

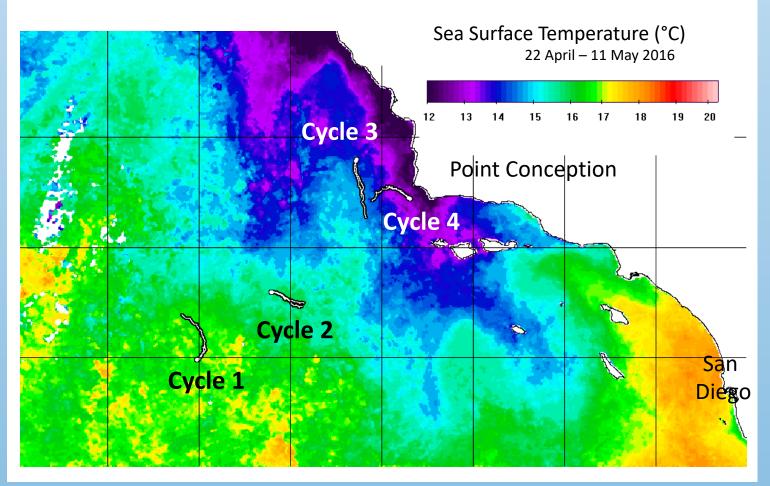
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# Questions

- Do zooplankton vertical habitats shift with major cross-shore environmental gradients?
- Does vertical habitat use covary with species' traits?
- Does feeding strategy shift within the zooplankton community in response to density stratification?

## Introduction

- Vertical gradients in temperature, food availability, and predation risk tend to be compressed in upwelling regions and expanded in the stratified offshore.
- If zooplankton actively select their vertical habitat in response to such environmental cues, their vertical distributions should change with distance offshore.



# Conclusions

- Clear vertical habitat shifts of DNA sequences as well as morphologically determined biomass
- OTU-specific vertical shifts best correlate with the depth of the 1% light level, a proxy for predation risk
- Stronger vertical shifts among carnivores than among herbivores
- Current feeding dominates, but feeding modes are more diverse offshore
- Offshore stratified waters, a spatial proxy for future oceans, indicate that warming may drive zooplankton deeper and shift the prey field available to both epipelagic and mesopelagic consumers

