# Co-occurrence networks of marine microbes in the Northern Gulf of Alaska

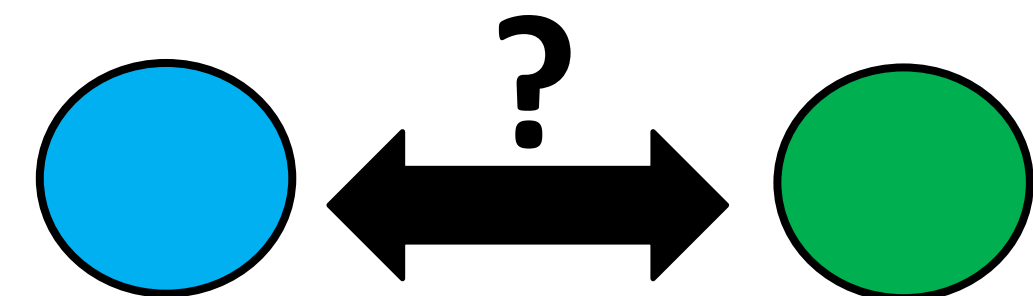Megan Brauner, Jacob Cohen, Brandon R. Briggs, Gwenn M. Hennon

## 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.
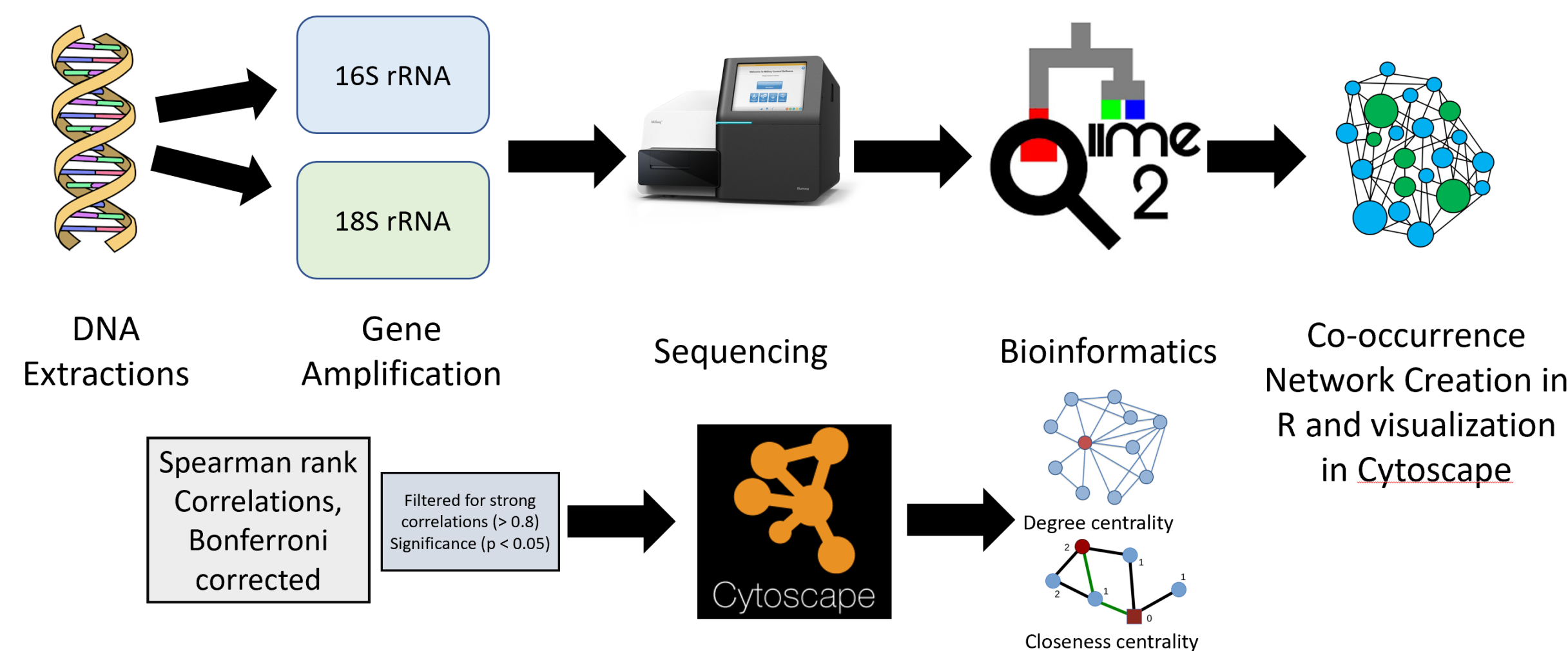
