Modeling of Biological and Abiotic Data to Predict Nuclear Process Marker Presence and Age

MTV Kickoff Meeting

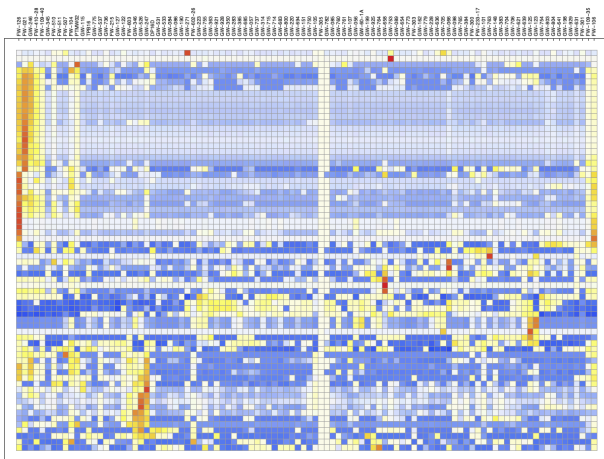**May 21, 2019**

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National Nuclear Security Administration

Geographic Sample

Physical/Chemical Measurement

Species Distribution

Chemistry

Species Distribution

Multiple-lines of evidence support biotic activities in chemical and physical processes
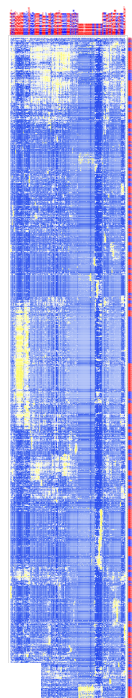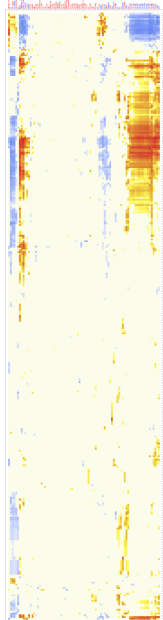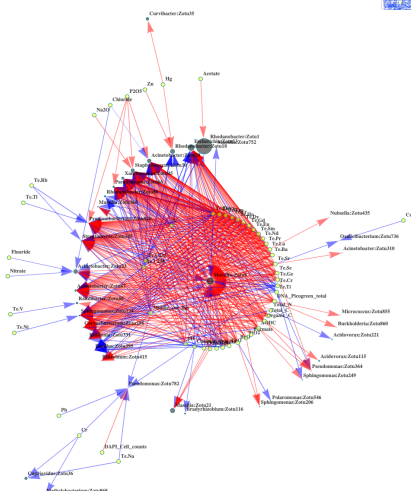
Introduction and Motivation

- We are looking to create an approach to discover and characterize mechanistic ecologist with suffient resolution to predict, control and design outcomes.

- Determining the link between genetic complement and fitness/activity in a variable environment and dissecting neutral from adaptive forces.

- Allow the detection and prediction of environmental processes from observation of biological elements (sequences can be amplified) and vice versa.

- Build information systems that allow access and analysis of diverse data, models and investigator conclusions.