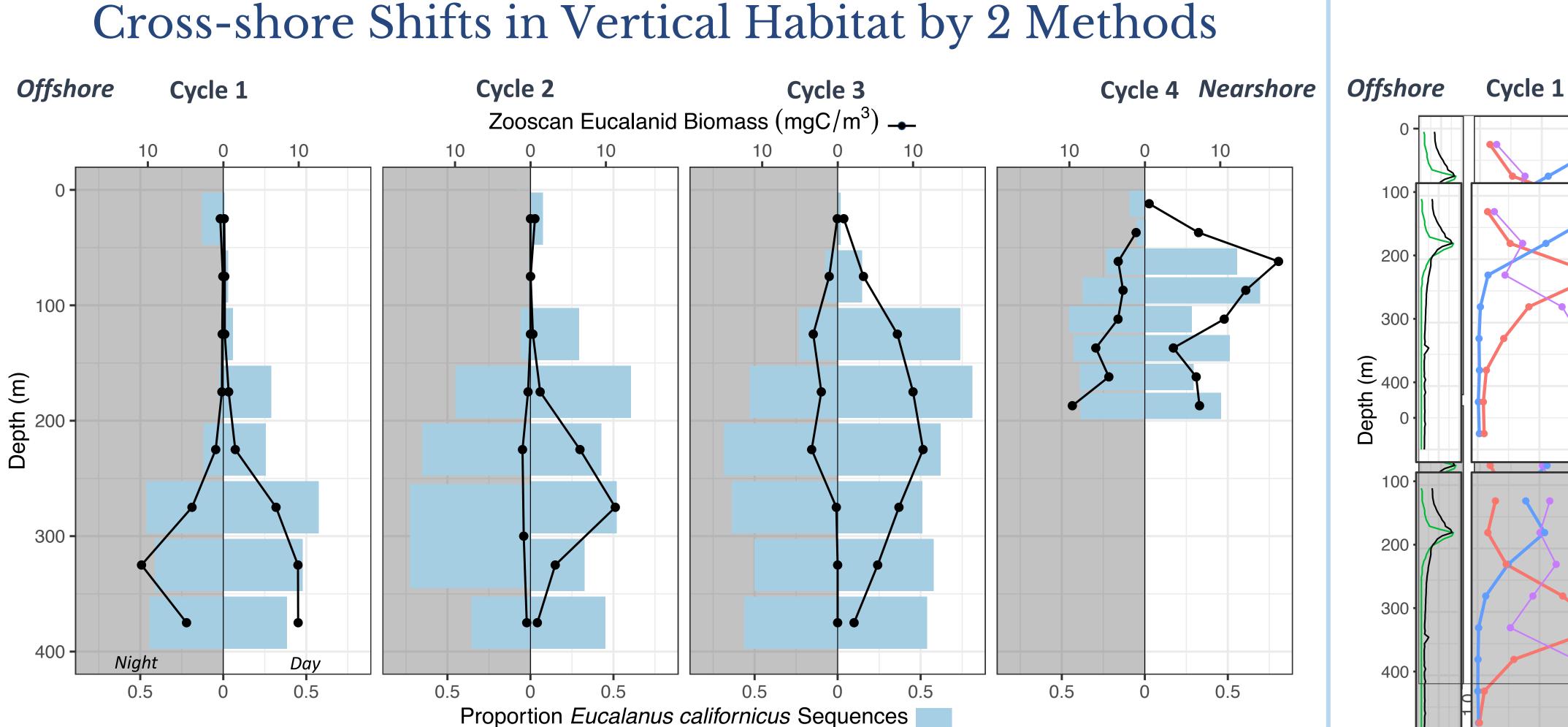
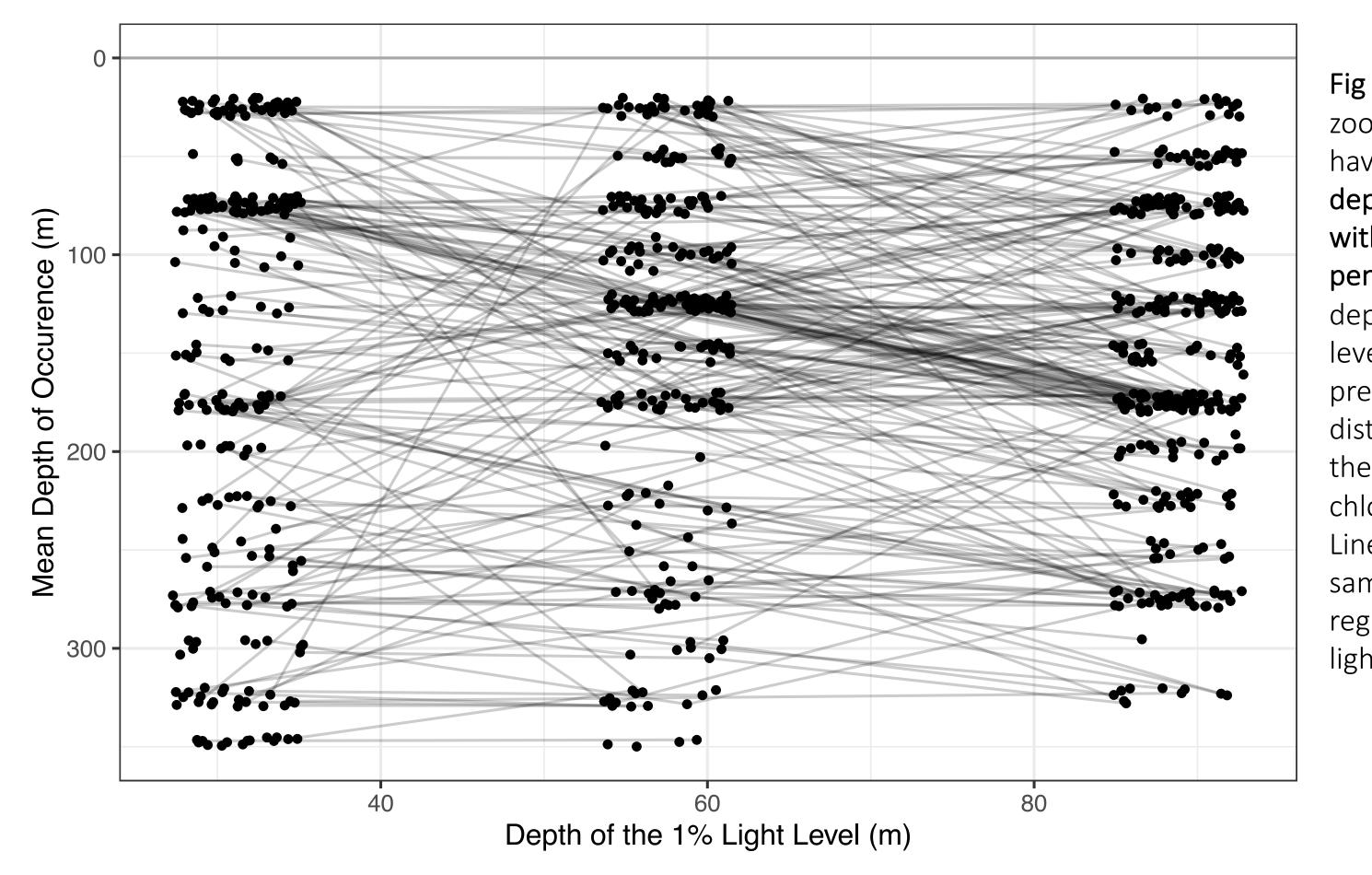


