# Patterns Influencing Species Interactions in North Pacific Marine Ecosystems

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SUMMARY:
Abundance and distribution of marine species varies across time and space, reflecting biological interactions, environmental forcing, and external perturbation. Understanding the relative influence of these drivers requires integrating community ecology with ecosystem approaches, which consider habitat, environmental gradients, and climate. We used time series of population dynamics and environmental indices in Northeast Pacific systems to explore physical-biological linkages underlying ecosystem structure and mechanisms driving stability and change over time. We use diet data to classify species to functional guilds, explore common trends within guilds and determine the extent to which species within and between guilds exhibit spatial overlap, resource partitioning, predatory and competitive interaction.

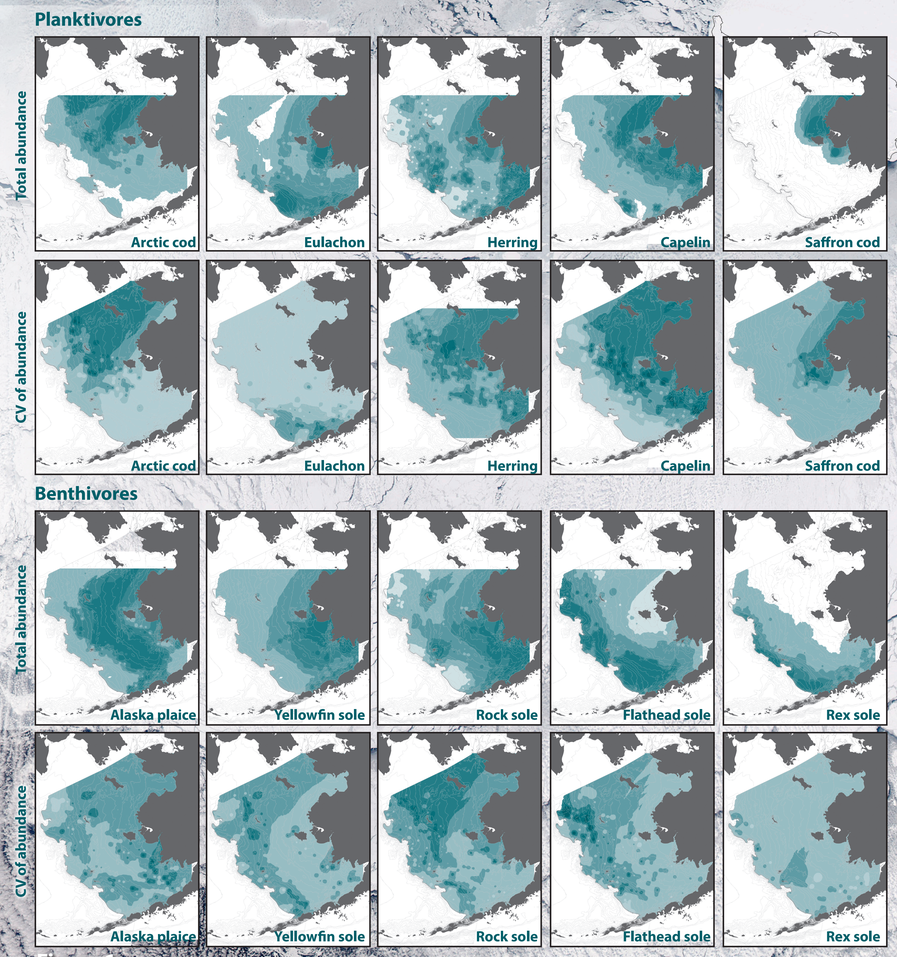


Figure 1

Spatial patterns in core (total abundance) and marginal habitat (coefficient of variation of abundance) suggest diverse responses to density dependence (Fig. 1). Whereas benthivores demonstrate highest variation at the margins of core habitat, (suggesting range expansion outside of core habitat during periods of high abundance), planktivores remain within core habitats as abundance varies (suggesting predatory or environmental constraints to range expansion and increased density constraints at high abundances).

Using random forests, we quantified relative importance, marginal effect, and critical thresholds for physical variables to species distribution. We then integrated single species outputs to determine how aggregate communities shift according to environmental gradients (schematic below). Location and importance of regression tree splits, which predict shifts in abundance on each environmental predictor gradient are aggregated for all species in the system (Fig. 5, gray histograms). Density plots (Fig. 5, lines) of the splits standardized by the observations indicate threshold shifts (ratios >1) in abundance of multiple species along the gradient of environmental predictors, or a rate of change in composition of the aggregate biological community. Barplots depict relative importance of predictor variables weighted across multiple species outputs. Biplots display survey stations (map, inset) in multidimensional space via ordination, such that coordinate position represents inferred biological community composition patterns along environmental gradients. To illustrate how individual species distribute across the system and orient according to environmental vector gradients, weighted mean abundance (1982-2012) was superimposed on these plots (Fig. 5, lower panels).

Using dynamic factor analysis, we distinguished common underlying trends within and among functional diet-based guilds. Correlation matrices display relationships between each functional guild in each LME (Figs. 2-4). In the eastern Bering Sea, abundance plots are displayed for each guild (Fig. 2, bottom plots), as well as plots of common underlying trends and the loading of each guild on each trend (Fig. 2, left). In the Bering Sea, guilds load primarily according to benthic versus pelagic pathways, such that motile invertebrates, crabs, benthivores, and demersal piscivores load similarly in contrast to invertebrate filter feeders, planktivores and pelagic piscivores. In the Gulf of Alaska (Fig. 3), loading appears based on trophic position with lower trophic levels loading more strongly on trend 1 and higher trophic levels on trend 2. In the Aleutian Islands (Fig. 4), loading on dominant trends is more diverse and may reflect alternating control based on bottom up and top down forcing. Lower level invertebrates load similarly on common trends but contrast to crab. Similarly, benthivores and planktivores load similarly, but contrast to demersal and pelagic piscivores respectively.

