

Thermodynamic network model for predicting effects of substrate addition and other perturbations on subsurface microbial communities

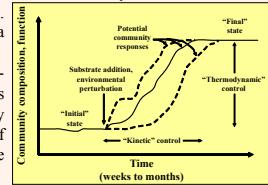
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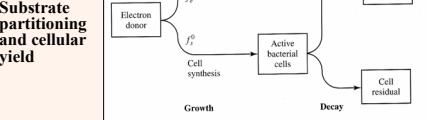
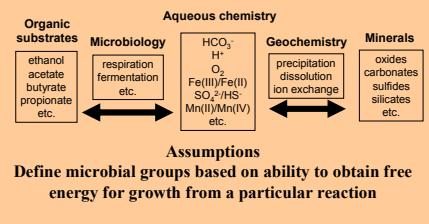
Introduction

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.



Model Development

Coupling Microbial and Geochemical Processes



Growth Equations (after Rittman and McCarty, 2001)

$$R_i = f_{e,i} R_{a,i} + f_{s,i} R_{c,i} - R_{d,i} \quad (1)$$

R_i = growth reaction for group i

$f_{e,i}$ = portion of electrons used for energy production

$f_{s,i}$ = portion of electrons used for cell synthesis

$R_{a,i}$ = electron acceptor half-reaction

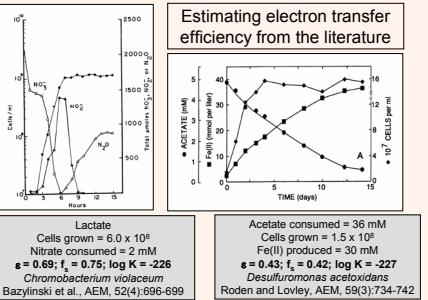
$R_{c,i}$ = synthesis reaction

$R_{d,i}$ = electron donor half-reaction

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

Model Development cont.

A graphical user interface was developed to implement this approach. The user selects electron acceptor, electron donor, nitrogen source, and electron transfer efficiency. Application computes overall growth equation and thermodynamic constants. Energy transfer efficiency, ϵ parameter must be known for each growth equation.

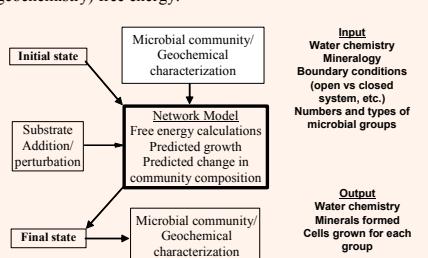


Coupling Microbiology and Geochemistry

The Geochemist's Workbench® is a set of software tools for manipulating chemical reactions, calculating stability diagrams and the equilibrium states of natural waters, tracing reaction processes, and plotting the results of these calculations.

Growth equations and free energy values for defined microbial groups are added to the existing chemical thermodynamic data base.

Reactions paths are computed as a series of equilibrium states by minimizing overall system (microbiology and geochemistry) free energy.



Model Validation

We intend to amplify 16S rRNA genes and separate products using denaturing gradient gel electrophoresis. Sequencing of the rRNA genes will allow us to identify the major components of the microbial community as well as to monitor changes in composition of the community. Second, we will quantify functional groups using a combination of functional genes assessed quantitatively by Quantitative-PCR and the analysis of lipid composition.

Acknowledgments

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For further information

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More information on this and related projects can be obtained at: <https://web.engr.oregonstate.edu/~istok/grl-main.htm>

Example 1

Reducing Area 2 groundwater/sediment system with ethanol.

Cell growth and minerals formed.

	moles	grams	volume (cm ³)
Iron Reducers	5.2 × 10 ⁻⁶ (48%)	0.059	0.059
Denitrifiers	5.0 × 10 ⁻⁶ (45%)	0.056	0.056
Sulfate Reducers	4.8 × 10 ⁻⁶ (4%)	0.005	0.005
Aerobes	2.4 × 10 ⁻⁶ (2%)	0.003	0.003
Magnetite	5.9 × 10 ⁻⁷	1.36	2.61
Calcite	5.3 × 10 ⁻⁷	0.053	0.02
Pyrite	4.1 × 10 ⁻⁴	0.05	0.01
Uraninite	4.9 × 10 ⁻⁶	0.001	0.0001
NiSS4	3.8 × 10 ⁻⁷	0.0001	0.00002
Tc257	9.7 × 10 ⁻⁶	0.00004	-

Example 2

Cell growth and minerals formed.

	Example 2 (moles)	Example 1 (moles)
Iron Reducers	4.5 × 10 ⁻⁶ (48%)	5.2 × 10 ⁻⁶ (48%)
Denitrifiers	4.1 × 10 ⁻⁶ (42%)	5.0 × 10 ⁻⁶ (45%)
Sulfate Reducers	2.7 × 10 ⁻⁶ (3%)	4.8 × 10 ⁻⁶ (4%)
Aerobes	2.0 × 10 ⁻⁶ (2%)	2.4 × 10 ⁻⁶ (2%)
Fermenters	7.4 × 10 ⁻⁶ (7%)	-
Magnetite	5.9 × 10 ⁻⁷	1.36
Calcite	5.2 × 10 ⁻⁷	0.053
Pyrite	4.1 × 10 ⁻⁴	0.05
Uraninite	4.9 × 10 ⁻⁶	0.001
NiSS4	3.8 × 10 ⁻⁷	0.0001
Tc257	9.7 × 10 ⁻⁶	0.00004
Pyrrohotite	6.2 × 10 ⁻⁶	-
Gibbsite	3.7 × 10 ⁻⁶	-

Example 3

Reoxidation of reduced system. Predicted change in community composition (NH₄⁺ not limiting).

	Example 2 (moles)	Example 3 (moles)
Iron Reducers	4.5 × 10 ⁻⁶ (45%)	~ 0
Denitrifiers	4.1 × 10 ⁻⁶ (42%)	0.019 (91%)
Sulfate Reducers	2.7 × 10 ⁻⁶ (3%)	~ 0
Aerobes	2.0 × 10 ⁻⁶ (2%)	9.7 × 10 ⁻⁶ (5%)
Fermenters	7.4 × 10 ⁻⁶ (7%)	9.0 × 10 ⁻⁶ (4%)

Example 4

Reoxidation of reduced system. Predicted change in community composition (NH₄⁺ limiting).

	Example 2 (moles)	Example 3 (moles)	Example 4 (moles)
Iron Reducers	4.5 × 10 ⁻⁶ (45%)	~ 0	~ 0
Denitrifiers	4.1 × 10 ⁻⁶ (42%)	0.019 (91%)	~ 0
Sulfate Reducers	2.7 × 10 ⁻⁶ (3%)	~ 0	5.4 × 10 ⁻⁶ (55%)
Aerobes	2.0 × 10 ⁻⁶ (2%)	9.7 × 10 ⁻⁶ (5%)	0
Fermenters	7.4 × 10 ⁻⁶ (7%)	9.0 × 10 ⁻⁶ (4%)	4.4 × 10 ⁻⁶ (45%)

