**Hypothesis/Central Question**

Methane (CH4) is a potent greenhouse gas emitted by archaea in anaerobic environments such as wetland sediments. Coastal wetlands are predicted to become increasingly saline as freshwater inputs decrease and sea levels rise as a result of climate change. Previous work has shown that increases in salinity generally decrease CH4 emissions, but there has been considerable variation in this effect, with some instances of *increased* CH4 flux. We measured microbial communities, biogeochemistry, and CH4 flux from field samples and lab experiments from four different sites across a wide geographic range – California, New Jersey, North Carolina, and South Carolina, USA. We sought to assess how site differences, biogeochemical legacies, and microbial ecology affect how CH4 emissions are influenced by increases in salinity.

We hypothesize that (1) CH4 and CO2 fluxes are positively correlated, along with organic carbon, ammonium, phosphate, and pH (2) CH4 flux and methanogen abundances are negatively correlated with salinity and alternative electron acceptors (nitrate, sulfate, iron, manganese) and taxa that reduce them, (3) discrepancies in CH4/salinity relationships are driven by differences in site history and biogeochemistry and site-specific microbial consortia that respond differently to environmental conditions, and (4) discrepancies between field and lab studies are driven by ecological dynamics such as dispersal and mixing.

**Summary/Results**

CH4 flux was positively correlated with CO2 flux in 2/3 sites where both were measured and was generally but not always positively correlated with carbon, ammonium, phosphate, and pH. All methanogen guilds were positively correlated with CH4 flux, but there was mixed support for negative relationships with alternative electron acceptors and taxa that reduce them. CH4/salinity relationships ranged from negative to neutral to positive and appeared to be influenced by broad site characteristics such as pH and plant composition, which also likely contributed to the large differences in microbial communities among the four sites. The activity of site-specific microbial taxa that may respond differently to salinity, even compared to taxa in the same genus, is likely an important driver of CH4 emissions. Microbial community assembly was governed by deterministic (nearest taxon index > 2) rather than stochastic processes in both field and laboratory samples. Our results highlight several variables that make it difficult to generalize CH4/salinity relationships.