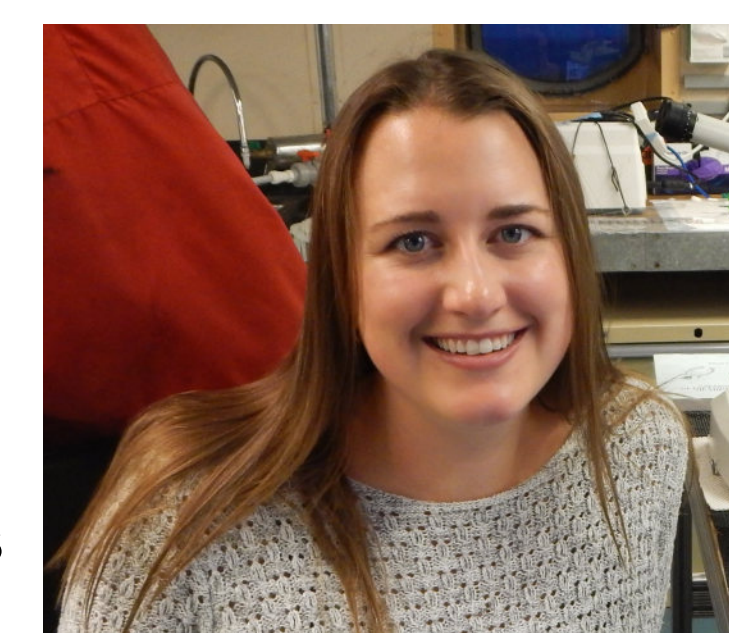


Zooplankton species and trait diversity in the Gulf of Alaska from the surface to the abyssopelagic



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Background Two cruises conducted in July 2019 provided a unique opportunity to survey zooplankton communities and pelagic diversity of the northern Gulf of Alaska from nearshore to deep oceanic environments to a depth of 4,300 m. Here we present preliminary results, primarily from traditional morphological analysis. We present contributions to species inventories for the region, explore community structure, and examine patterns of different metrics of diversity across inshore-offshore and depth gradients.

Faunal Groups and Species Patterns

Methods:

Stratified zooplankton samples were collected with fine (150- μ m) and coarse (505- μ m) mesh nets in the Northern Gulf of Alaska during July 2019 (Fig. 1). We collected paired samples for morphological and molecular analysis. Samples were analyzed to determine species composition and abundance. Community structure was explored with hierarchical clustering, non-metric multidimensional scaling (nMDS), and permutational multivariate analysis of variance (PERMANOVA) in Primer v7 software.

