal{S}_2 o \mathcal{S}_2$

 $\mathcal{S}_1 \to \emptyset$

 $\mathbf{s}_{3} = [0, 1]^{T}$ $\begin{array}{c} \mathcal{S}_{2} \rightarrow \mathcal{S}_{2} + \mathcal{S}_{2} \\ \mathcal{S}_{1} \rightarrow \mathcal{S}_{1} + \mathcal{S}_{2} \\ \emptyset \rightarrow \mathcal{S}_{2} \end{array}$ $\mathbf{s}_{4} = [1, -1]^{T}$ $\begin{array}{c} \mathcal{S}_{2} \rightarrow \mathcal{S}_{1} \\ \mathcal{S}_{1} + \mathcal{S}_{2} \rightarrow \mathcal{S}_{1} + \mathcal{S}_{1} \\ \mathcal{S}_{2} + \mathcal{S}_{2} \rightarrow \mathcal{S}_{1} + \mathcal{S}_{2} \end{array}$

The stoichiometry only measures the **net** change (increase in products – decrease in reactants), whereas propensities depend only on *reactants*.

For this reason, the same stoichiometry can correspond to many different propensity functions. Stoichiometry **should not** be used to guess the propensity – nor vice-versa!

Final Notes: Reducing Model Size Using Separation of Timescales

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Is the law of mass action **required** for the definition of propensity functions?

Michaelis-Menten Dynamics:



Law of Mass action is always correct for a completely modeled system, but model simplifications can lead to different propensities not given by law of mass action

Example 1: Birth Decay Process



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Example 1: Birth Decay Process



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Example 2: Bursting Gene Expression



Example 2: Bursting Gene Expression



Example 4: Stochastic Oscillator



Example 4: Stochastic Oscillator



Example 3: Genetic Toggle



Example 3: Genetic Toggle

