Title: Constructing microbial networks from Genome Scale Metabolic Models.

Authors: James D. Brunner[1,2] (jdbrunner@lanl.gov), Michaeline Albright[1], **John Dunbar**[1]

Institutions: [1]Biosciences Division, Los Alamos National Laboratory, Los Alamos, New Mexico; [2]Center for Nonlinear Studies, Los Alamos National Laboratory, Los Alamos, New Mexico

Project Goals:

1. Construct species-species interaction networks from genome-scale metabolic models within an environmental context.

2. Investigate the stability of species-species interactions as environmental context is changed.

3. Produce accurate predictions of stable microbial community composition outcome after perturbation of community composition and environmental context.

Abstract: Interactions between microbial species have become a popular basis for dynamical and predictive models that seek to understand how microbial populations organize and affect their environment. However, the poor predictive power of pairwise network models with static parameters suggests that interactions are in turn affected by their environment, and are therefore context dependent. Genome scale metabolic modeling offers techniques to understand the behavior of a microbe in a specific metabolic environment. One method for combining genome scale models into a community model, called community dynamics flux balance analysis, offers a way to create a dynamical system which couples the microbial community with its environment. However, this system suffers from complexity and non-smooth behavior, and does not directly reveal any interaction between microbes, making manipulation of the community difficult. We use the community dynamic flux balance analysis system as a basis from which to derive the implied interactions between species, and so create an environmental-context dependent networks of species interactions. These networks can be used to study how interactions between microbes change with a changing environment, and provide predictions of microbial community changes, including engraftment of invading taxa.