

Modeling Biological Systems With Cybernetic Control Laws and Steady State Flux Distributions

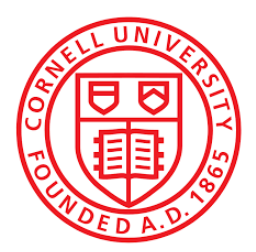
Master of Science Exam

Department of Chemical and Biomolecular Engineering

Kritika Kashyap

Committee Member : Jeffrey D. Varner (Chair)

Matthew DeLisa

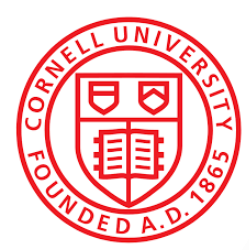


Overview

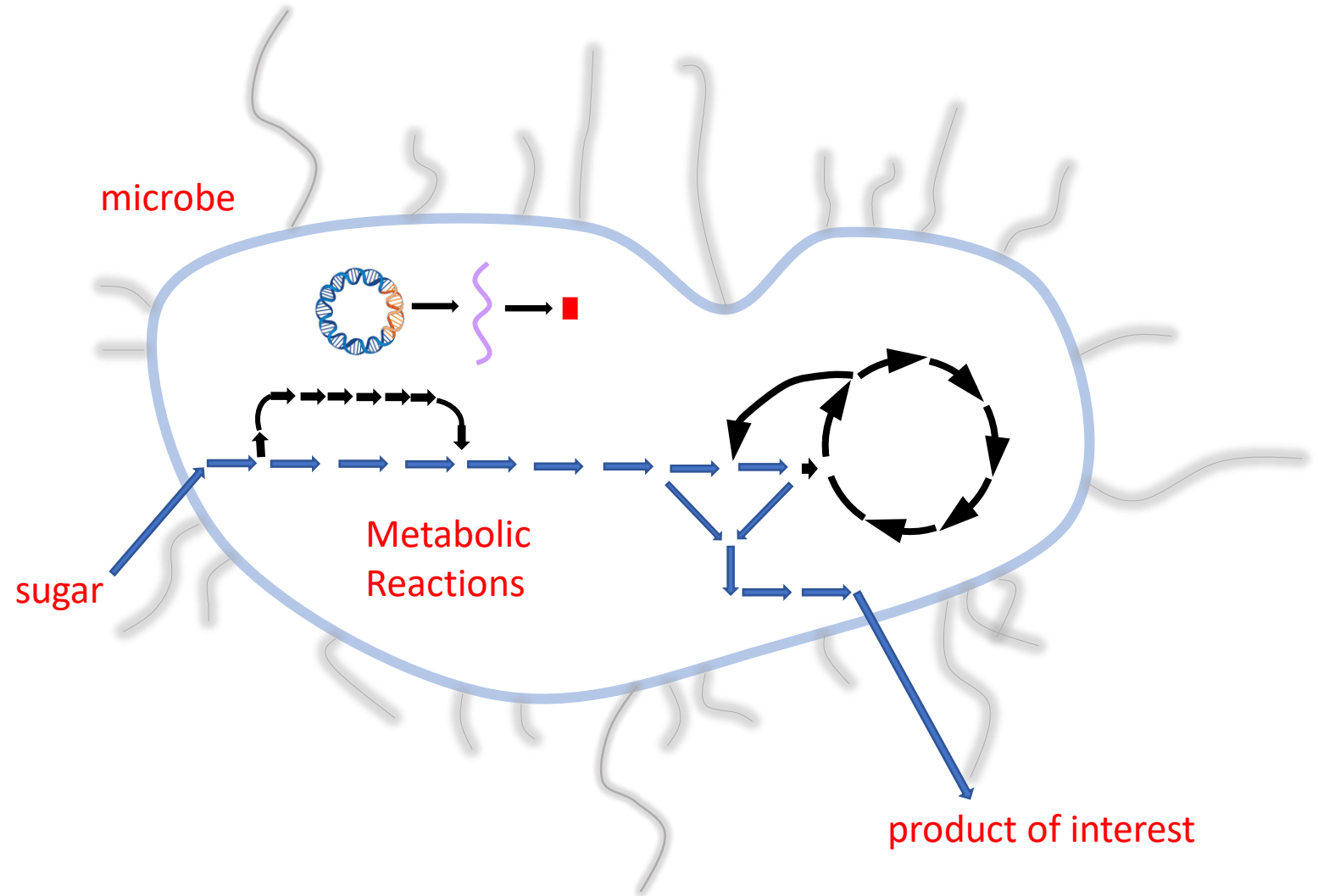
Review Basic
Concepts

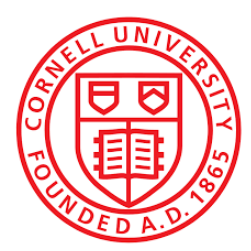
Model of
Escherichia coli
(*E. coli*) cells

Model of *Chinese*
Hamster Ovary
(*CHO*) cells



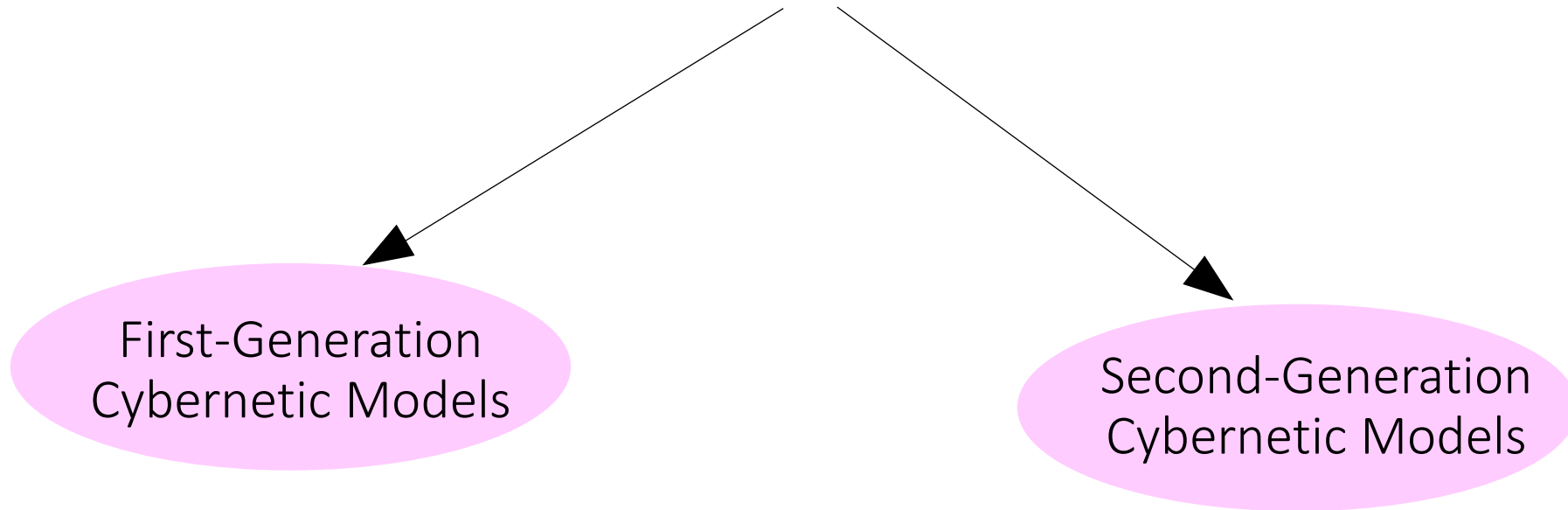
Motivation : Metabolic Engineering of Organisms

