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### **BACKGROUND/OBJECTIVES**

Via interspecies metabolic exchanges, microbial communities are able to convert chemical nutrients into complex chemical compounds, which can be used for production of biofuels and biomaterials.

#### Motivation:

Perform *in silicio* studies of microbial consortia to evaluate their potential use in producing biofuels and biomaterials, eliminating pollutants, treating wastewater, or other biotechnology applications.

#### **Objective:**

Formulate a mathematical model to simulate the behavior of a microbial system and predict flowrates of metabolites.

#### INTRODUCTION

This is a simulation of a well-characterized, natural, hot spring microbial mat community in Yellowstone National Park [1]. It contains a sulfatereducing bacteria (SRB) and two photoheterotrophic bacteria, filamentous anoxygenic bacteria (FAP) and Synechococcus spp. (SYN). This mat is a good case study for microbial communities because the guilds exhibit different behaviors between day & night, and the community contains all of the prototypical metabolite exchange interactions described in [2].

### **INTERACTION TYPES**



Figure 1: Yellow & blue circles: 2 different guilds. Red circles: metabolite. Aquamarine: environment. *Interaction diagrams adapted from* [2]

# FLUX BALANCE ANALYSIS (FBA)



FBA writes a flux balance for each metabolite in the metabolism and assumes quasi-steady state. This creates an undetermined linear program, which FBA solves by assuming that the microorganism will try to maximize its growth rate.

# QUANTIFYING INTERSPECIES METABOLIC EXCHANGES IN MICROBIAL COMMUNITIES WITH **DYNAMIC FLUX BALANCE ANALYSIS**

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#### **Model Assumptions**

- Cost coefficients for biomass flux are normalized
- . Concentration of metabolites exchanged by more than one organism
- are at steady state
- Residence time of community is 59 weeks
- 4. Mass fraction of carbon in each guild is 1/2

### RESULTS



**Figure 3:** FAP reaches maximum growth rate once critical light intensity is reached

## REFERENCES

- 1. Taffs, R. *et al.* BMC Systems Biology, 2009, 3:114.
- 2. Zomorrodi AR, Maranas CD PLoS Comput Biol 8(2): e1002363. doi:10.1371/journal.pcbi.1002363



MIT, DEPARTMENT OF CHEMICAL ENGINEERING

**FUTURE WORK** Apply methodology to consortia in bioprocesses such as fermentation or **Three mass balances** *Metabolites (i) entering mat from atmosphere* production of biofuels. Consider the accumulation of metabolite within guild for use at different time in the diel cycle.  $\frac{dc_i}{dt} = n_{in,j} + \sum (-f_{i,k})C_k - \frac{c_i}{\tau}$ **SUMMARY** *Metabolites (j) consumed/produced in mat* Community behavior highlights:  $\frac{dc_j}{dt} = \sum_{i} (-f_{j,k})C_k - \frac{c_j}{\tau}$ • SYN outcompeted the other guilds because it can choose not to share essential metabolites. • Uptake of ammonia and acetate by FAP is limited by light available. *Biomass (k)*  $\frac{dC_k}{dt} = \left(\frac{f_k C_{mole}\mu}{x_k}\right) C_k - \frac{C_k}{\tau}$ • SRB reaches a constant growth rate with FAP because FAP is inter-(3)acting syntrophically with SRB via hydrogen exchange. Definitions Advantages of modeling approach:

 $c_i$  - concentration of metabolite i

 $C_k$  - concentration of guild k

 $n_{in,j}$  - system inlet molar flowrate of metabolite j  $f_{i,k}$  - flux of metabolite *i* exchanged in guild *k* 

 $\tau$  - residence time

 $C_{mole}$  - moles of carbon per mole of biomass  $\mu$  - molecular weight of carbon

 $x_k$  - mass fraction of carbon in guild k



**Figure 5:** CO2 uptake and O2 release by photosynthetic community

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. Mass of each guild is considered when performing FBA. 2. Normalizing the maximum biomass fluxes forces independent guilds to share with dependent guilds.

Modeling challenges faced:

Absence of experimentally determined flux values for the individual guilds.

2. Determining reasonable assumptions about the community.