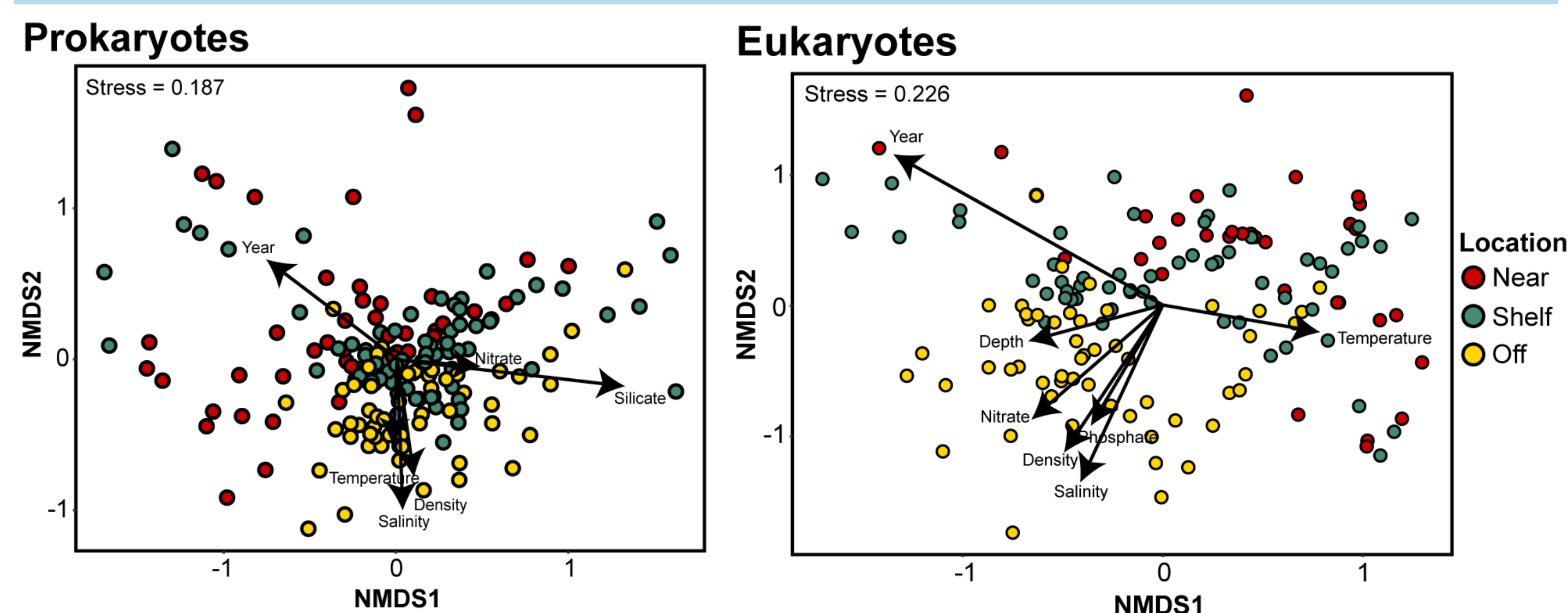Nearshore • On Shelf • Off Shelf
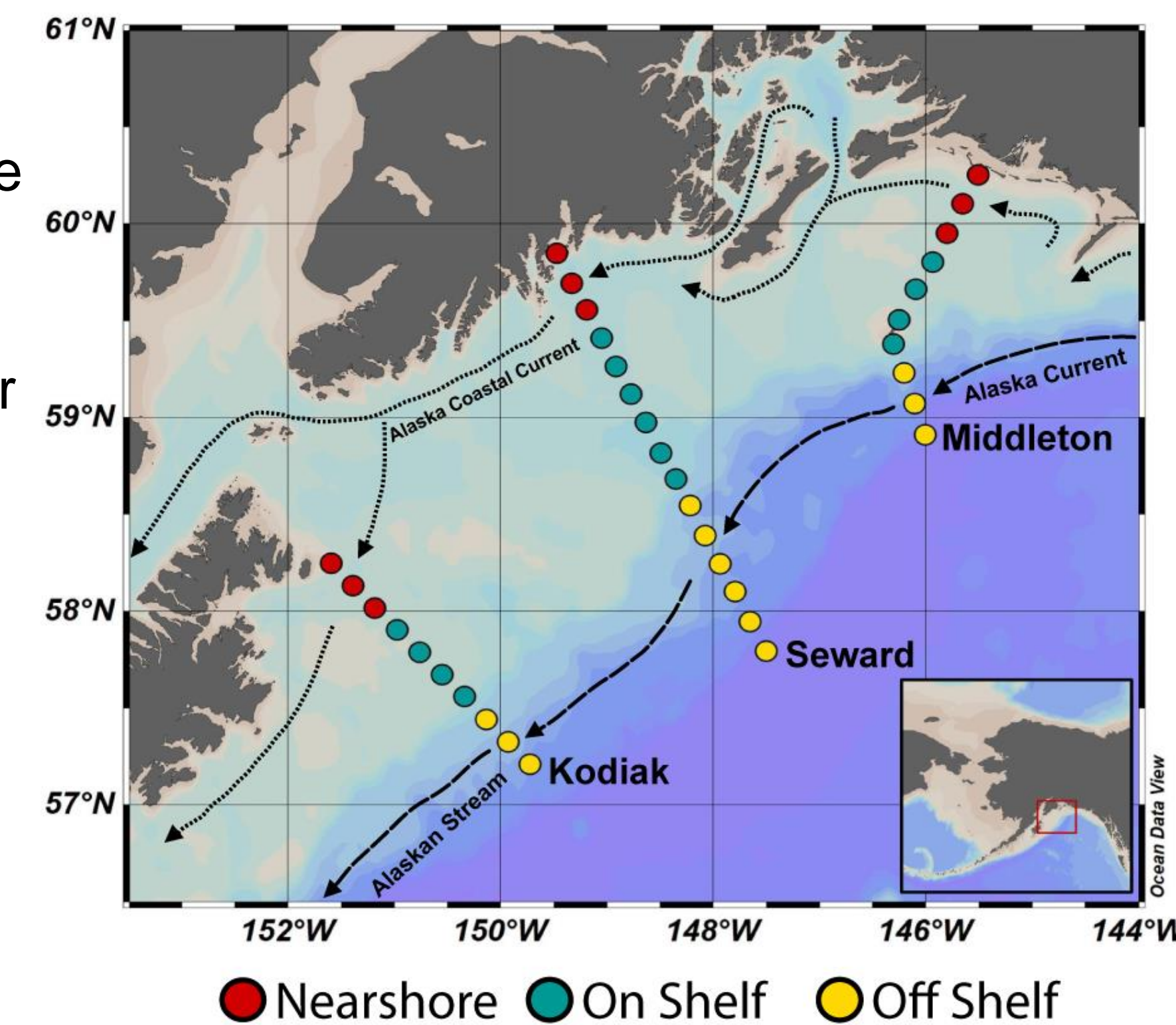
## Big Question