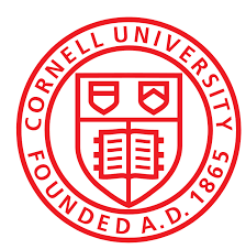




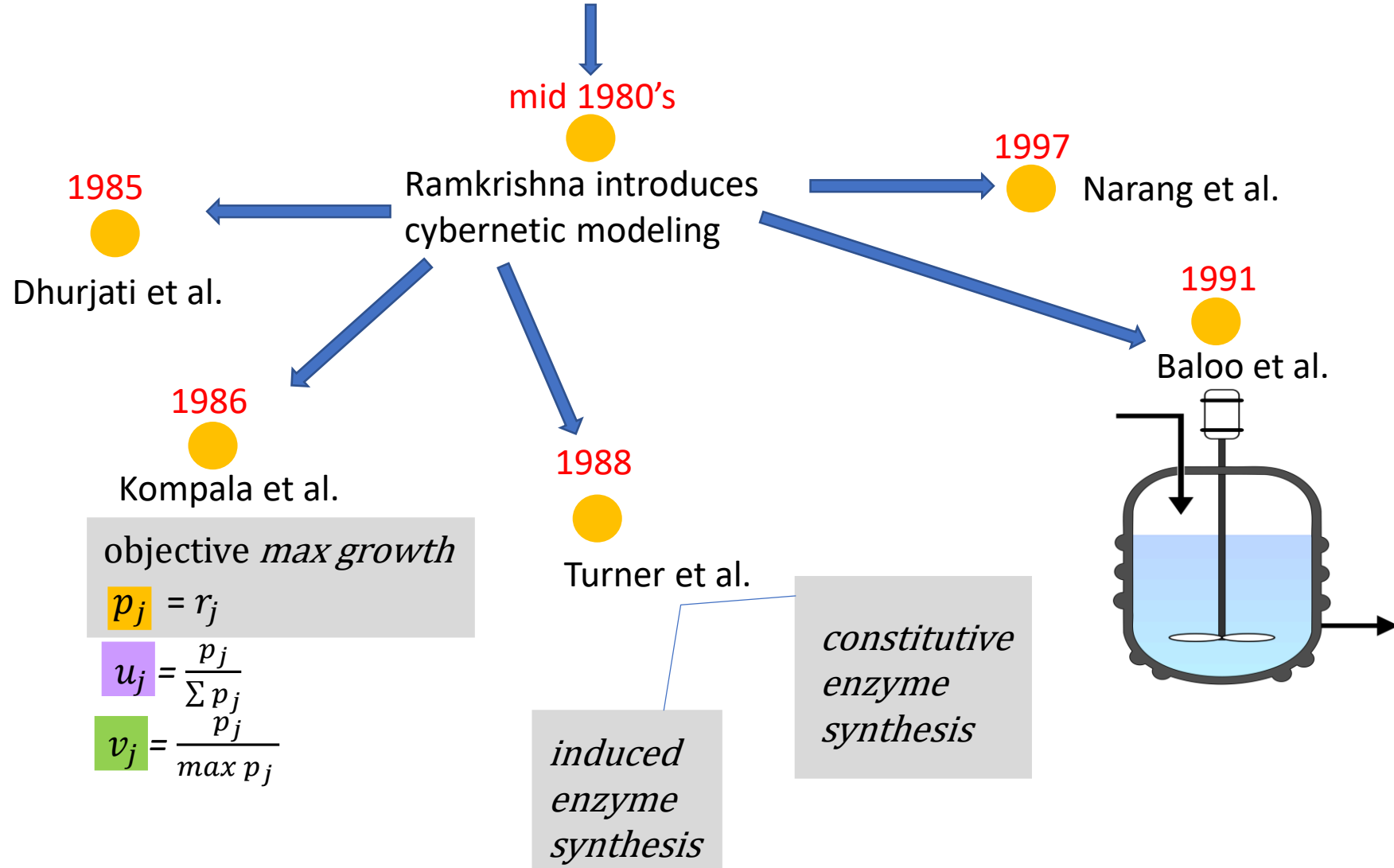
Cybernetic Models

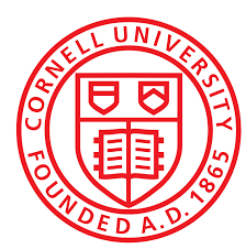
1. Assumption : The ultimate goal of an organism is to grow and survive
2. A cell will act, sense, compare itself to its goal and self correct its inner functions until it can successfully achieve its goal





First-Generation Cybernetic Models





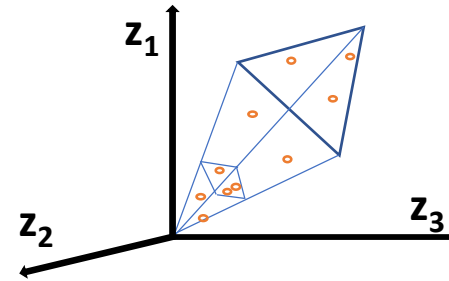
Second-Generation Cybernetic Models

1996
Straight et al.

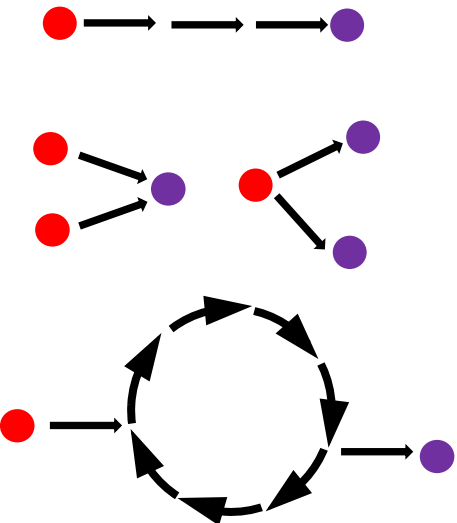
1999
Varner et al.
Local Control *Global Control*

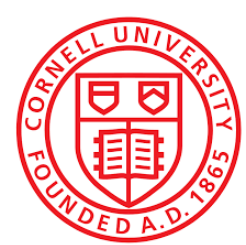
2007
Young et al.

2008
Kim et al.



Flux Analysis

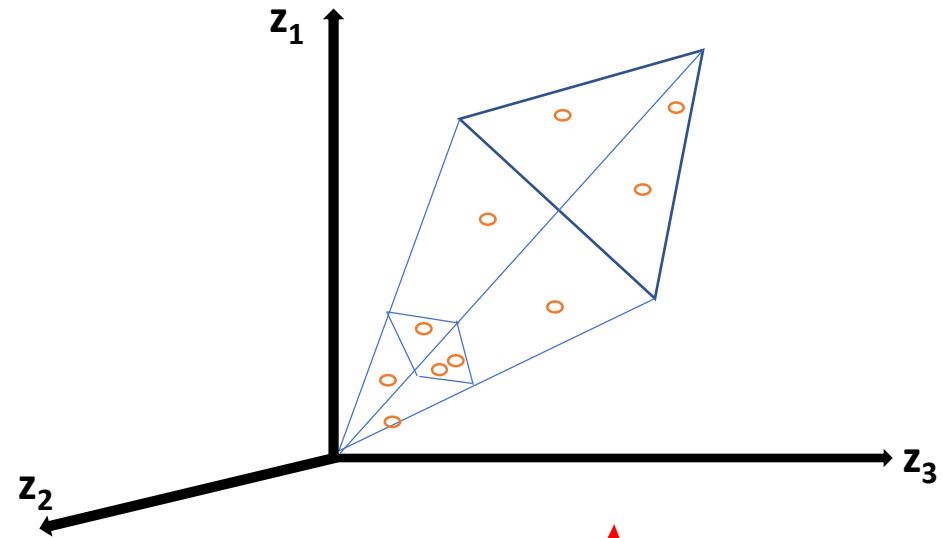




What are elementary flux modes?

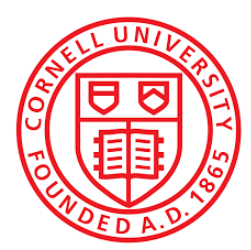
$$\sum_{j=1}^R S_{ij} z_j = 0 \quad \text{for all } i = 1, \dots, M$$
$$j = 1, \dots, R$$

(Steady state assumption)
constraints
 $lb_j \leq z_j \leq ub_j$



Computationally Expensive

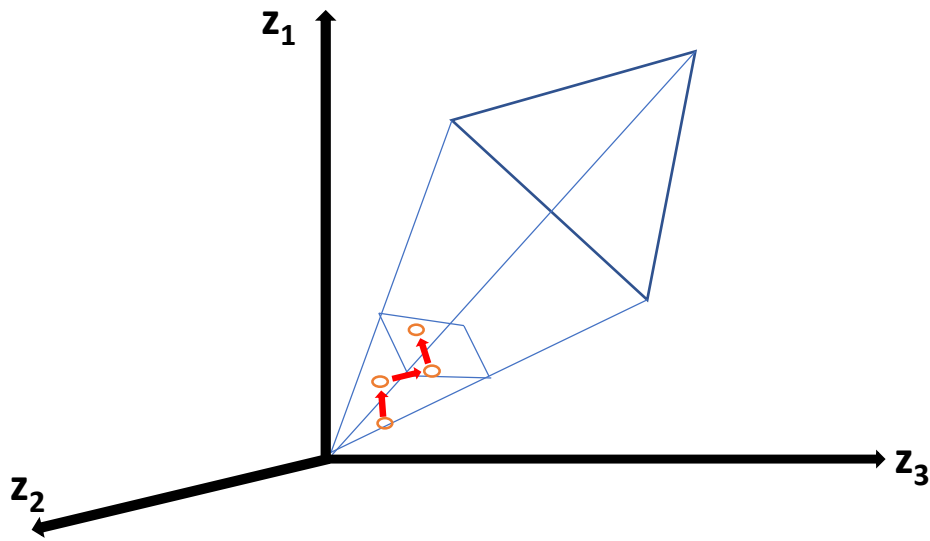
Mathematically
Challenging



Steady State Flux Analysis

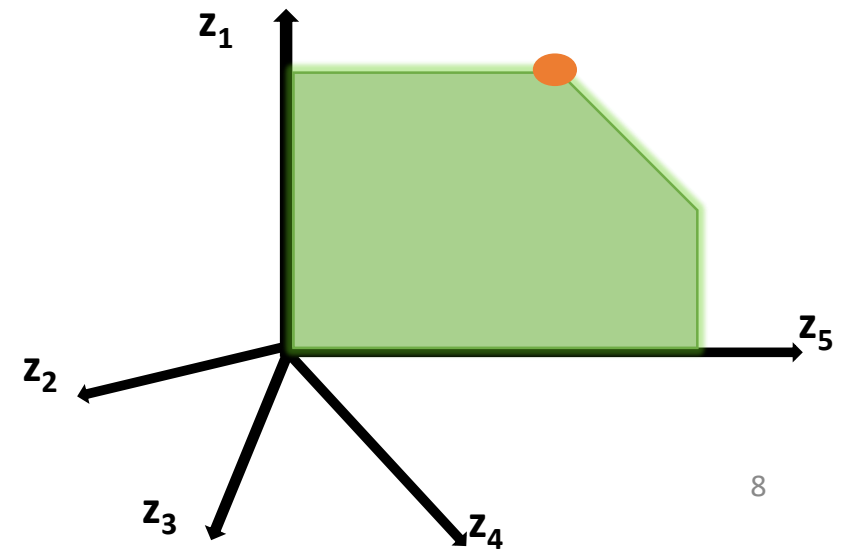
Markov-Chain
Monte-Carlo

UnBiased Flux Analysis



Flux Balance
Analysis

Biased Flux Analysis



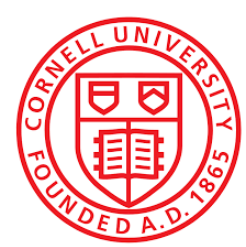


Extracellular fluxes are relatively easier to measure and are used to constrain the solution space

