

## ENIGMA Science Focus Area

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<http://enigma.lbl.gov>

**Project Goals: ENIGMA (Ecosystems and Networks Integrated with Genes and Molecular Assemblies) uses a systems biology approach to understand the interaction between microbial communities and the ecosystems that they inhabit. To link genetic, ecological, and environmental factors to the structure and function of microbial communities, ENIGMA integrates and develops laboratory, field, and computational methods.**

The goal of Ecosystems and Networks Integrated with Genes and Molecular Assemblies (ENIGMA) scientific focus area is to develop an unprecedented mechanistic and predictive understanding of the assembly, activity, stability and resilience of complex microbial communities in variable conditions. Established in 2009, ENIGMA is a collaborative consortium of 23 investigators at fourteen institutions located across the country and is led by principals at the Lawrence Berkeley National Laboratory. We are focused on sediment and groundwater communities and the processes that impact (and are impacted by) anthropogenic contaminants resulting from legacy nuclear programs at the Oak Ridge National Laboratory (ORNL). At the Oak Ridge Reservation (ORR) we perform sophisticated field experiments to measure the natural and anthropogenically perturbed dynamics of these geochemical processes and microbial community assembly and activity. From these we infer the chemical, physical and microbial interactions most predictive of these dynamics and estimate the ecological forces, both stochastic and deterministic, that shape community function. We then dissect the causal basis for these observations through laboratory studies of representative organisms in isolation and when they are part of synthetic or naturally derived assemblies. By using a unique array of culturing, genetic, physiological, bioreactor, and imaging technologies to map gene function and energy/material flow within and among cells, we determine how different genetic capabilities and regulatory strategies adapt microbes to ORR relevant conditions and to each other, thereby delivering an unprecedented mechanistic understanding of complex environmental bioprocesses and ecology.

Our prior high spatial resolution survey of ORR biogeochemical features identified the strongest correlations among chemical and physical environmental parameters and microbial community structure and function. We now seek to dissect the contributions of biotic, abiotic, stochastic and deterministic factors controlling community assembly, system-level processes, and system resilience. This overarching goal addresses one of the grand challenges identified in the most recent DOE Grand Challenges Report: to “define the levels of biological organization most relevant to scaling from single cells to ecosystems and global cycles; capture how that organization varies in time and space; and identify critical interactions that dictate rates of carbon, nutrient, and energy transformation in different environments.”

To address this major challenge, the ENIGMA team has organized itself and its scientific/technological platforms into complementary campaigns for iterative field, laboratory, and computational analyses. We: 1) characterize stochastic and deterministic variations in community structure over time and space at the ORR in both unstimulated and stimulated conditions; 2) employ field and laboratory bioreactor systems that sustain both planktonic and attached communities to simulate simulating ORR environmental conditions, testing alternative mechanisms of community assembly and resilience; 3) design and employ methods for enriching and isolating key interacting sub-communities and active microbes representative of the condition-dependent diversity observed at the site; 4) develop and employ high-throughput experimental and computational technologies for the genetic manipulation of diverse environmental microbes to assess gene function, regulatory-network structure and adaptive genetic; 5) identify adaptive genetic elements that are laterally transferred among microbes in the field through analysis of and examination of the global plasmid pool; 6) Design and employ new metabolomics technologies and high-throughput physiological characterization platforms to gain insight into the flow of materials and energy through isolates and communities; 7) apply genetic, physiological, and bioreactor technologies to refine understanding of factors controlling the activities and persistence of sulfate and nitrate respiring populations in the field; 8) use experimental evolution of mono- or co-cultures in constant and fluctuating environments to elucidate species- and community-level mechanisms of adaptation and resilience to environmental stress.

We then integrate field observations, laboratory simulations of the environment, and genetic and metabolic experimentation to create the beginnings of a mechanistic, energetic and ecological model of how differential levels of nitrate, pH, oxygen, metals (essential, e.g. molybdenum, and toxic), and carbon coupled with physical dispersal processes affect community assembly at the ORR.

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