Hypothesis/Central Question:

Methane (CH4) is an important greenhouse gas that is emitted by archaea in anaerobic environments such as wetland sediments. Coastal and estuarine wetlands are predicted to become increasingly saline as freshwater inputs decrease and sea levels rise as a consequence of climate change. While previous work has shown that increases in salinity generally decrease methane emissions, there has been considerable variation in this effect, with even some instances of increased methane emissions following increases in salinity. Here we present microbial (16S rRNA gene sequencing), biogeochemical, and greenhouse gas flux data from a combination of field surveys, field experiments, and laboratory incubation experiments from four different sites across a wide geographic range – California, New Jersey, North Carolina, and South Carolina, USA - to assess how biogeochemical legacies and microbial ecology affect how methane emissions are influenced by increases in salinity.

We hypothesize that (1) CH4 and CO2 fluxes are positively correlated, along with metrics of organic carbon content, ammonium, and phosphorus (2) CH4 flux and methanogen abundances are negatively correlated with salinity and alternative electron acceptor abundances (nitrate, sulfate, iron, manganese) and taxa that reduce those compounds, (3) discrepancies in salinity-methane responses are driven by differences in site history and biogeochemistry and site-specific microbial consortia at the operational taxonomic unit (OUT) level that have different responses to environmental conditions, and (4) discrepancies between field and laboratory studies are driven by ecological dynamics such as dispersal and mixing that occur only in the field.

Summary/Results:

Microbial alpha-diversity metrics (richness, Shannon diversity) generally decreased with increased salinity. Microbial community composition varied significantly among the sites, salinity classes (freshwater vs. oligohaline), and sediment depths (0-5 cm vs. 5-15 cm range). Despite broad taxonomic differences among the four sites, there were still some consistent taxa that responded to increasing salinity both across natural salinity gradients and in experimental salinity manipulations in the field and laboratory. However, there were few consistent responses regarding the hypothesized links between microbes and methane emissions. Methane/salinity relationships ranged from negative to neutral to positive and appear to be influenced by broad site characteristics such as pH and plant composition, which in turn affect microbial community composition. The activity of site-specific microbial OTUs that may respond differently to environmental parameters including salinity, even compared to taxa in the same genus, are likely important drivers of methane emissions and render it difficult to make generalizations about methane/salinity relationships.