$$\max c^T z$$

(Steady state assumption)
constraints
 $lb_j \leq z_j \leq ub_j$





Markov-Chain Monte-Carlo Sampling

1. Implement following constraints to get the solution space :

$$\sum_{j=1}^R S_{ij} z_j = 0 \quad \text{for all } i = 1, \dots, M$$

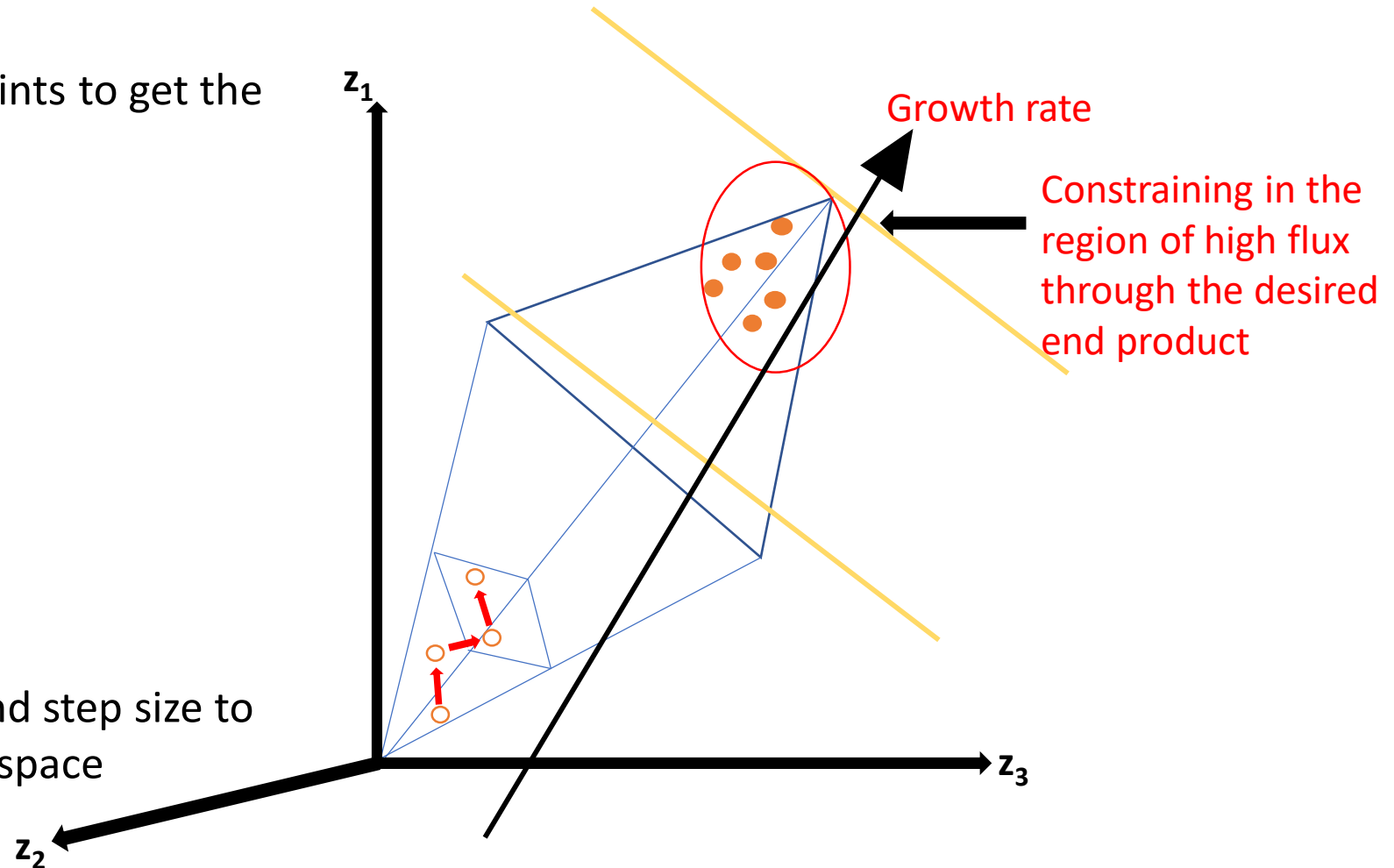
$j = 1, \dots, R$

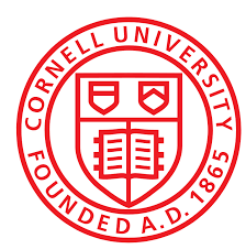
(Steady state assumption)

constraints

$$lb_j \leq z_j \leq ub_j$$

2. Select an initial point
3. Choose a random direction and step size to reach next point in the solution space





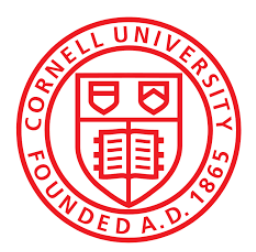
FBA vs Markov-Chain Monte-Carlo

Flux Balance Analysis

1. Assumes an objective function like growth maximization
2. Artificial objective functions are used to generate multiple flux distributions
3. Solution time is within seconds

Markov-Chain Monte-Carlo

1. No growth maximization assumption
2. A sample of feasible flux distribution is obtained
3. Solution time ranges in minutes to an hour



Hybrid Cybernetic Models

Kinetic Expressions

+

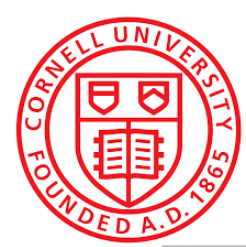
Metabolic Reaction Network

+

Cybernetic Control Laws



Hybrid Cybernetic Models



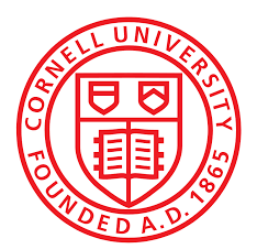
Contribution

Central Carbon stoichiometry (*E. coli*) + Constraints on extracellular fluxes + Flux Balance Analysis + Cybernetic Control Laws + Kinetic Rate Expressions = Hybrid Cybernetic Model with FBA

Central Carbon stoichiometry (*E. coli*) + Constraints on extracellular fluxes + Markov-Chain Monte-Carlo + Cybernetic Control Laws + Kinetic Rate Expressions = Hybrid Cybernetic Model with MCMC

Genome scale stoichiometry (*CHO-K1*) + Constraints on extracellular fluxes + Flux Balance Analysis + Cybernetic Control Laws + Kinetic Rate Expressions = Hybrid Cybernetic Model with FBA

Genome scale stoichiometry (*CHO-K1*) + Constraints on extracellular fluxes + Markov-Chain Monte Carlo + Cybernetic Control Laws + Kinetic Rate Expressions = Hybrid Cybernetic Model with MCMC

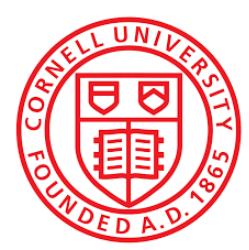


Overview

Review Basic
Concepts

Model of
Escherichia coli
(*E. coli*) cells

Model of *Chinese*
Hamster Ovary
(*CHO*) cells



Hybrid Cybernetic Models

Rate Expressions

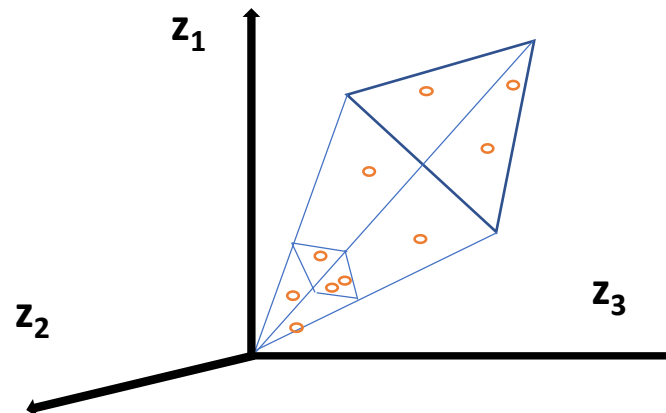
$$r_{M,l} = k_{M,l} e_l \frac{s_l}{K_l + s_l}$$

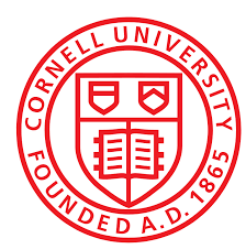
$$r_{E,l} = k_{e,l} \frac{s_l}{K_l + s_l}$$

Cybernetic Control Laws

$$u_l = \frac{z_{s,l} r_{M,l}}{\sum_{l=1}^L z_{s,l} r_{M,l}}$$

$$v_l = \frac{z_{s,l} r_{M,l}}{\max_{l=1,\dots,L} z_{s,l} r_{M,l}}$$





The E. coli System

Model Equations and Assumptions

Batch fermentation of E. coli has been simulated. A reaction network of 118 reactions and 62 metabolites was used. Dynamics within the central carbon metabolism were the focus. Cell death has been ignored.

Specific growth rate for each mode is given as

$$r_{G,l} = z_{biomass,l} r_{M,l}$$

Total growth rate of the system is written as

$$\mu = \sum_{l=1}^L r_{G,l} v_l$$

The abundance of extracellular species is given as

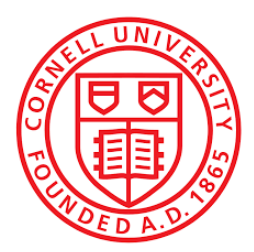
$$\frac{ds_i}{dt} = \sum_{j=1}^R \sum_{l=1}^L s_{i,j} z_j r_{M,l} v_l c$$