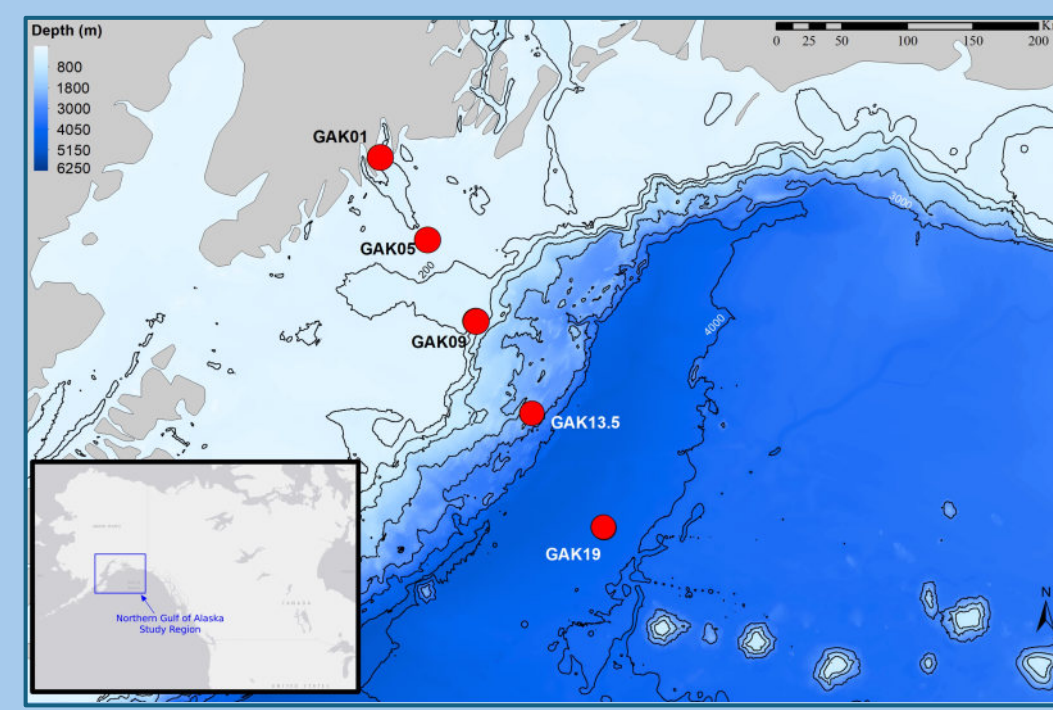


Figure 1. Study area of July 2019 cruises in the Gulf of Alaska.

Results:

- The 150- μ m net was dominated numerically by copepods. Copepods were also a dominant component of the 505- μ m net; however, other groups such as chaetognaths, mysids, and decapods were important contributors to the larger size spectra. We report new copepod species observations for the North East Pacific* such as *Heteroptilus acutilobus*, *Mormonilla phasma*, and others.
- We observed faunal groupings along a depth gradient, with additional structure in epipelagic layers along an inshore-offshore axis (Fig. 2). Distinct zooplankton assemblages were observed in the Upper Epipelagic, Lower Epipelagic, Mesopelagic, and Bathypelagic domains (150- μ m PERMANOVA; $p < 0.001$) (505- μ m PERMANOVA; $p < 0.001$).
- Some copepod families, such as the Augaptilidae, exclusively occurred in the mesopelagic & bathypelagic domains. These families exhibited vertical partitioning of the water column, with different genera occupying separate depth strata (Fig. 3).

* North East Pacific (Gulf of Alaska, "P" station, British Columbia) Zone on the Biodiversity of Marine Planktonic Copepods webpage (Razouls et al.), accessed Dec 2023.

