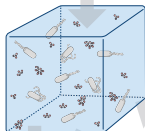
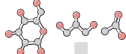


Develop physiologically-grounded models of the ecology of microbial communities

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

nutrient inflow



death

growth

metabolic details

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

physiological details

$$\begin{aligned} \partial_t \text{Species}_1 &= k_{translation} ([Precursors_1]) M_{ribosomes,1} \\ &\vdots \\ \partial_t \text{Species}_N &= k_{translation} ([Precursors_N]) M_{ribosomes,N} \end{aligned}$$

ecological details

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

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