Pseudoenzyme levels are governed by

$$\frac{de_l}{dt} = \alpha_l + r_{E,l} u_l - (\beta_l + \mu) e_l$$

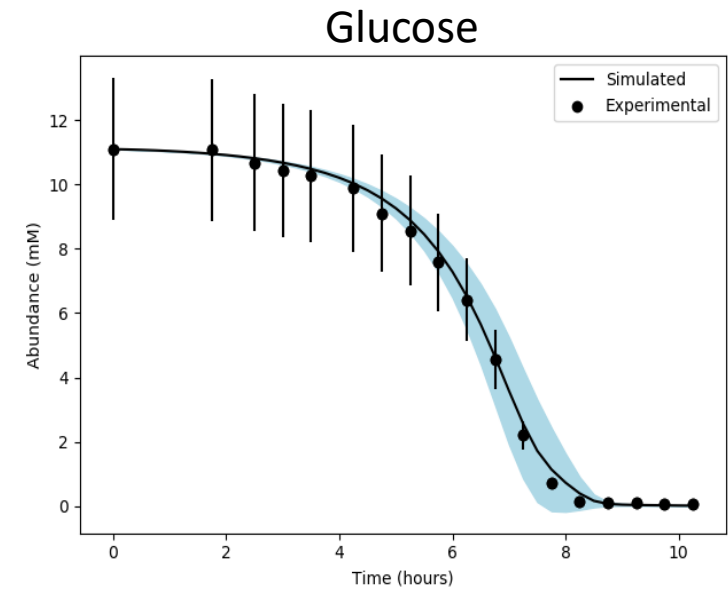
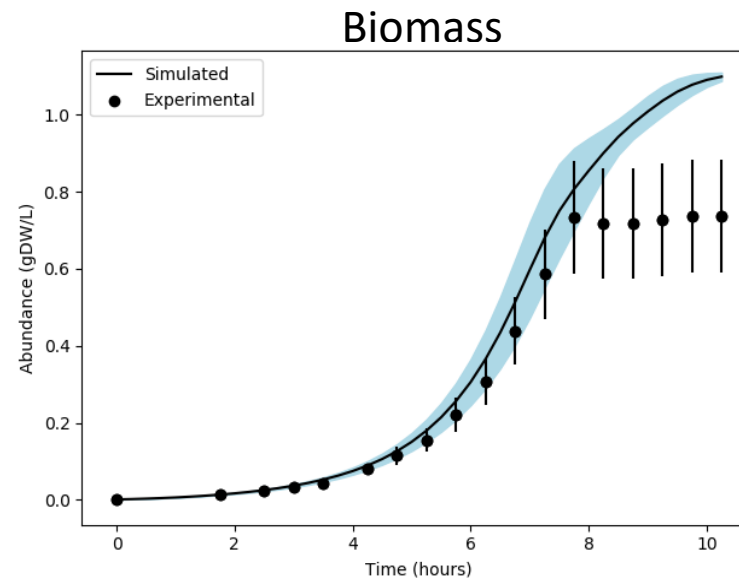
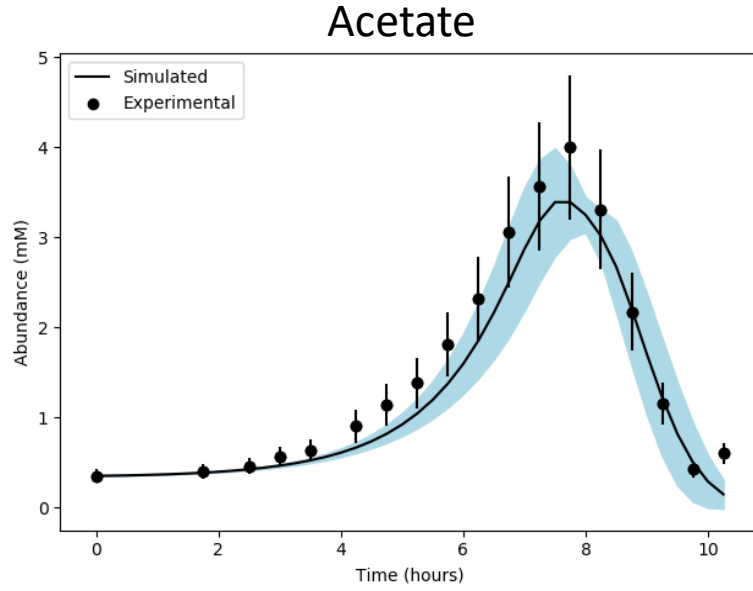
Cell mass is governed by

$$\frac{dc}{dt} = \mu c$$

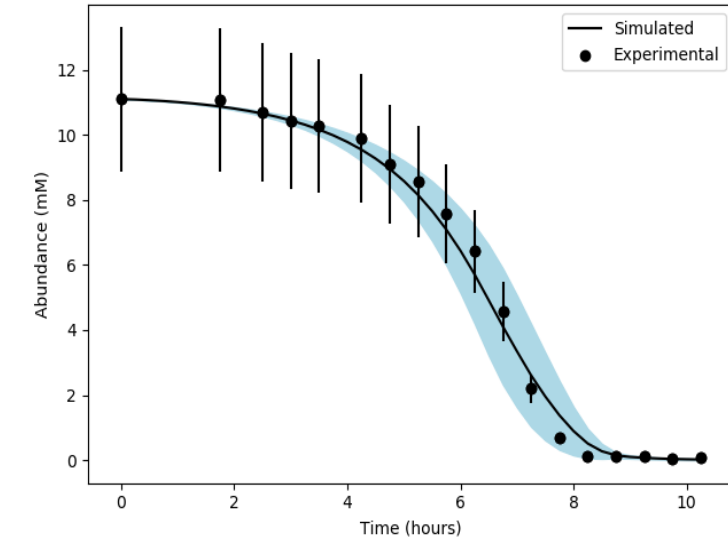
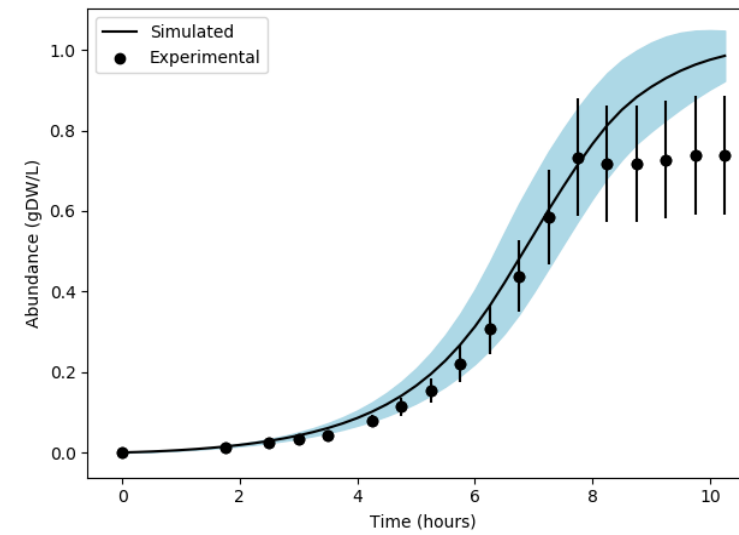
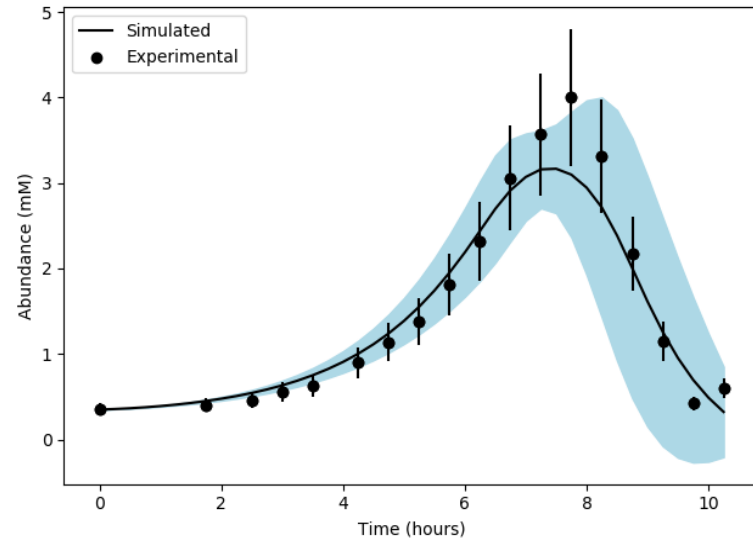


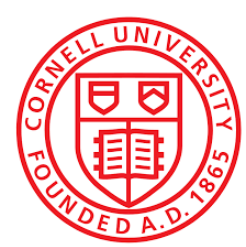
Results

HCM-FBA



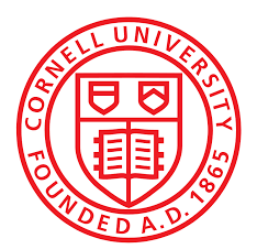
HCM-MCMC





Summary

1. 29 flux modes were generated using FBA and MCMC sampling
2. The framework selects glucose as the preferred substrate
3. There is a clear switch in substrate utilization when glucose is exhausted. Acetate uptake begins at this time
4. HCM-MCMC has no performance penalty compared to HCM-FBA
5. HCM-MCMC offers a better solution strategy than HCM-FBA by eliminating the need to define an objective function that might not be biologically relevant

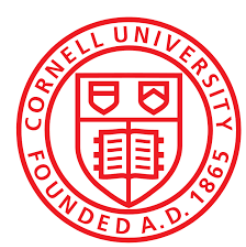


Overview

Review Basic
Concepts

Model of
Escherichia coli
(*E. coli*) cells

Model of *Chinese*
Hamster Ovary
(*CHO*) cells



Chinese Hamster Ovary System

Model Equations and Assumption

Fed-batch based kinetics are performed for *CHO-K1* cells has been simulated. A reaction network of 4723 reactions and 2773 metabolites was used. Cell death has been ignored. Volumetric flow rate will affect dynamics of this system.