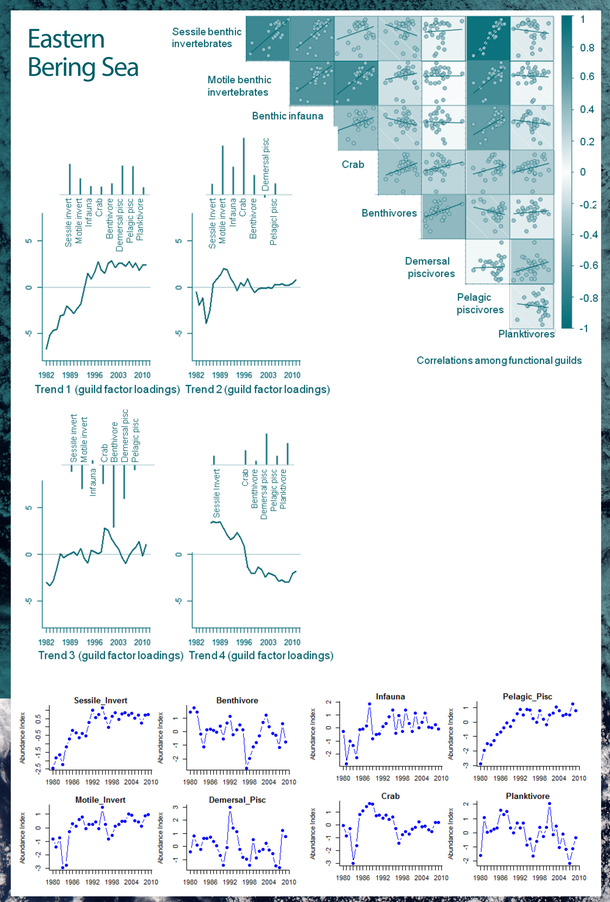


Figure 2

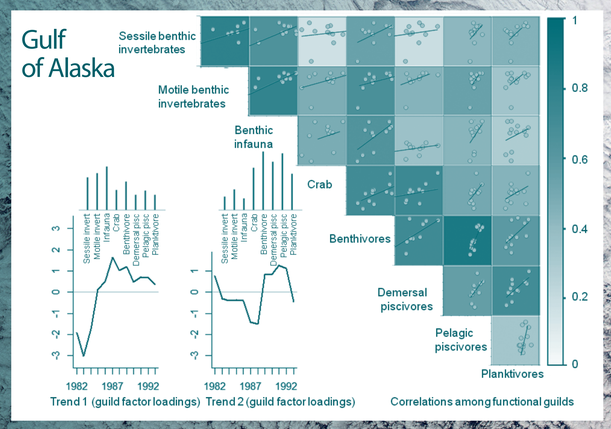


Figure 3

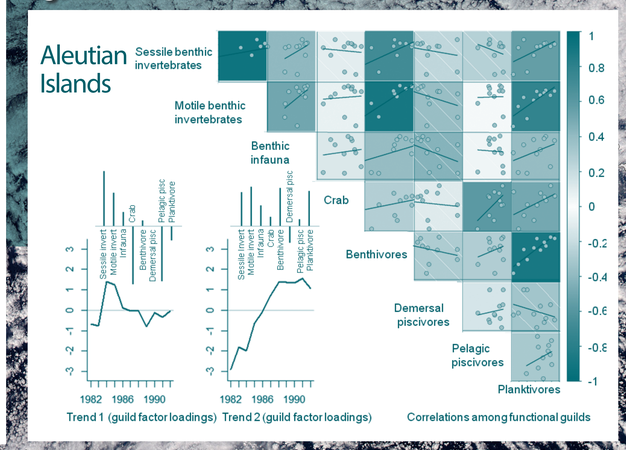


Figure 4

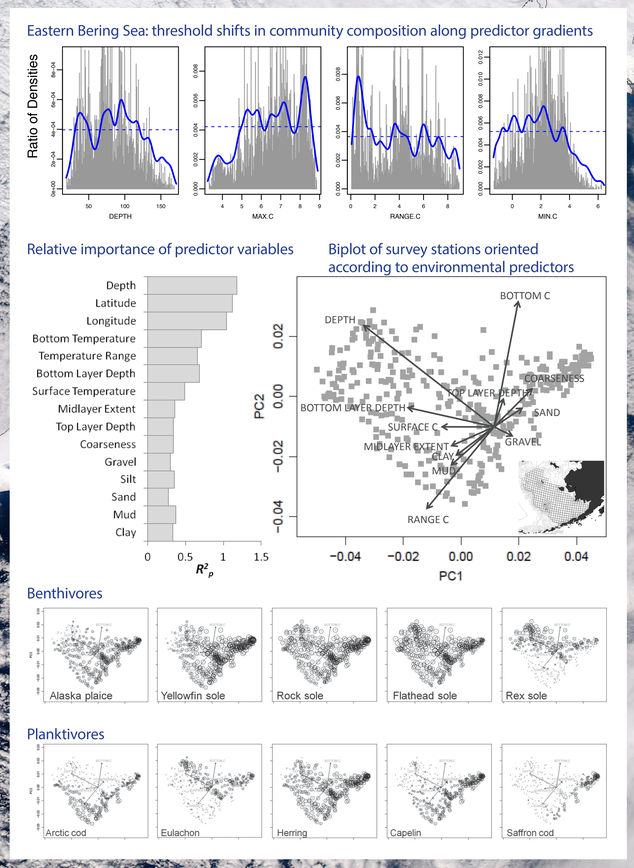


Figure 5

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