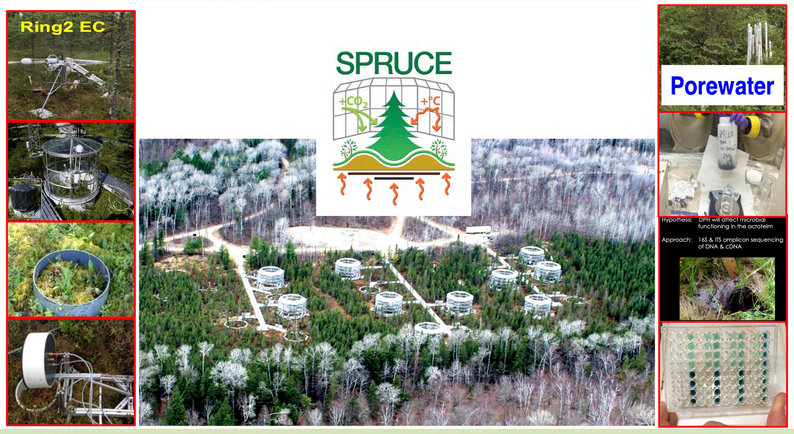
Integrating multiple sources of data with the ELM-SPRUCE model to understand microbial mechanisms of CH_4 cycling under warming and elevated CO_2 in the S1 bog

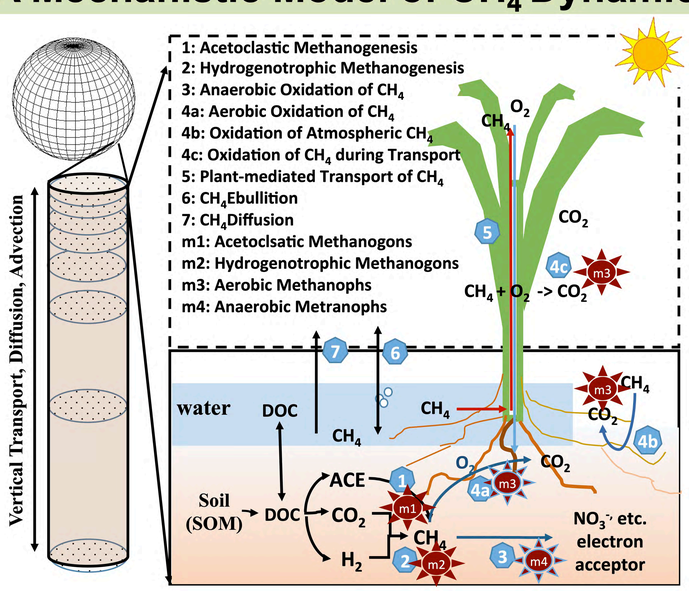
Xiaofeng Xu[1], Jingwei Zhang[1], Daniel M. Ricciuto[2], Fegnhui Yuan[3], Xiaoying Shi[2], Xiaojuan Yang[2], Melanie A. Mayers[2], Christopher W. Schadt[2], Joe E. Kosta[4], Jeff Chanton[5], Rachel Wilson[5], Scott Bridgham[6], Jason Keller[7], Jessica Gutknecht[3], Natalie Griffiths[2], Hongyi Zhao[1], Peter E. Thornton[2], Paul J. Hanson[2]

1. Biology Department, San Diego State University, San Diego, CA, USA; 2. Climate Change Science Institute and Environmental Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, USA.; 3. Department of Soil, Water, and Climate, University of Minnesota; 4. School of Biological Sciences, Georgia Institute of Technology; 5. Florida State University; 6. The Institute of Ecology and Evolution, University of Oregon; 7. Schmid College of Science and Technology, Chapman University; (XX: xxu@sdsu.edu)