Feed stream enters the reactor at a volumetric flow rate F

$$F = \frac{dV}{dt}$$

Rate of dilution can be written as

$$D = \frac{F}{V_0 + Ft}$$

The abundance of extracellular species is given as

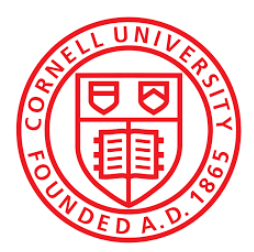
$$\frac{ds_i}{dt} = D(s_f - s) + \sum_{j=1}^R \sum_{l=1}^L S_{i,j} Z_{i,j} r_{M,l} v_l c$$

Pseudoenzyme levels are governed by

$$\frac{de_l}{dt} = \alpha_l + r_{E,l} u_l - (\beta_l + \mu) e_l$$

Cell mass is governed by

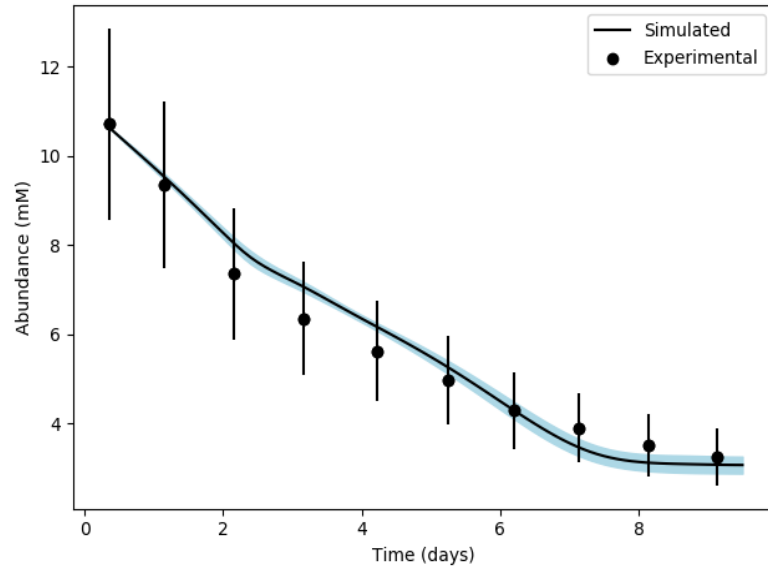
$$\frac{dc}{dt} = (\mu - D) c$$



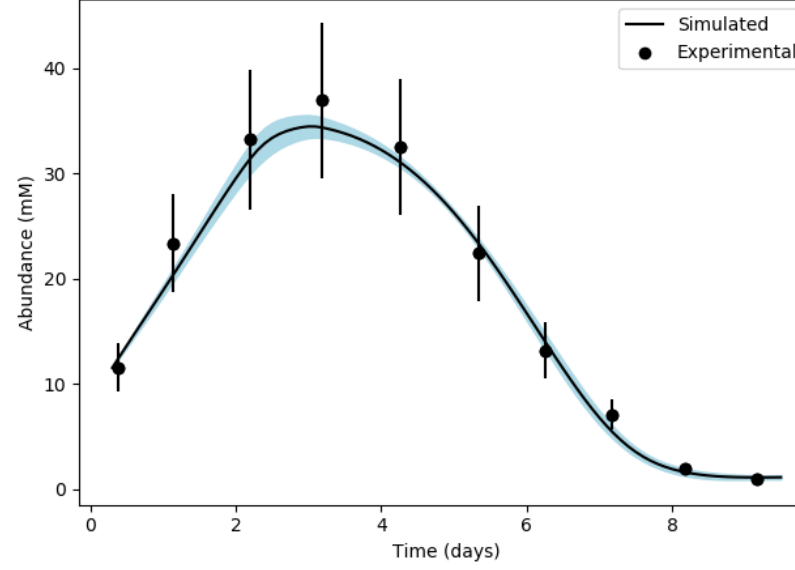
Results

HCM-FBA

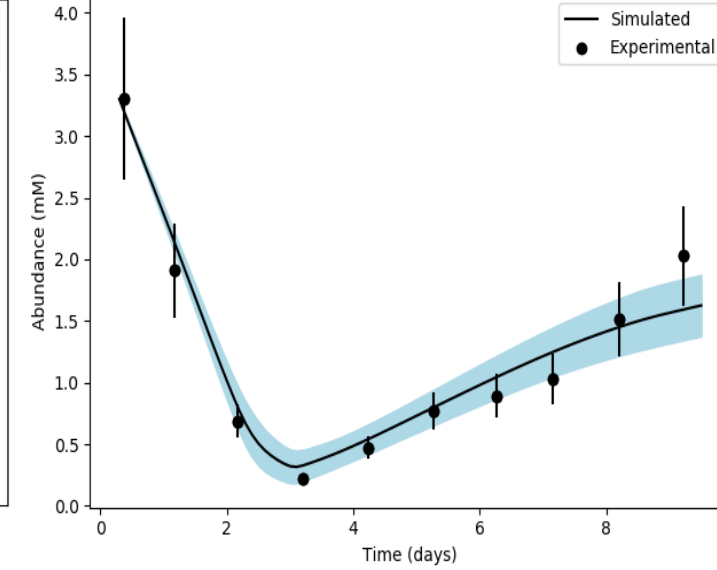
Serine



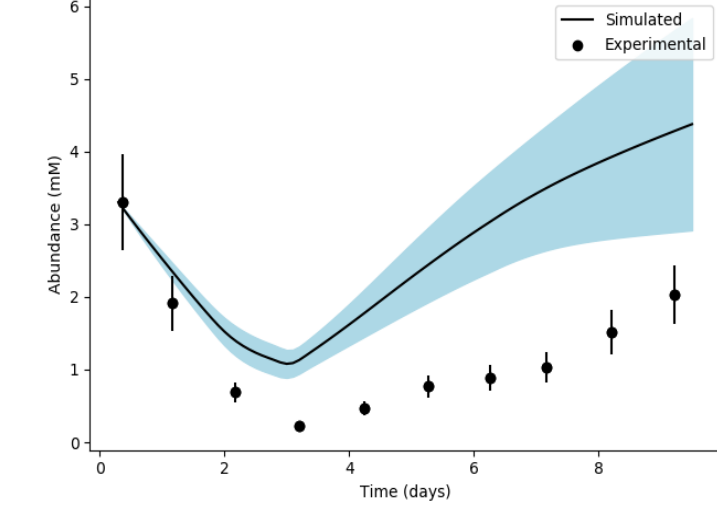
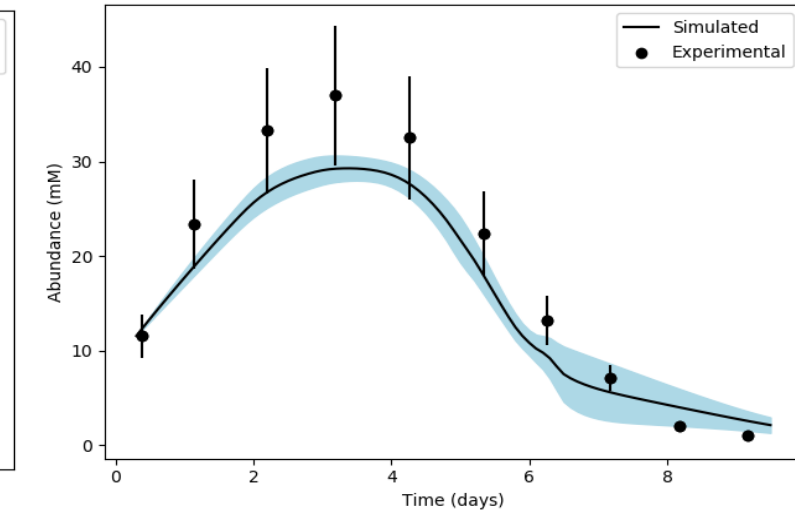
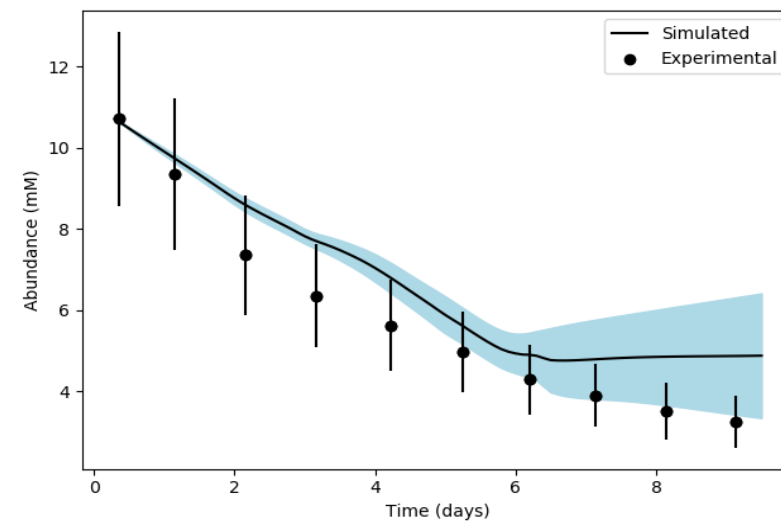
Lactate