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

## Methods

DNA Extractions → Gene Amplification → 16S rRNA / 18S rRNA → Sequencing → Bioinformatics → Co-occurrence Network Creation in R and visualization in Cytoscape

Spearman rank Correlations, Bonferroni corrected → Filtered for strong correlations (> 0.8) Significance (p < 0.05) → Cytoscape → Degree centrality, Closeness centrality

## Nutrients Influence Microbial Communities

Prokaryotes (Stress = 0.187)

Eukaryotes (Stress = 0.226)

Location: Near (red), Shelf (teal), Off (yellow)

Nonmetric multidimensional scaling (NMDS) ordination of variation in prokaryotic and eukaryotic water community structure. Color represents significant differences in sample locations; Near (red), Shelf (teal), and Off (yellow). Vectors represent significant correlations (p < 0.05) with environmental variables.

## Networks & Potential Key Microbial Players

Shelf

Near

Off

● Archaea  ● Bacteria  ● Eukaryota
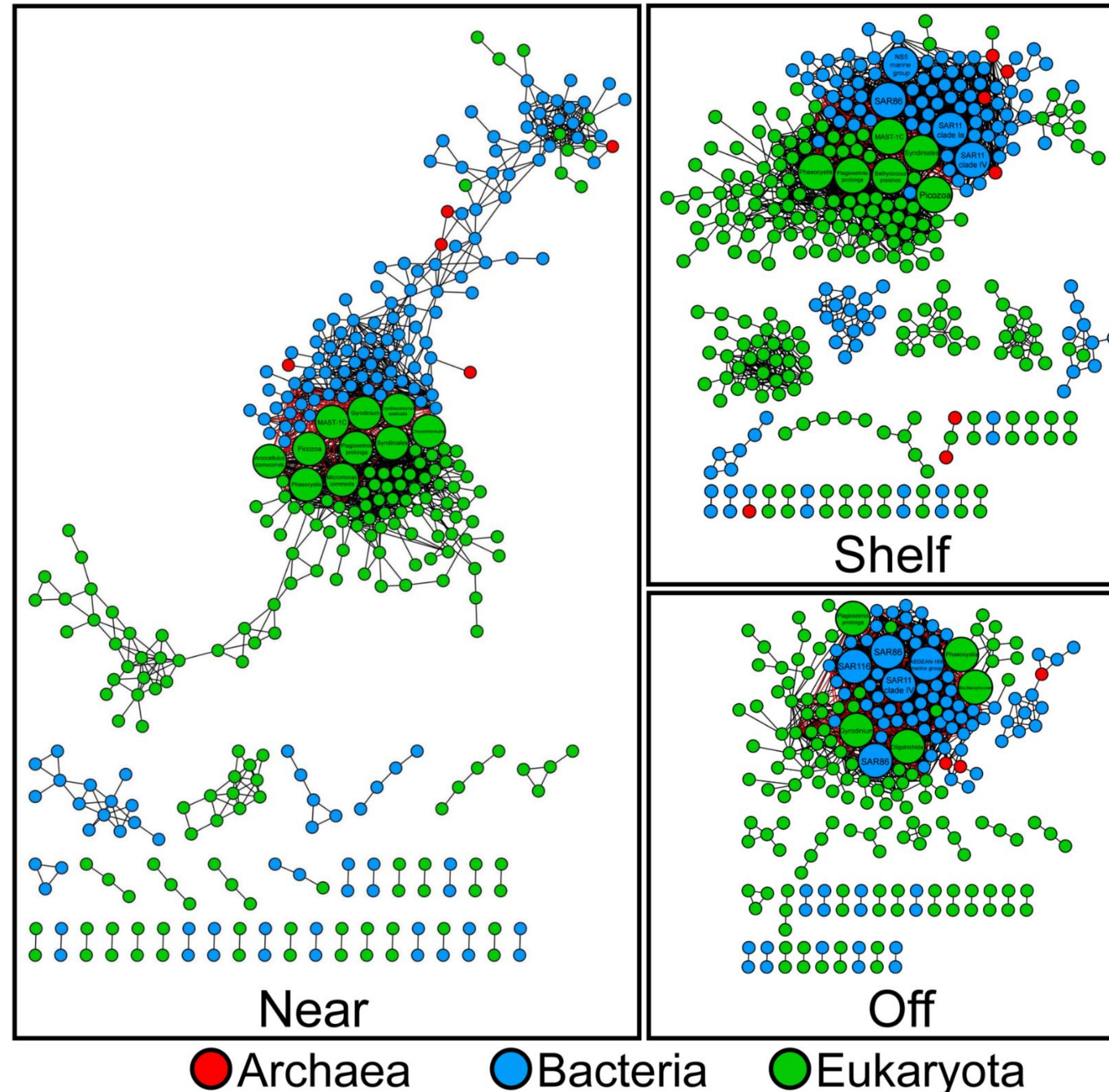
Co-occurrence networks of operational taxonomic units (OTUs) (nodes) with statistically significant Spearman rank correlations (>0.8, Bonferroni corrected p < 0.05) including positive (black) and negative (red) (edges). Nodes are color coded by taxonomy; Archaea (red), Bacteria (blue), and Eukaryota (green). Larger nodes have the highest degree centrality and are potential key microbial players.
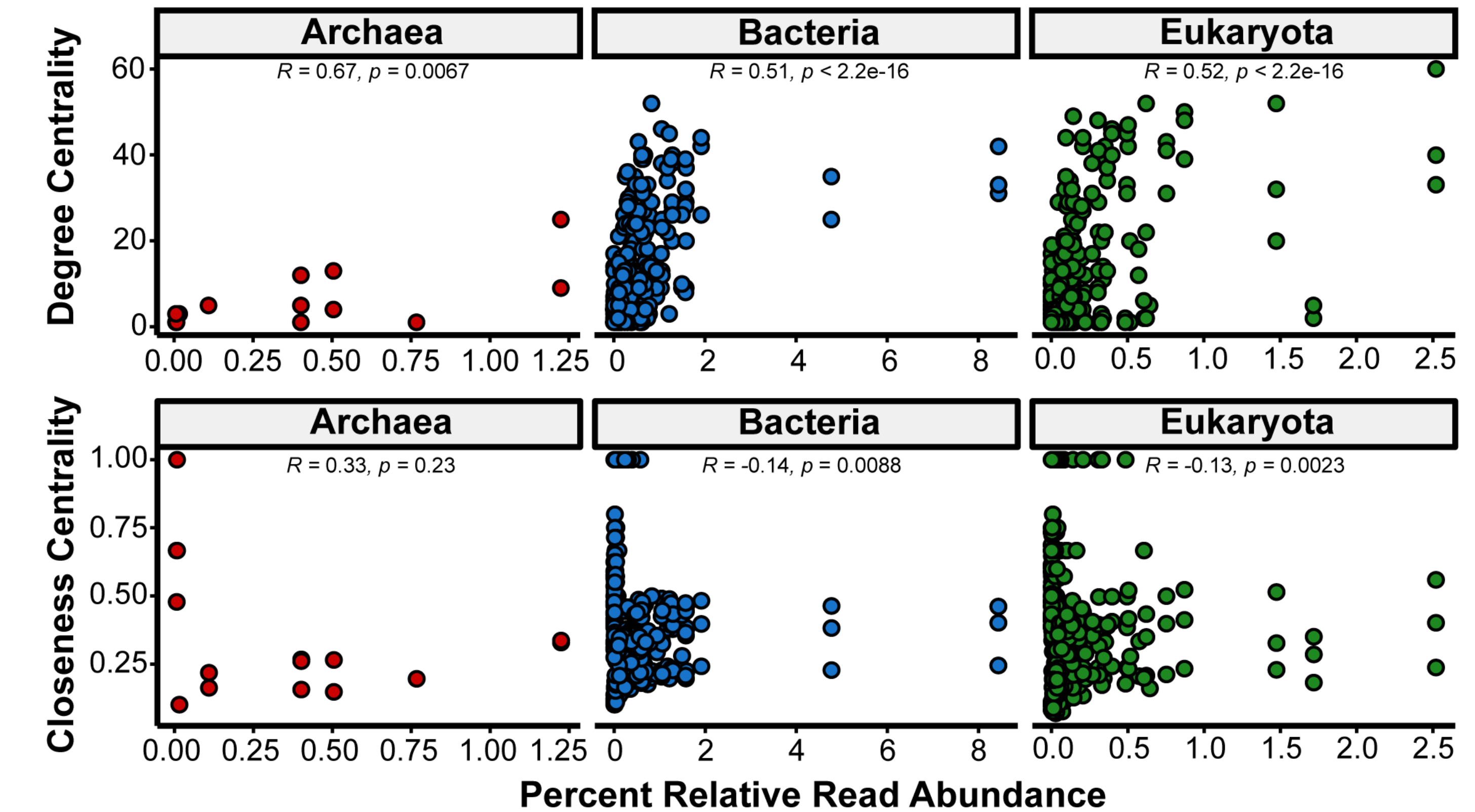
## Subnetworks of Predatory BALOs