KBase
PREDICTIVE BIOLOGY

DOE Systems Biology Knowledgebase

National Nuclear Security Administration

BERKELEY LAB
Lawrence Berkeley National Laboratory

Mission Relevance

- We are seeking models that link chemical/physical inputs to the environment from nuclear materials processing and testing to sensitive biological outcomes.
  - The taxonomic, genetic, and activity diversity give a complementary high-dimensional readout of environmental status.
  - The sequence-based methods are amplifiable from the environment.
  - Microbes can accumulate/integrate/transport information over time and space
  - Microbes can be ultimately engineered to be more specific/sensitive readouts.
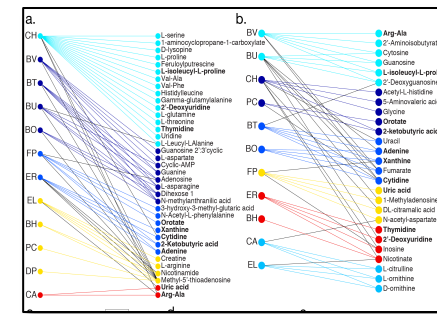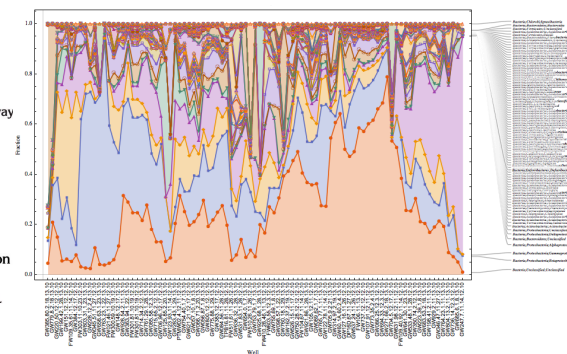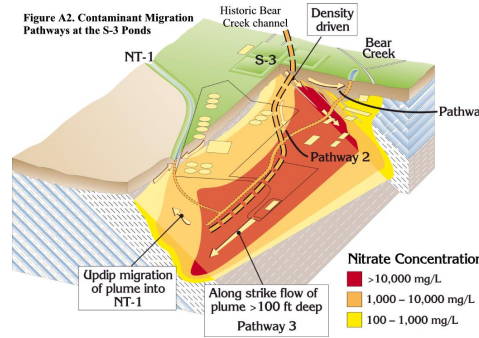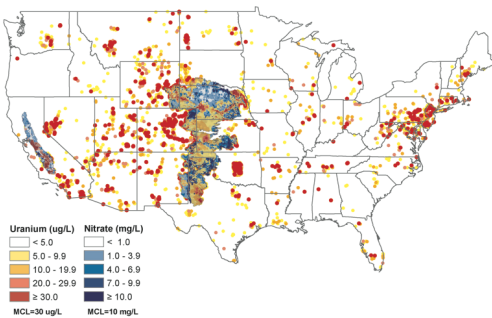
Technical Work Plan

- Year 1-
  - Utilizing infrastructure we've built with Alm, Hazen and others as part of large DOE program, experimental design for environmental sampling to characterize sites suspected to have differential markers of nuclear-activities.
  - Experimental sampling of existing sites and initial survey of new terrestrial and coastal locations.
  - KBase datatypes to serve these data and analyses.

- Year 2-
  - Time series sampling; sample analysis protocol optimization;
    - front-end computational pipelines deployed in KBase
    - Initial integrative analysis of historical and year 1 data.

- Year 3/4-
  - Continued time-series sampling; individual isolate/single cell analysis for markers of accumulation/activity; iterative sampling design; Ongoing analysis and initial predictive models; design of model tests.

- Year 5- As year 3 & 4 but now with specific sampling and analysis to test model predictions.

Expected Impact

- New biological mechanisms of sensing and processing of nuclear industrial material by environmental microbiomes

- Models of distribution and flow of biological effects

- New models that link biological observation to predictions of space/time presence of nuclear processing in terrestrial and coastal environments.

MTV Impact

- MTV will:
  - provide an engaged group of experts in the physical and chemical processes and other detection systems that will inform where biological markers will be most informative and effective.
  - Provide opportunity for scientist exchanges for cross-training;
  - Provide opportunities for new scientific approaches combining physical and chemical as well as biological approaches to detection and prediction and control.
- Our lab is a tightly integrated across U.C. Berkeley/LBNL and has a long history of graduate of personnel into long term positions at the Labs.
- We collaborate with a wide set of people in academics, government both domestically and Internationally. Hazen and Alm are very long term collaborators in a major DOE program with complementary goals.
- We would love to collaborate with experts in environmental impacts of nuclear processes; investigators working on field sensors; and experts in data analysis and prediction.

Conclusion

- With Hazen and Alm , we hope to:
  - Provide robust models that will link metafunctional genomics measurements to time/space prediction of when and where key nuclear processes are detected.
  - We hope to elucidate the basic biology of microbial response to these processes.
  - We hope to create an infrastructure for disseminating, integrating and analyzing these data in the DOE Systems Biology Knowledgebase.

Acknowledgements

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