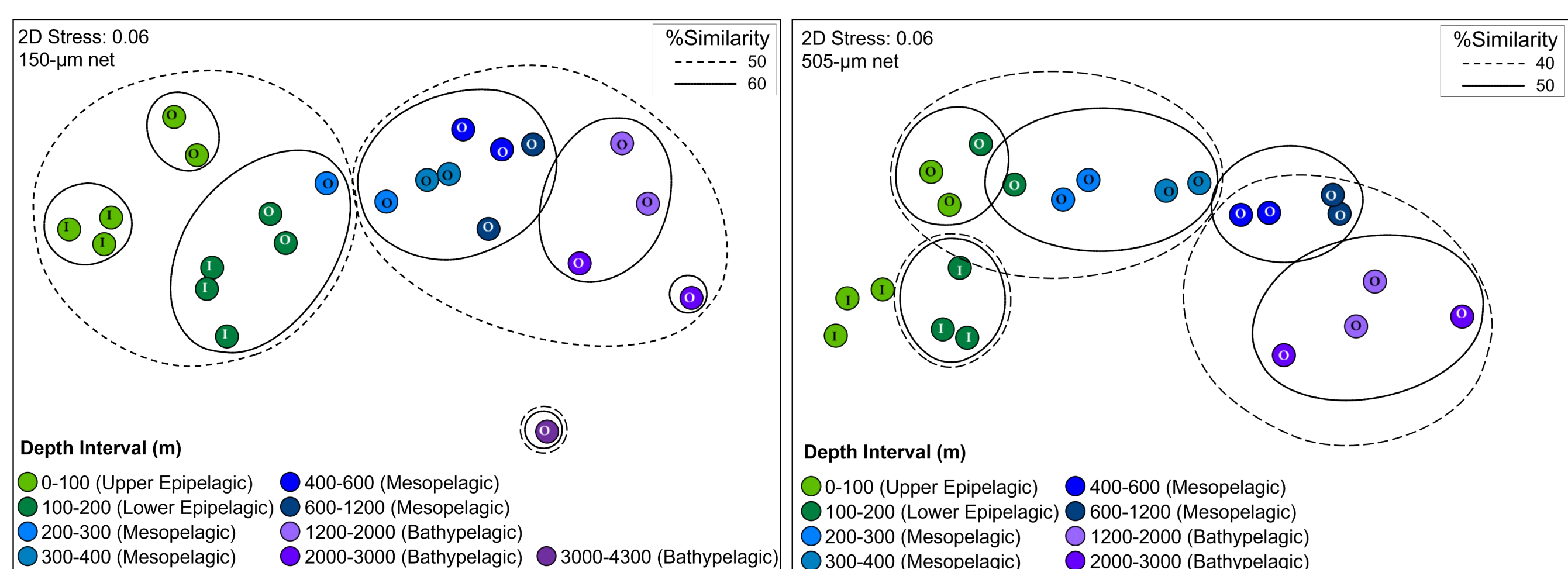


Figure 2. Non-metric multidimensional scaling (nMDS) of zooplankton community abundance data from the 150- μ m net (left) and 505- μ m net (right) overlain with clusters as determined by hierarchical clustering routine. Samples are symbolized by depth interval (m) with like colors representing major oceanic domains. Letters inside circles indicate Inshore (I) or Offshore (O).

