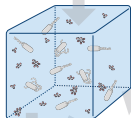
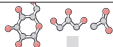


Develop physiologically-grounded models of the ecology of microbial communities

$$Environment = f(t, [N], [P], [C]...)$$

nutrient inflow



death



growth



metabolic details

$$\begin{aligned} \partial_t \text{Precursors}_1 &= \sum_i^{\text{nutrients}} k_{\text{metabolism},i}^{(1)} ([\text{Nutrient } i]) M_{\text{metabolism},i}^{(1)} \\ &\vdots \\ \partial_t \text{Precursors}_N &= \sum_i^{\text{nutrients}} k_{\text{metabolism},i}^{(N)} ([\text{Nutrient } i]) M_{\text{metabolism},i}^{(N)} \end{aligned}$$

physiological details

$$\begin{aligned} \partial_t \text{Species}_1 &= k_{\text{translation}}([\text{Precursors}_1]) M_{\text{ribosomes},1} \\ &\vdots \\ \partial_t \text{Species}_N &= k_{\text{translation}}([\text{Precursors}_N]) M_{\text{ribosomes},N} \end{aligned}$$

ecological details

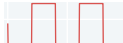
$$\partial_t \text{Biomass} = \sum_j^N \text{Species}_j - k_{\text{death}} \text{Species}_j$$

Predict and test how dynamic environments drive species composition within synthetic communities

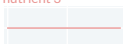
nutrient 1



nutrient 2



nutrient 3



time

in silico community