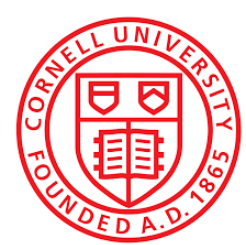


Glutamine



HCM-MCMC





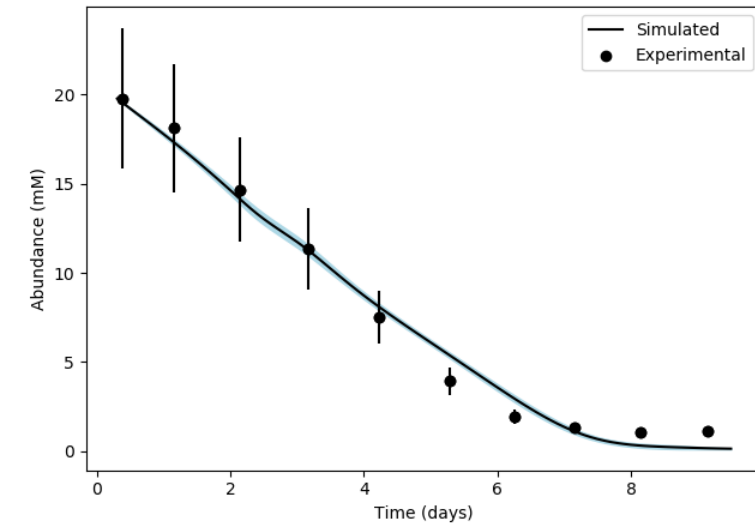
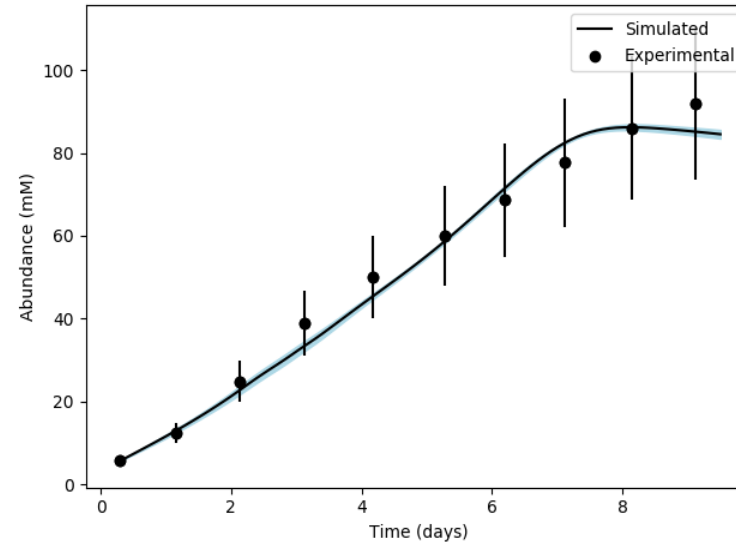
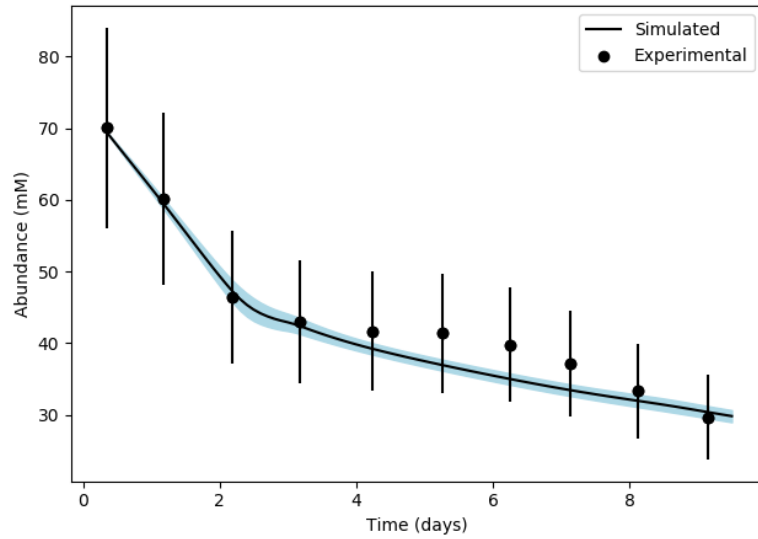
Results

Glucose

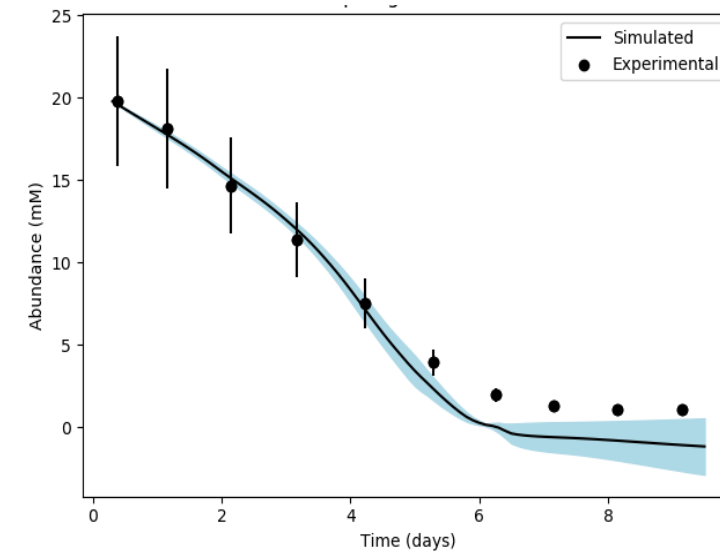
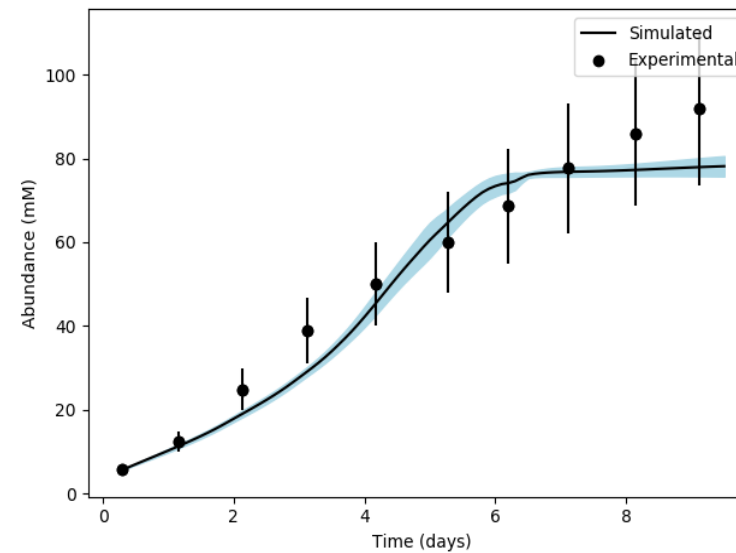
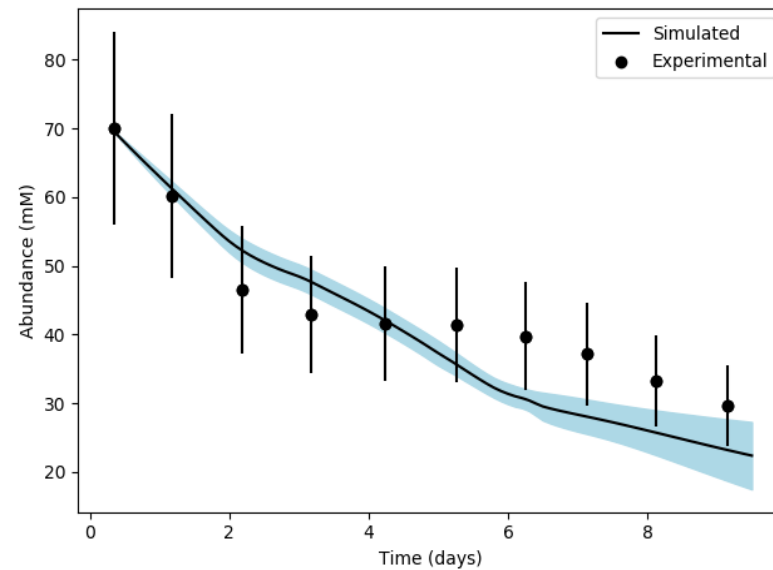
Biomass

