Molecular level *in silico* analysis of mass and energy flows in microbial communities

R.P. CARLSON* AND R. TAFFS

Department of Chemical and Biological Engineering, Thermal Biology Institute, Montana State University, Bozeman, MT 59717 (*correspondence: rossc@erc.montana.edu)

Motivation

Complex microbial communities drive the Earth's biogeochemical cycles. In spite of their importance, the biochemical interactions within these communities are not yet well understood, nor are many *in silico* methodologies available for studying them.

Results

Three *in silico* methodologies were developed for studying mass and energy flows in microbial communities on the molecular level. Each approach has distinct advantages and disadvantages suitable for analyzing systems with different degrees of complexity and *a priori* knowledge. These methodologies were tested and compared using the extensive data from the phototrophic, thermophilic mat communities at Octopus and Mushroom springs in Yellowstone National Park. The models included three community guild members: cyanobacteria, filamentous anoxygenic phototrophs, and sulfate reducing bacteria. The *in silico* models were used to explore fundamental microbial ecology questions including the prediction and explanation for measured relative abundances of the oxygenic phototrophic primary producer cyanobacteria and the filamentous anoxygenic phototrophic bacteria. The three approaches represent a flexible toolbox which can be rapidly adapted to study other microbial systems with a variety of electron donors and acceptors on scales ranging from individual cells in a pure culture to entire ecosystems represented by metagenomic data.

Asian aerosols: Current and future distributions and implications to air quality and regional climate change

GREGORY R. CARMICHAEL[1]*, BHUPESH ADHIKARY[1], SARIKA KULKARNI[1], DAVID STREETS[2] AND QIANG ZHANG[2]

[1]Center for Global & Regional Environmental Research, The University of Iowa, Iowa City, IA 52242 (*correspondence: gcarmich@engineering.uiowa.edu) (bhupesh-adhikary@uiowa.edu, sarika-kulkarni@uiowa.edu)

[2]Argonne National Laboratory, 9700 S Cass Ave., Argonne, IL 60439 (dstreets@anl.gov, zhang@anl.gov)

Asian environments contain high levels of aerosols and these have profound impacts on human health and on climate change. Vast regions (>80%) in Asia have $PM_{2.5}$ concentrations that exceed on an annual basis the WHO guideline of 10 $\mu g/m^3$, often by factors of 2 to 4. The high aerosol loadings cause a significant dimming at the surface, and mask ~45% of the warming by greenhouse gases. In this paper, we present results using the STEM chemical transport model to help describe the regional distributions and seasonal cycles of Asian aerosols. The seasonal cycles of Asian aerosols are shown to be driven by seasonal variations in emissions associated with combustion processes such as open biomass burning and heating cycles, monsoonal flows that bring strong on-shore flows across large regions, and strong flows across arid and semi-arid regions resulting in large quantities of wind blown dust. We also discuss some of the important impacts of Asian aerosols on human health and the climate system. Finally, we look to the future and discuss the implications for aerosol emissions in Asia, and the opportunities for win-win straegies built upon addressing air quality and climate change together. Throughout the paper we focus special attention on black carbon (BC) because of its unique role as the aerosol that acts like a greenhouse gas and warms the atmosphere, and its importance in human health effects.