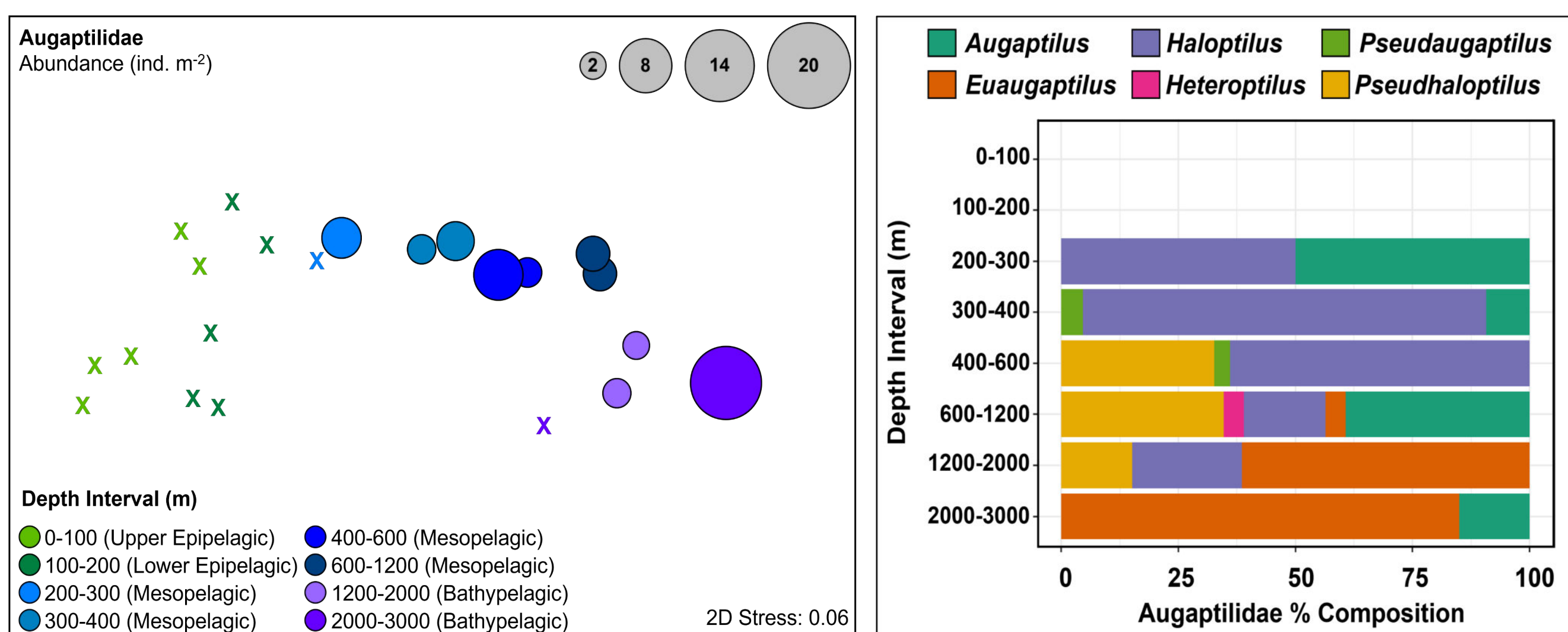


Figure 3. Augaptilidae abundance (ind. m^{-2}) overlain on nMDS plot (left) and percent composition of the family Augaptilidae by depth (right). Data from 505- μ m net.

Traditional Diversity Indices

Methods:

The number of taxonomic categories (richness) and Gini-Simpson index (evenness) was calculated for each sample in Primer v7 software.

Results:

- In both the 150- μ m and 505- μ m nets the number of taxonomic categories peaked in mesopelagic layers (Fig. 4).
- Epipelagic layers in the 505- μ m net had similar numbers of taxonomic categories; the number of taxonomic categories observed in the same layers in the 150- μ m net was more varied.
- Evenness in the 150- μ m net was relatively constant below 300 m.