SPRUCE Measurements on CH_4



A Mechanistic Model of CH_4 Dynamics



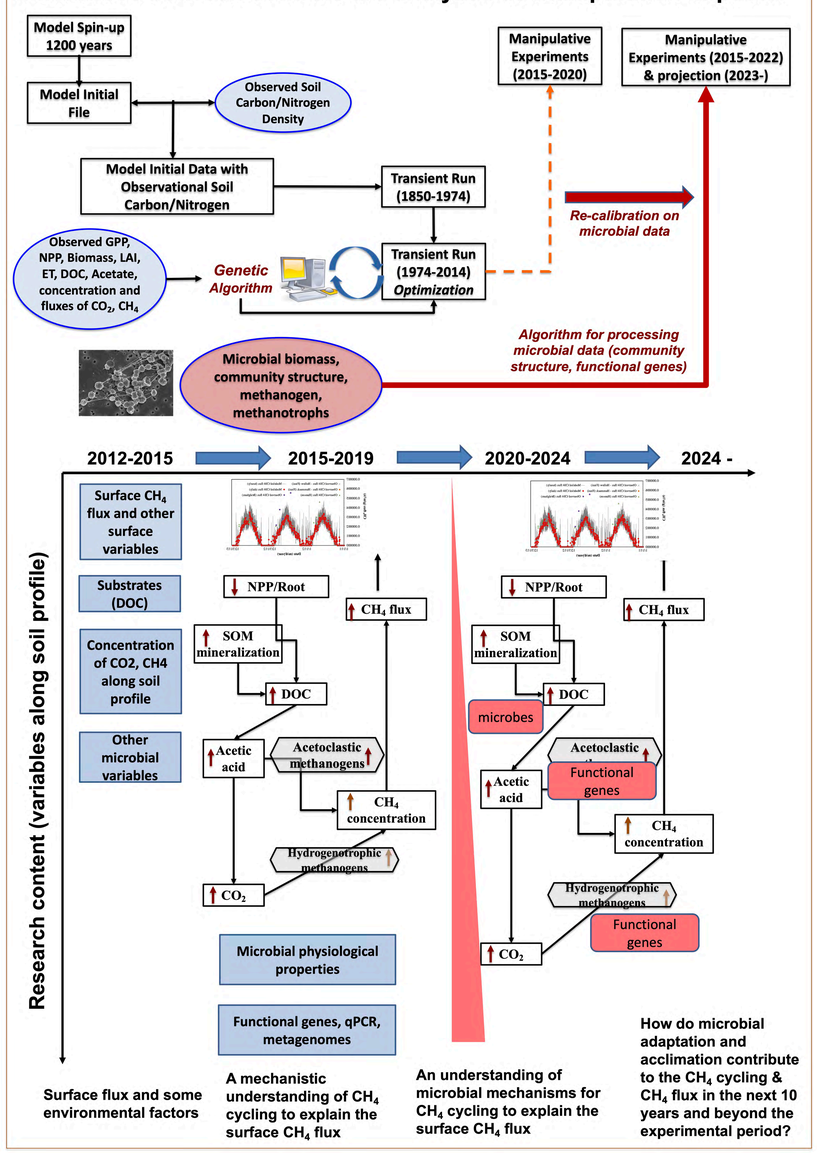
Questions

- How do microbial communities (bacteria vs. fungi; methanogens vs. methanotrophs) affect the CH_4 dynamics?
- How do acetoclastic and hydrogenotrophic methanogenesis along soil profile affect CH_4 dynamics?
- Warming and eCO_2 are additives or not in stimulating CH_4 cycling?
- Are soil microbes in deep soil more sensitive to warming?

Model Optimization & Implementation

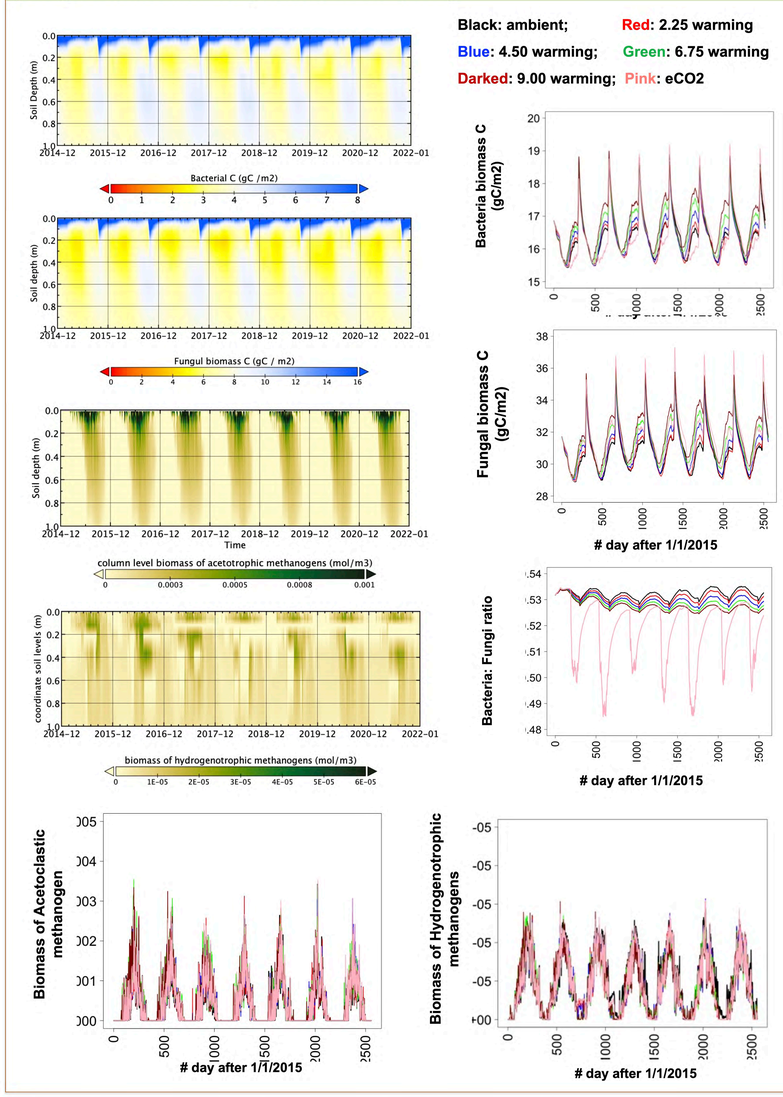
Model optimization for observational data of NPP, vegetation biomass, LAI, water table, Dissolved Organic Carbon (DOC), acetic acid, CH_4 flux, CH_4 concentration, microbial biomass C, **bacteria, fungi, relative abundance of acetoclastic methanogenesis, hydrogenotrophic methanogenesis, etc (new efforts).**

Model initialization in 1974 with observational soil carbon density; transient runs cover 1974-2015; warming & eCO_2 runs for 2015-2030; differences between controls are analyzed as manipulation impacts.



Preliminary results

(only microbial outputs are shown)



- ✓ See the left figures (middle panel) for the logic of this research; many ecosystem-level results have been shown previously and published.
- ✓ Microbial physiology and gene abundance data are used for parameterizing the model. The data-model integration effort is ongoing, and more results are expected. Based on the present analysis, functional genes can be used to parameterize the model to improve model simulations on CH_4 cycling. Warming has stronger impacts than eCO_2 on stimulating microbial functions on carbon cycling and CH_4 production.

This study has been sponsored by DOE.