Near    Shelf    Off
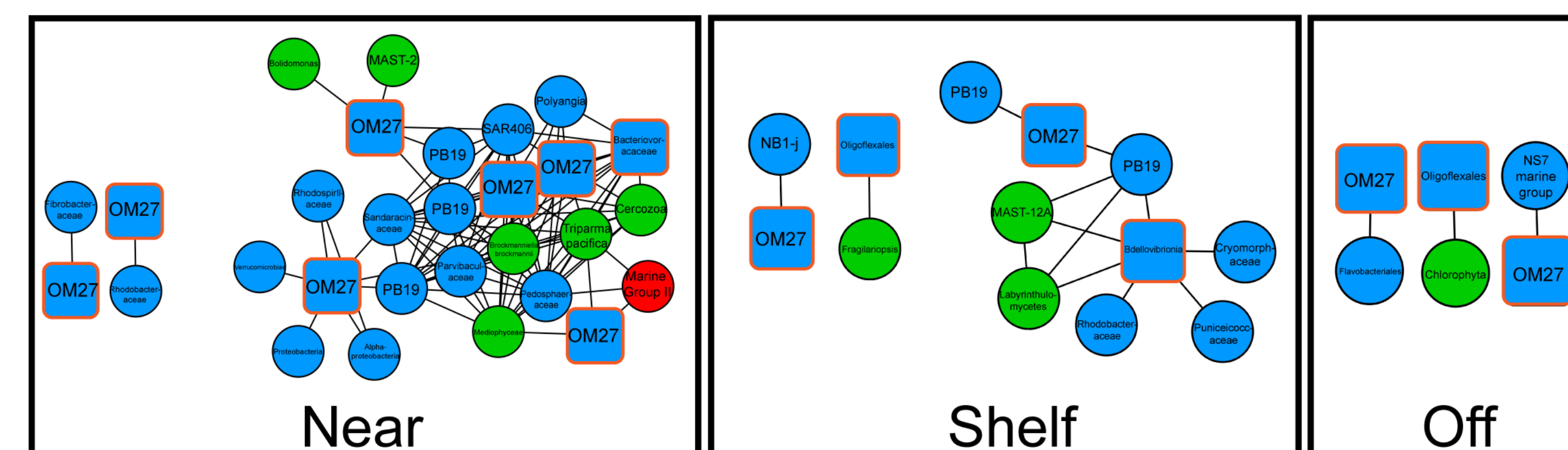
Subnetworks of predatory Bdellovibrio and like organisms (BALOs) (squares with orange border) and significantly correlated nodes including potential bacterial prey (blue circles) and associations with eukaryotes (green circles).