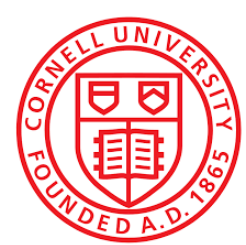
Asparagine

HCM-FBA



HCM-MCMC

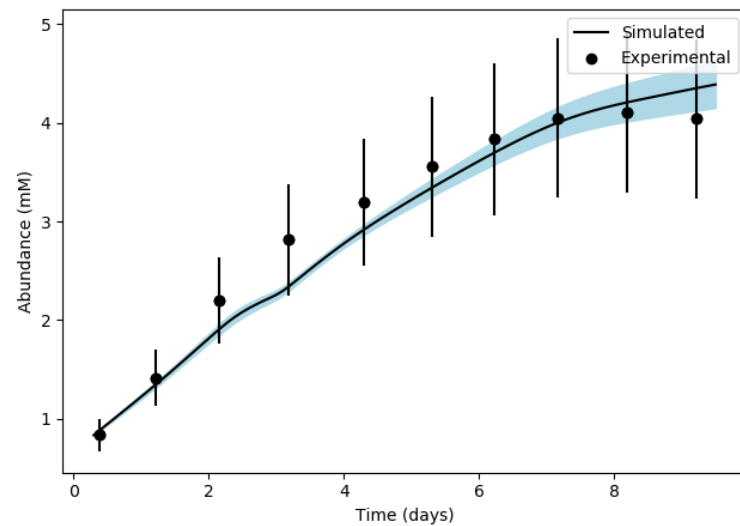




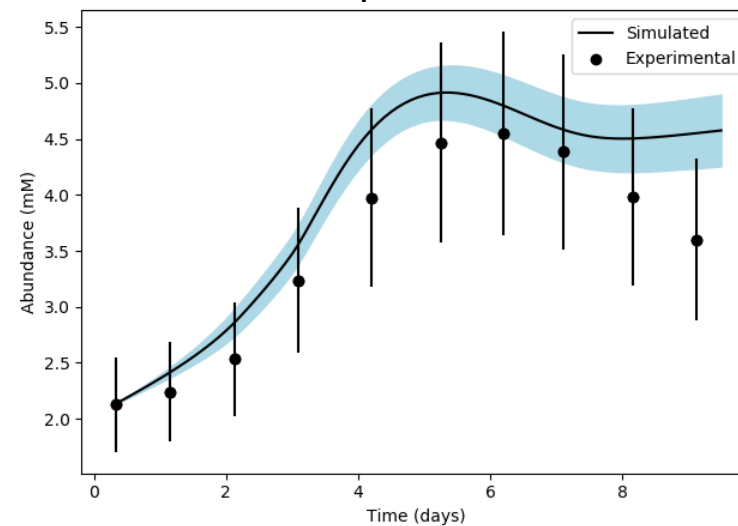
Results

HCM-FBA

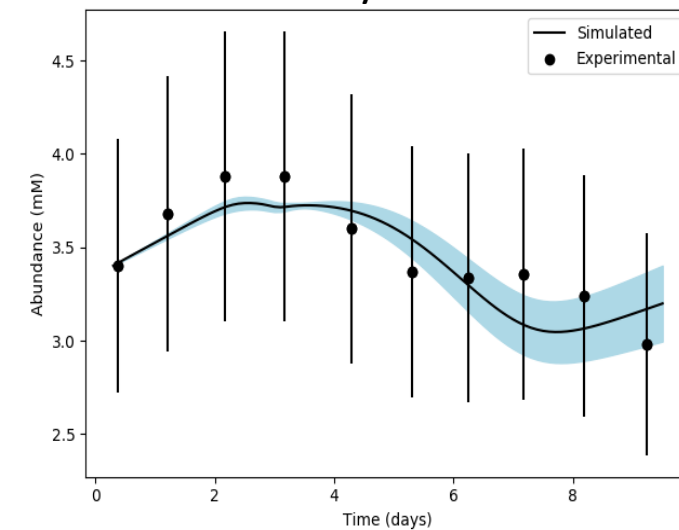
Glutamate



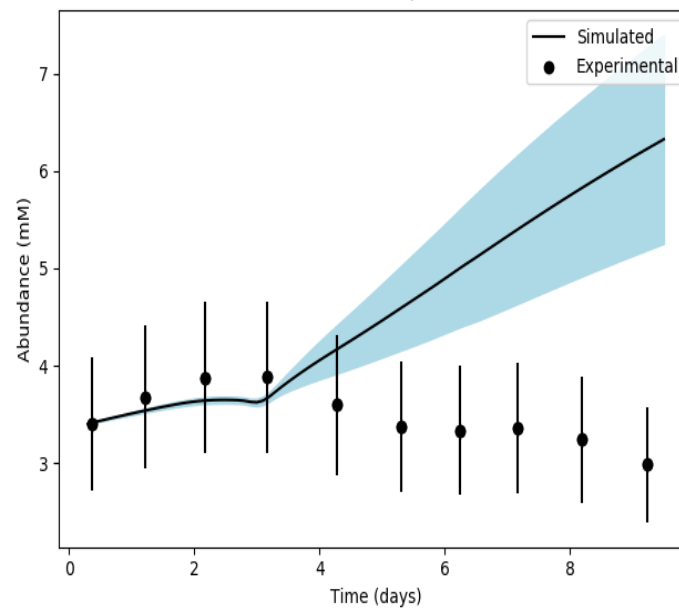
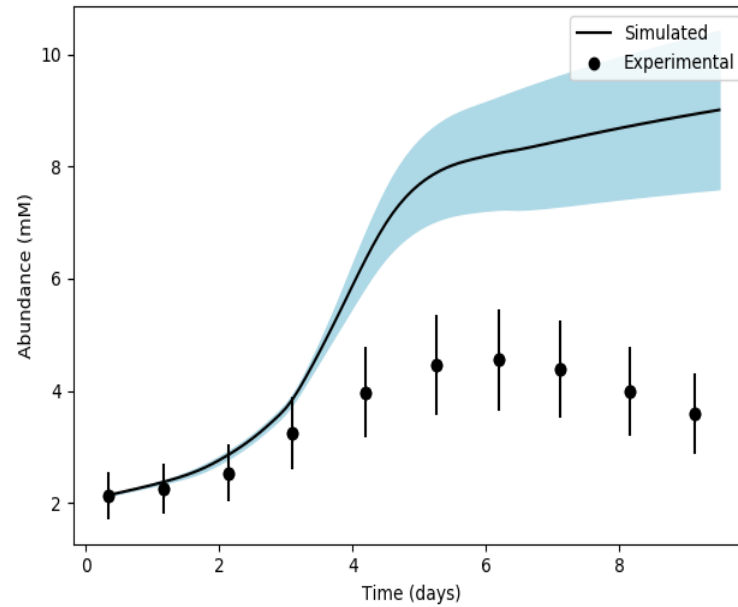
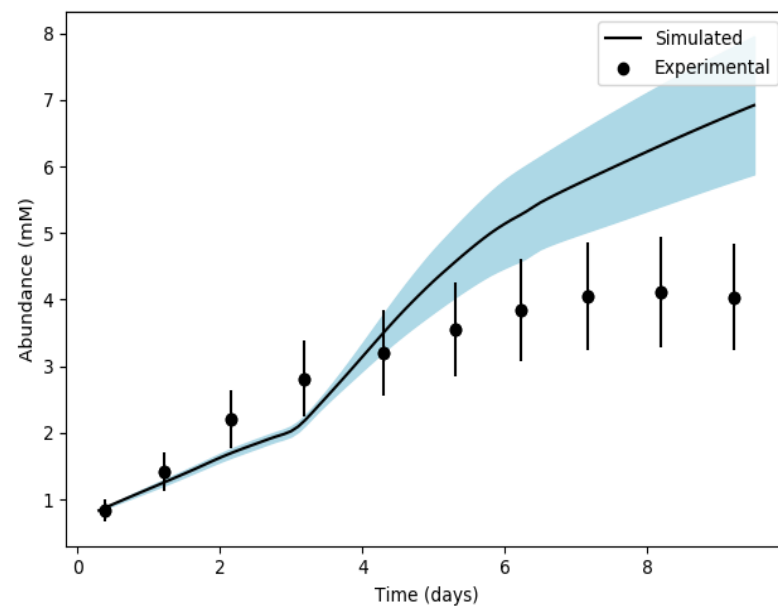
Aspartate

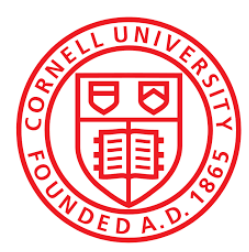


Glycine



HCM-MCMC

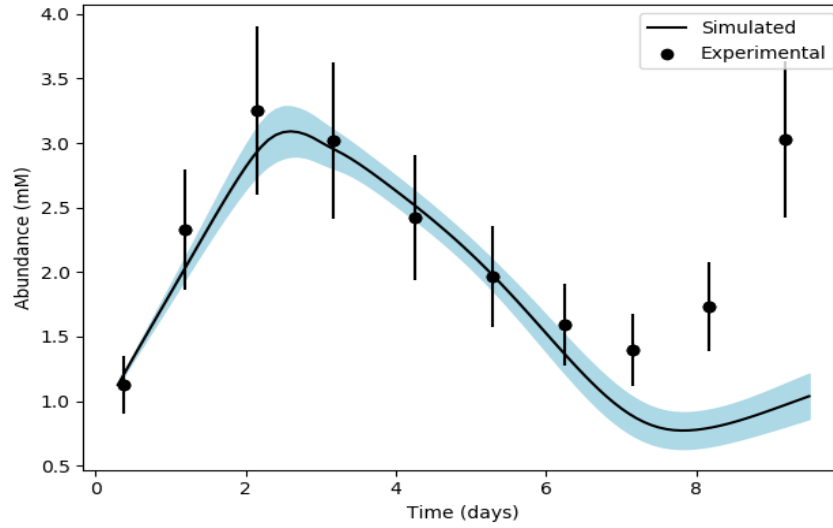




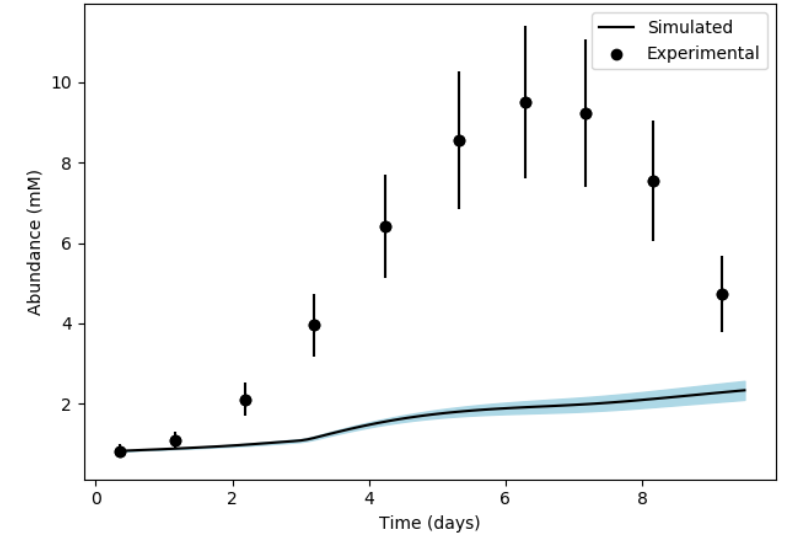
Results

HCM-FBA

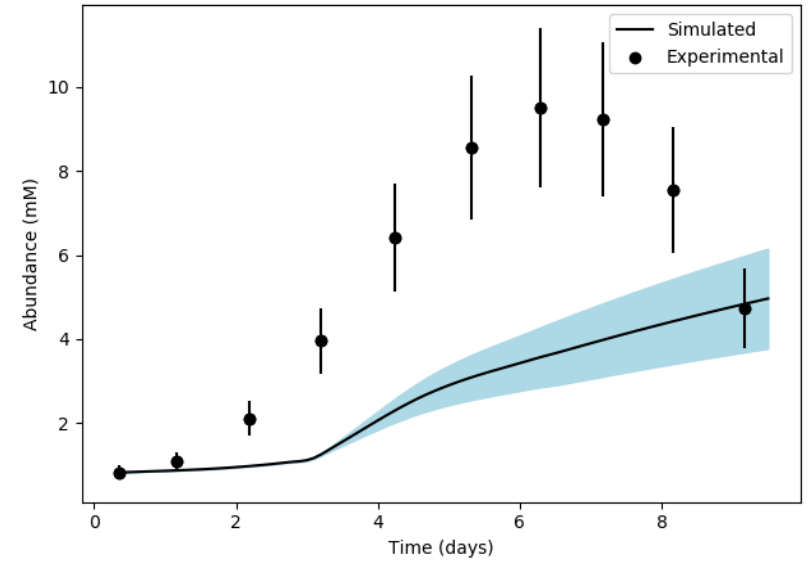
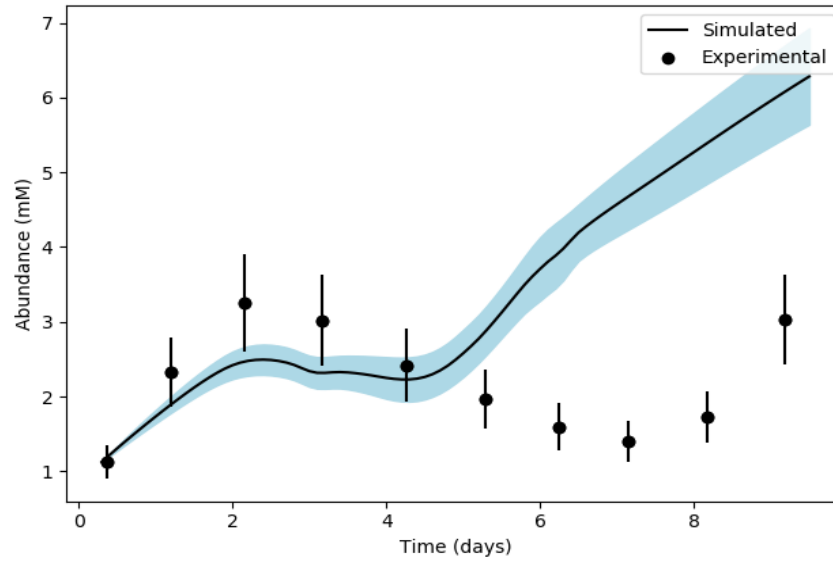
Ammonia