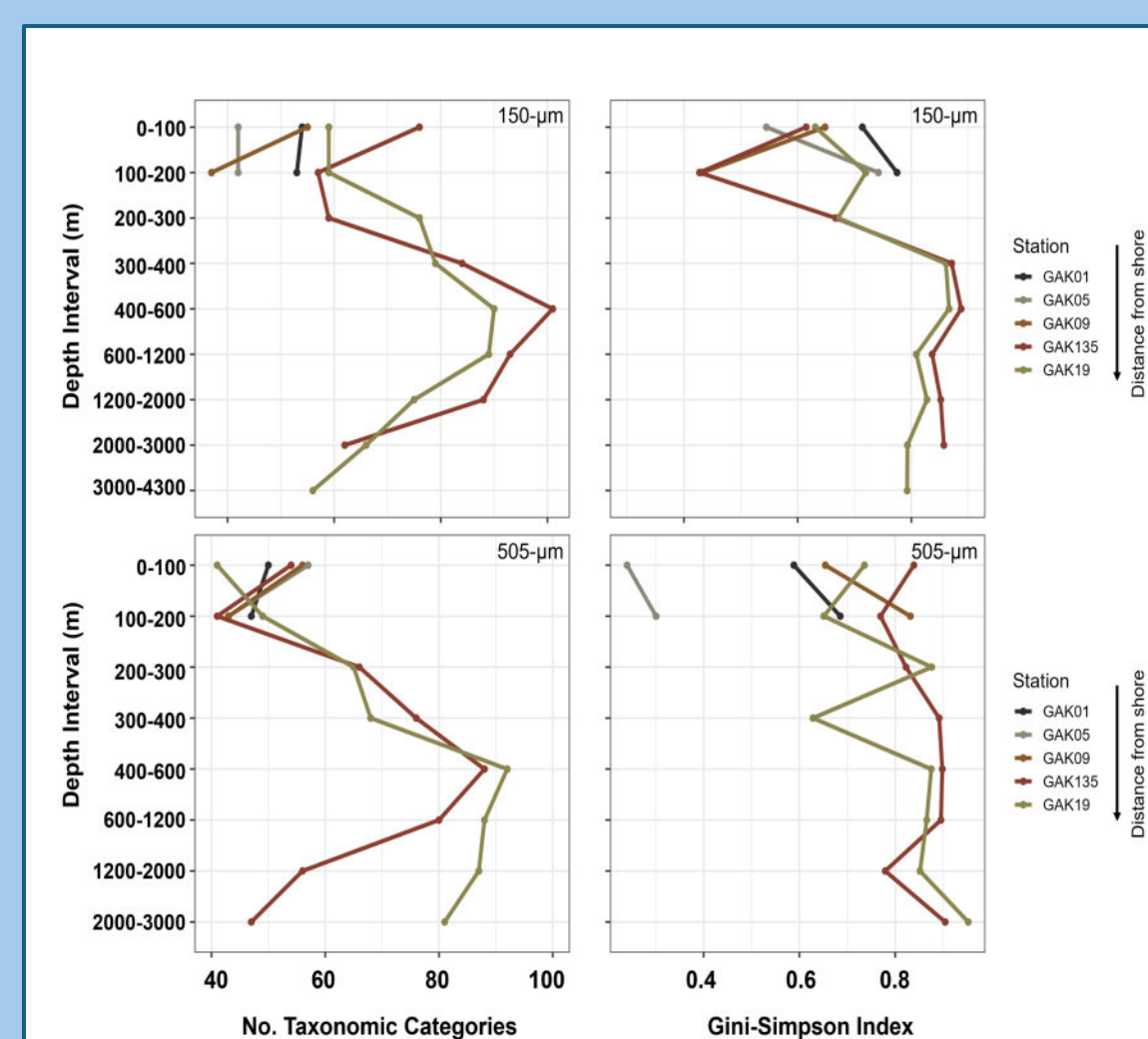


Figure 4. Number of taxonomic categories for the 150- μ m (top left) and 505- μ m (bottom left) nets. Gini-Simpson index for the 150- μ m (top right) and 505- μ m (bottom right) nets.

Taxonomic Diversity

Methods:

Average Taxonomic Distance (AvTD) indicates the taxonomic breadth of a community and offers a different facet of diversity than richness. AvTD can capture differences in communities that would be considered equivalent in terms of richness alone: five species in one family vs. five species in five different families. AvTD was calculated for the copepod community at offshore stations from the 150- μ m net in Primer v7.

Results:

- AvTD increased with depth within the epipelagic domain and decreased with depth within the mesopelagic & bathypelagic domains (Fig. 5).
- AvTD increased at transition zones between major oceanic domains; e.g. from epipelagic to mesopelagic and from mesopelagic to bathypelagic.