## Potential Key Microbial Player Stats

Potential key microbial players for each network and the associated degree and closeness centrality measurements

| Near | | | Shelf | | | Off | | |
|---|---|---|---|---|---|---|---|---|
| Organism | Degree | Closeness | Organism | Degree | Closeness | Organism | Degree | Closeness |
| Eukaryota; Cryothecomonas aestivalis | 49 | 0.237 | Eukaryota; Dino-Group-I | 52 | 0.433 | Eukaryota; Gyrodinium | 60 | 0.559 |
| Eukaryota; Dino-Group-I | 48 | 0.237 | Eukaryota; Phaeocystis | 50 | 0.413 | Bacteria; AEGEAN-169 | 52 | 0.500 |
| Eukaryota; MAST-1C | 48 | 0.242 | Eukaryota; Plagioselmis prolonga | 47 | 0.417 | Eukaryota; Bacillariophyceae | 52 | 0.515 |
| Eukaryota; Chrysochromulina sp. | 44 | 0.235 | Bacteria; SAR11 Clade IV | 45 | 0.397 | Eukaryota; Phaeocystis | 48 | 0.523 |
| Eukaryota; Picozoa sp. | 42 | 0.235 | Eukaryota; MAST-1C | 45 | 0.406 | Eukaryota; Plagioselmis prolonga | 47 | 0.521 |
| Eukaryota; Arcocellulus cornucervis | 42 | 0.234 | Eukaryota; Picozoa sp. | 44 | 0.401 | Bacteria; SAR116 | 46 | 0.491 |
| Eukaryota; Plagioselmis prolonga | 42 | 0.234 | Eukaryota; Bathycoccus prasinos | 43 | 0.398 | Bacteria; SAR11 Clade IV | 45 | 0.489 |
| Eukaryota; Gyrodinium | 40 | 0.239 | Bacteria; SAR11 Clade Ia | 42 | 0.402 | Eukaryota; Oligotrichida | 45 | 0.498 |
| Eukaryota; Phaeocystis | 39 | 0.232 | Bacteria; SAR86 | 42 | 0.397 | Bacteria; SAR86 | 44 | 0.482 |
| Eukaryota; Micromonas commoda | 34 | 0.237 | Bacteria; NS5 marine group | 40 | 0.392 | Bacteria; SAR86 | 43 | 0.486 |

## Relative Read Abundance & Centrality

Archaea R = 0.67, p = 0.0067
Bacteria R = 0.51, p < 2.2e-16
Eukaryota R = 0.52, p < 2.2e-16

Archaea R = 0.33, p = 0.23
Bacteria R = -0.14, p = 0.0088
Eukaryota R = -0.13, p = 0.0023

Degree (top) and closeness (bottom) centrality measurements plotted against relative read abundance for operational taxonomic units (OTUs) for Archaea, Bacteria, and Eukaryota.

## Discussion

- Both prokaryotic and eukaryotic microbial communities showed significant correlations in environmental variables including location, temperature, salinity, nitrate, and silicate concentrations.
- 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 shifted to dominantly bacteria.
- Predatory BALO bacterial nodes were more abundant and connected in nearshore network compared to the offshore network. Suggesting higher concentrations of microbes and contact rates which could increase the chance of success for predatory bacteria.
- Species with high degree and closeness centrality could play a role within the community and removal could affect the resilience of the community.
- Positive correlations between degree centrality and relative read abundance suggest abundance influences microbial connectivity as more abundant are more connected. While negative correlations between closeness centrality and relative read abundance suggest less abundant microbes are more central.

## Implications

Different regions support different microbial communities and different potential interactions. Removal of a key player or an environmental change within those regions could push the community past resilience into a new state.