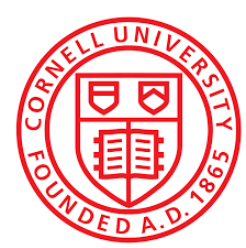


Alanine



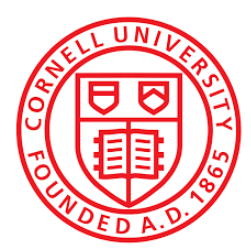
HCM-MCMC



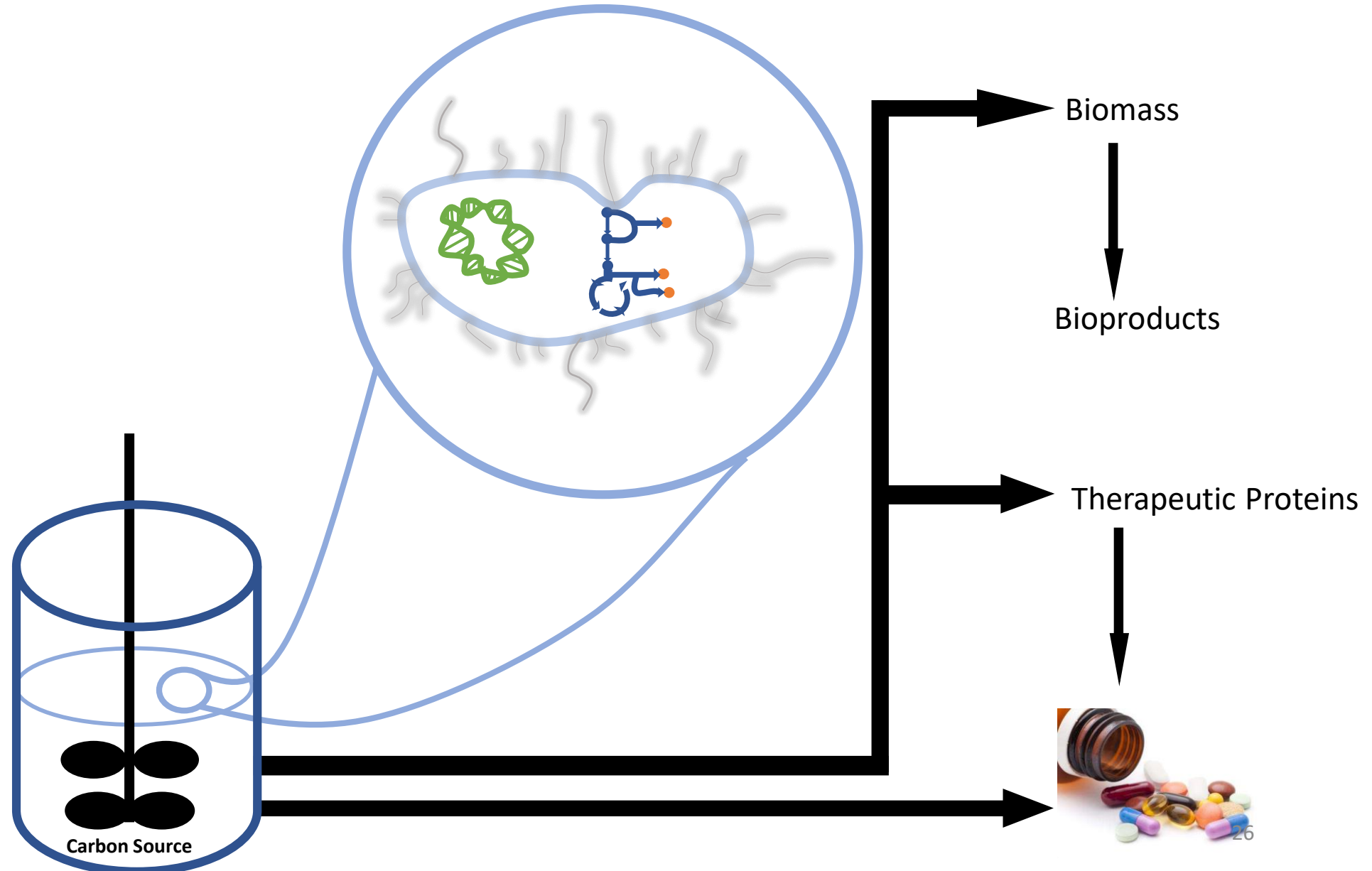


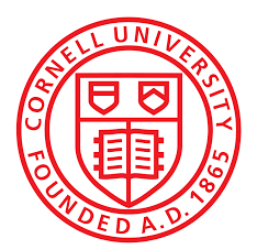
Summary

1. 3 flux modes have been used to describe dynamics
2. *E. coli* shows single-substrate kinetics. *CHO-K1* demonstrates multi-substrate kinetics
3. *E. coli* shows sequential uptake pattern. *CHO-K1* demonstrates *simultaneous uptake pattern*
4. *Glutamine, glucose, lactate, asparagine and serine are important for biomass production*

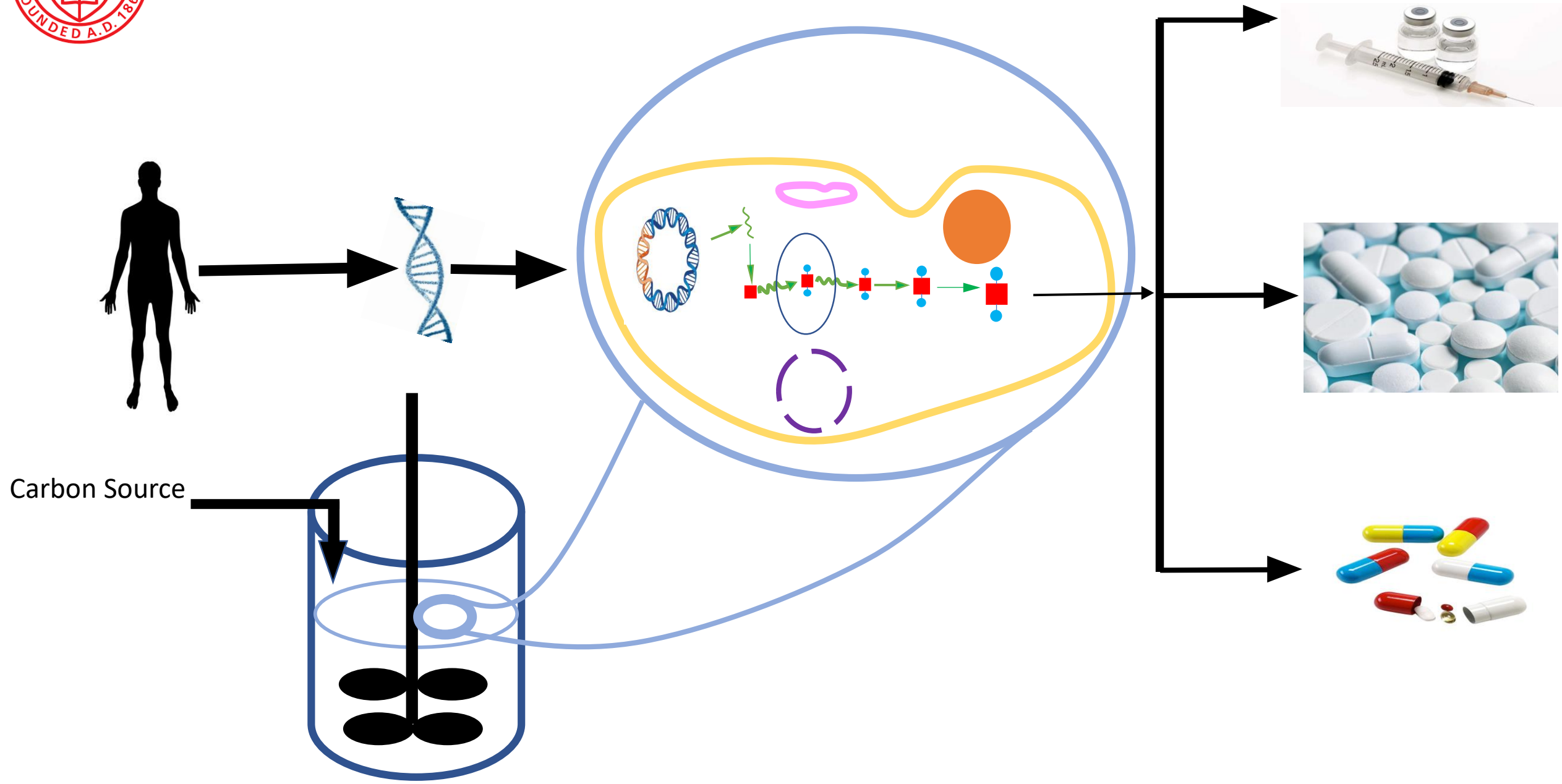


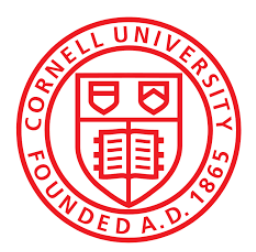
Future Work : Implementing New Age Biology





Future Work : Producing glycosylated proteins





Acknowledgement

Prof. Varner

Prof. DeLisa

Dr. Michael Vilkhovoy

All members of Varner lab