The overall goal of this project is to develop and test a thermodynamic network model for predicting the effects of substrate additions and environmental perturbations on the composition and functional stability of subsurface microbial communities. The hypothesis is that a thermodynamic analysis of the energy-yielding reactions performed by broadly defined groups of microorganisms can be used to make quantitative and testable predictions of the change in microbial community composition that will occur when a substrate is added to the subsurface or when environmental conditions change (Fig. 1).

**Introduction**

The network model will be used to predict the effects of substrate additions on the microbial community composition by predicting the growth of major metabolic groups of organisms (acetobes, fermenters, denitrifiers, Fe(III)/sulfate/metal reducers). Model predictions will be tested by quantifying changes in the abundance of each of these groups using a combination of functional genes and lipid analysis.

**Approach**

The network model will be used to predict the effects of substrate additions on the microbial community composition by predicting the growth of major metabolic groups of organisms (acetobes, fermenters, denitrifiers, Fe(III)/sulfate/metal reducers). Model predictions will be tested by quantifying changes in the abundance of each of these groups using a combination of functional genes and lipid analysis.

**Model Development**

*Equation 1:*

\[ R_j = f_a R_{a} + f_{b} R_{b} - R_{j} \]

Equation 1 is written once for every combination of donor and acceptor utilized by each metabolic group.

**Model Comparison – FRC**

Area 1 – FW21 Site Groundwater

**Fig. 2.** Donor addition stimulates range of in situ microbial activities at FRC.

**Fig. 3.** Proposed network model predicts the effect of donor addition on growth of these major metabolic groups.

**Model Comparison – Old Rifle**

Area 2 – GW835 Site Groundwater

**Fig. 3.** Proposed network model predicts the effect of donor addition on growth of these major metabolic groups.

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