Community resilience / Starting state / New state
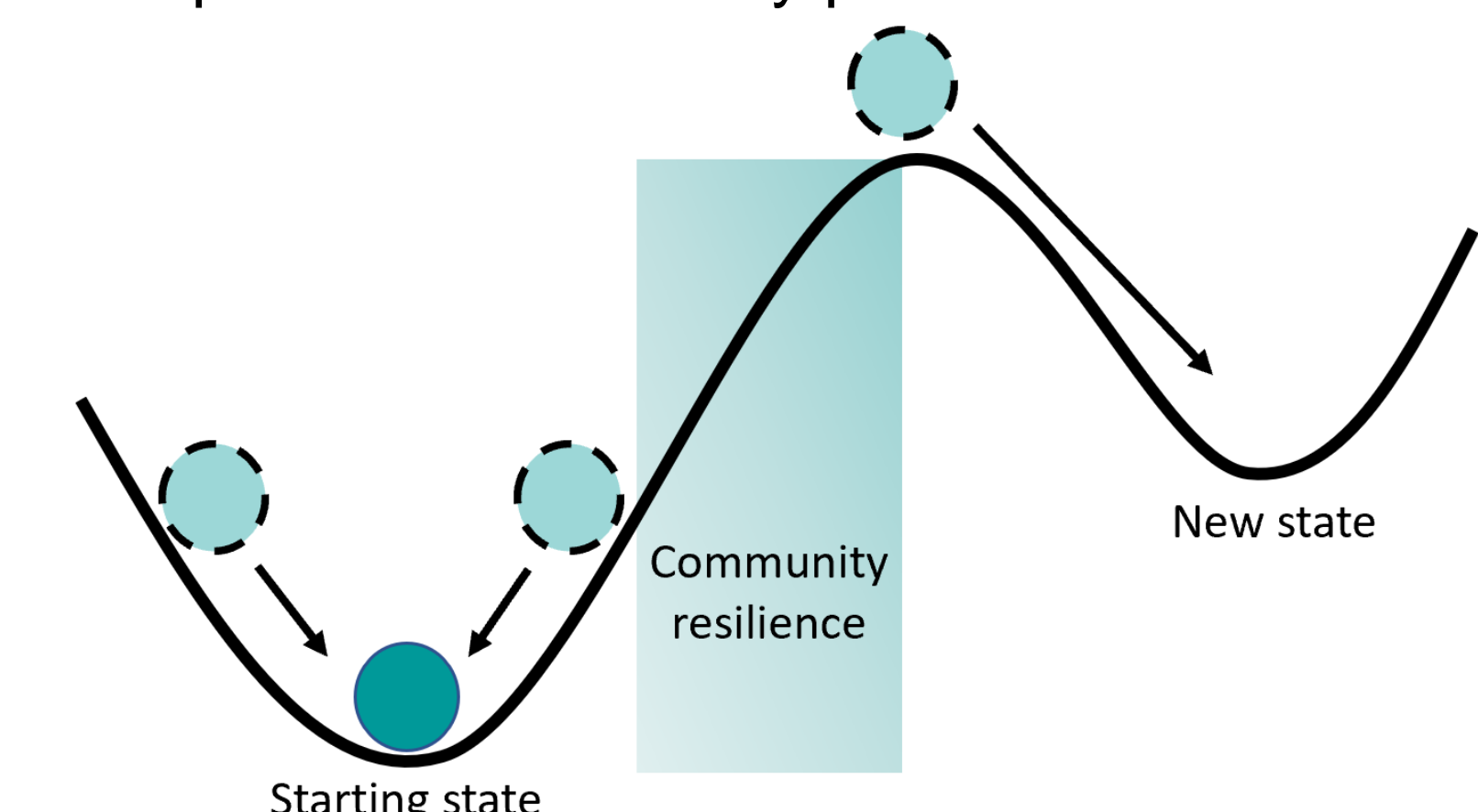
## Acknowledgments

I would like to thank Kyle Dilliplaine, Kodi Haughn, and the Strom lab for all their help and support on this project. This work was supported by funding from NSF Biological Oceanography (OCE 1851101), the Northern Gulf of Alaska Long Term Ecological Research program (OCE 1656070) and NSF (OPP 1937595). We acknowledge that we work on the ancestral lands and waters of the Dena'ina, Eyak, and Sugpiaq-Alutiiq peoples.