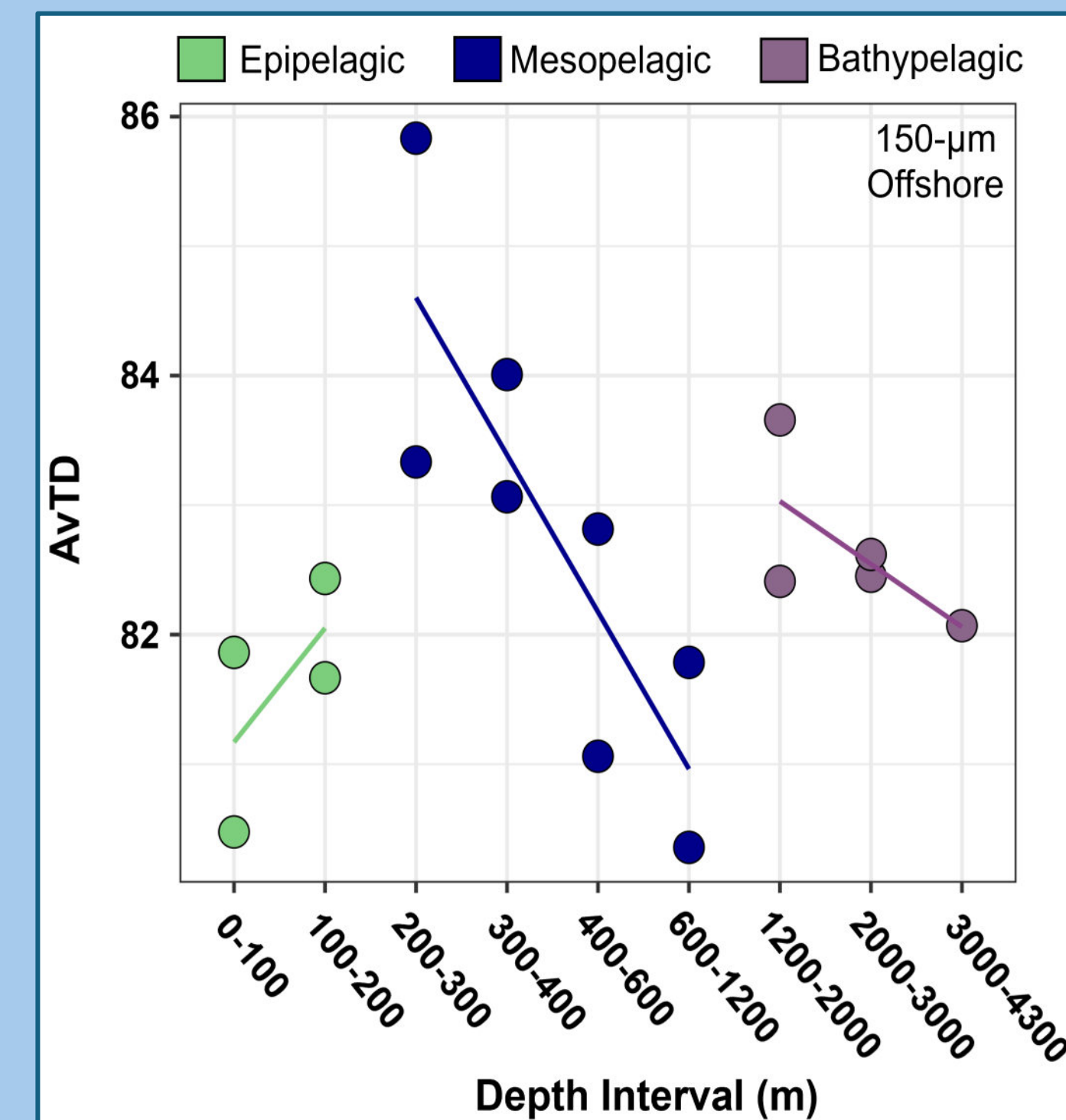


Figure 5. AvTD by depth interval with trend line for each major oceanic domain.

Genetic Diversity

Methods:

Samples for DNA metabarcoding were collected along with samples for traditional morphological analysis. Bioinformatics and analyses were conducted following the methods of Questel et al. (2021). Data are based on nuclear 18S-V4 rRNA and mitochondrial COI Amplicon Sequence Variants (ASVs) for metazoan plankton clustered at 97% and 96% similarity, respectively.

Results:

- The number of COI ASVs was highest in the epipelagic domain for the 150- μ m net. Trends for the number of ASVs and the Gini-Simpson Index were not consistent between markers for the 150- μ m net (Fig. 6).
- Depth-related trends for number of ASVs observed in the 505- μ m net were consistent between markers and peaked in the mesopelagic (Fig. 6).

