Co-occurrence Networks of Marine Microbes in the Northern Gulf of Alaska
Megan Brauner, Jacob Cohen, Brandon R. Briggs, Gwenn M. Hennon

Introduction
- The Northern Gulf of Alaska (NGA) is a highly productive region that is experiencing rapid changes in nutrient fluxes due to climate change.
- The Alaska Coastal Current moves along the coast providing nearshore and shelf communities with high micronutrients from terrestrial freshwater runoff.
- Samples from summer 2018-2021 were sequenced for the 16S (V4) and 18S (V9) rRNA genes to characterize microbial communities and their potential interactions.

Big Question
What microbial taxa are key players in each region and do potential interactions differ?

Networks & Potential Key Microbial Players
Co-occurrence networks of operational taxonomic units (OTUs) (nodes) with statistically significant Spearman rank correlations (p < 0.05) including positive (black) and negative (red) (edges). Larger nodes have the highest degree centrality and are potential key microbial players.

Plagioselmis prolonga subnetworks
- Nearshore
- Shelf
- Offshore

Discussion
- Both prokaryotic and eukaryotic microbial communities showed significant correlations to physico-chemical conditions.
- Nearshore network had the largest number of nodes, and all potential key players were eukaryotes. While offshore network had the lowest number of nodes and potential key players included both eukaryotes and bacteria.
- Predatory BALO nodes were more abundant and connected in nearshore network compared to the offshore network. Higher contact rates nearshore could increase the chance of success for predatory bacteria.
- Species with high degree and closeness centrality such as *Plagioselmis prolonga* could play a key role within the community and removal could affect the resilience of the community.

Implications
Networks differ by region implying different potential interactions. Transitions between ecosystem states may occur with removal of a key player or environmental change such as a marine heatwave.

Acknowledgments
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