

# Enzyme-Substrate Dynamics & Michaelis-Menten Model

Tianyun (Jason) Lin

Lab 6, C&SB 150, Spring 2019

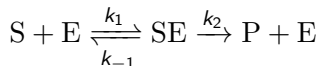
May 10th, 2019

- Two .m files for today's lab: `enzymekin.m` and `QSSA_func.m` (download from CCLE lab assignment 6 portal).
- Can also download lecture8 note for more information on MM model.

# Outline for today

- Review Michaelis-Menten Model.
- Model and simulate MM model through Matlab.
- Incorporate Quasi-Steady State Approximation (QSSA) into the model.

# Michaelis-Menten Model



- Translate the chemical reaction into equations for each compartment.
- What quantity is not changing?

# Quasi-Steady State Approximation (QSSA)

- What's the assumption?
- What's the amount of complex under the assumption of QSSA?
- What about  $\frac{dP}{dt}$  and  $\frac{dS}{dt}$ ?
- When is QSSA a good approximation and when is QSSA a bad approximation?

# MM Model - System description in Matlab

```
function [dxdt] = QSSA_func(t,x,K1,K1MINUS,K2,e0)
% Single Substrate-Enzyme Reaction
% R1: S + E -- k1 --> ES
% R2: ES -- k1minus --> E + S
% R3: ES -- k2 --> E + P
% ----Original----
s=x(1); e=x(2); c=x(3); p=x(4);
dsdt = %% REPLACE %%;
dedt = %% REPLACE %%;
dcdt = %% REPLACE %%;
dpdt = %% REPLACE %%;
% ----sQSSA----
% Constraints
%     e(t) + c(t) = e0
% Assumption
%     dcdt ~ 0
%_s_qssa = x(5); p_qssa = x(6);
% Pack output
dxdt=[dsdt;dedt;dcdt;dpdt];
return
```

# MM Model - Simulation in Matlab

- Use `enzymkin.m` to simulate and plot the MM model.
- First, you need to enter corresponding parameters and initial conditions:

```
K1      = %% REPLACE %%;  
K1MINUS = %% REPLACE %%;  
K2      = %% REPLACE %%;
```

```
% Initial conditions x0.
```

```
s0 = %% REPLACE %%;  
e0 = %% REPLACE %%;  
c0 = %% REPLACE %%;  
p0 = %% REPLACE %%;
```

## Note:

- For question3, when you modify the code in `QSSA_func.m`, remember that you are adding two differential equations into your model. Therefore, make sure to also update the number of input/output variables to match the change.
- Also change the code for plotting in the `enzymkin.m` to accommodate for the modification (basically adding two items for plotting two more curves.)