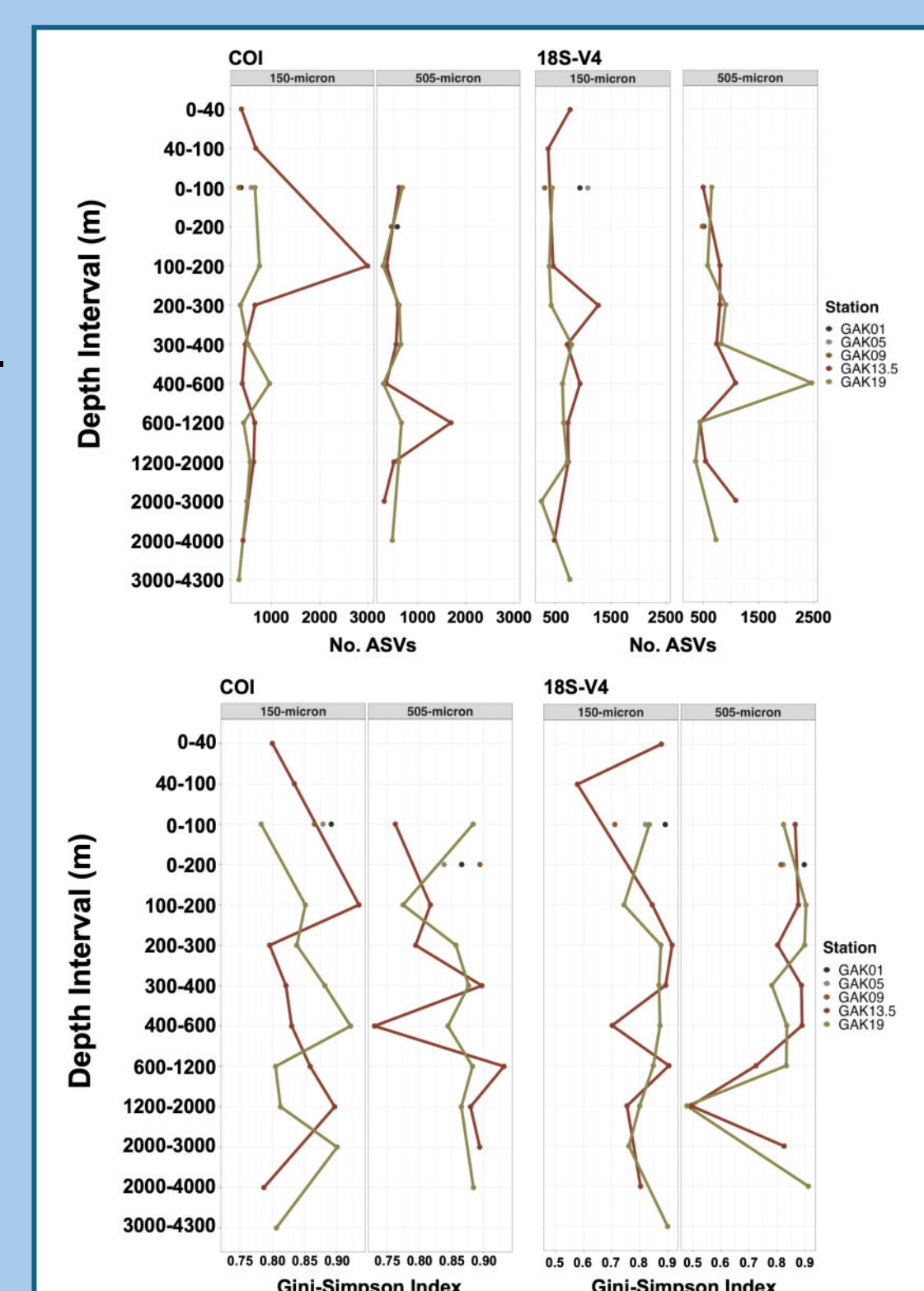


Figure 6. Number of ASVs (top) and Gini-Simpson Index (bottom) observed for metazoan plankton for COI and 18S-V4 for each mesh.

* For more information, please see talk by J. Questel in Session 4 *

Trait Diversity

Methods:

We assigned trophic traits (herbivore, omnivore, carnivore, omnivore-detritivore) to copepod taxa using published literature and trait databases. Using copepod abundance data from the 150- μ m net and the trait matrix, we calculated Community Weighted Mean (CWM) value of each trait using the FD package in R. CWM of trait values were plotted to explore spatial patterns.

Results:

- Communities in the upper epipelagic (0-100 m) on the shelf were dominated by herbivorous copepods (Fig. 7). Epipelagic communities past the shelf break were not as heavily dominated by herbivores compared to the shelf.
- Communities in the meso- and bathypelagic domains past the shelf break were dominated by omnivore-detritivores (Fig. 7).

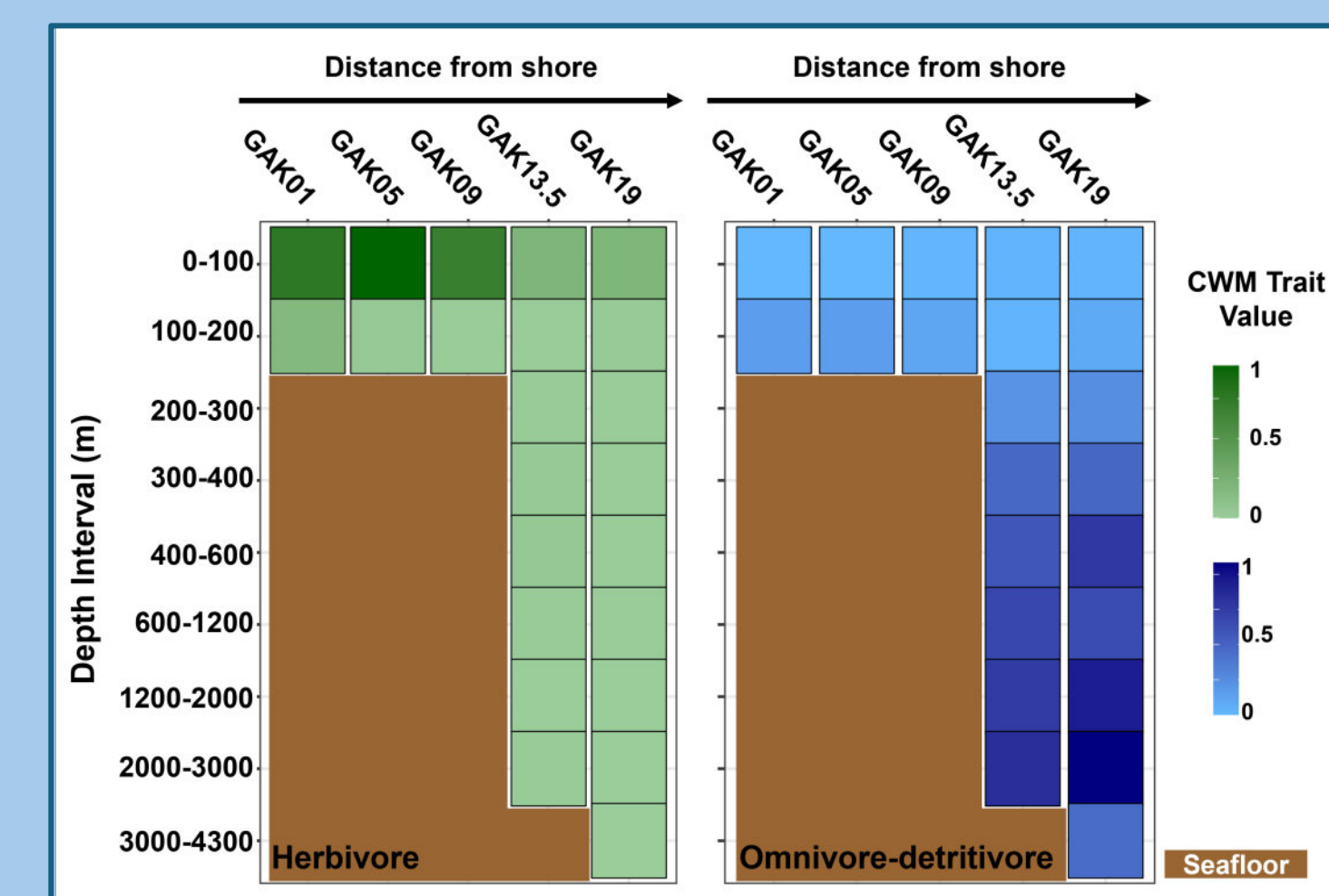


Figure 7. CWM value for herbivore (left) and omnivore-detritivore (right) traits plotted along an inshore-offshore transect.

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Conclusion and Discussion

- These efforts contribute to zooplankton biodiversity estimates in the North Pacific; additional study of the deep sea is needed to more completely characterize diversity \rightarrow more samples to be processed from 2019 cruises; another deep-sea cruise is planned for 2024.
- Zooplankton communities observed during these surveys were highly structured with depth. A second layer of separation was observed within the epipelagic domain along an inshore-offshore axis. Future analyses will consider environmental parameters as a structuring factor in zooplankton communities.
- Taxonomic breadth of the copepod community as assessed by the 150- μ m net decreased with depth within the mesopelagic and bathypelagic domains, indicating the dominance of a few highly speciose copepod groups.
- Diversity trends for the 505- μ m net as assessed by morphological and metabarcoding techniques showed consistent depth-related patterns. Trends for the 150- μ m net were not consistent between methodologies. Metabarcoding techniques captured higher levels of diversity, likely driven by hidden diversity, which is difficult to capture with traditional morphological approaches.
- Consideration of functional traits, such as trophic group, can give insight to community structure and function but is limited by the availability of data regarding these traits - particularly for deep sea taxa.