Fig 1. Both ZooScan-assessed biomass (circles and lines) and mtCOI DNA sequences (blue bars) reveal that the highest abundance of eucalanid copepods is found in subsurface waters, with the abundance peak deepening with distance offshore. There is good correspondence between the two methods, and sequencing appears to be more sensitive near the surface, where eggs and nauplii may be concentrated.

# Vertical Response to an Environmental Gradient



## Methods

Sampling Zooplankton were collected with vertically stratified paired day and night MOCNESS tows along an environmental gradient in the California Current Ecosystem (Cycles 1 - 4, above left) in April 2016, and split for preservation in 5% Formalin or 95% buffered EtOH (Matthews et al. 2021).



# The power of zooplankton metabarcoding: Resolving changes in habitat use by zooplankton across the California Current Ecosystem

ZooScan Morphological Analysis

Zooplankton were imaged with a ZooScan, sorted into 27 taxonomic categories using machine learning, and all image classifications verified manually (Gorsky et al. 2010).

## Traits

Traits were assigned to OTUs based on taxonomy. Traits included maximum size, diet, feeding behavior, spawning strategy, presence of asexual reproduction, DVM behavior, and carbon content

Metabarcoding Analysis mtCOI (Leray et al. 2013) and 18S (v4-v5, Zhan et al. 2013) were amplified in triplicate with a 2-step PCR and library prep (Sommer et al. 2017). Bioinformatic analyses were conducted in QIIME2 (Bolyen et al. 2019). ASVs were inferred with DADA2 (Callahan et al. 2016), then clustered at 97% similarity to obtain COI OTUs. Taxonomy was assigned using the MetaZooGene database with an 80% confidence cutoff.

# Habitat Shifts by Diet

Fig 2. Many zooplankton OTUs have deeper mean depth of occurrence with increasing light penetration. The depth of the 1% light level is a better predictor than distance offshore or the depth of the chlorophyll maximum. Lines connect the same OTUs sampled in regions of different light penetration

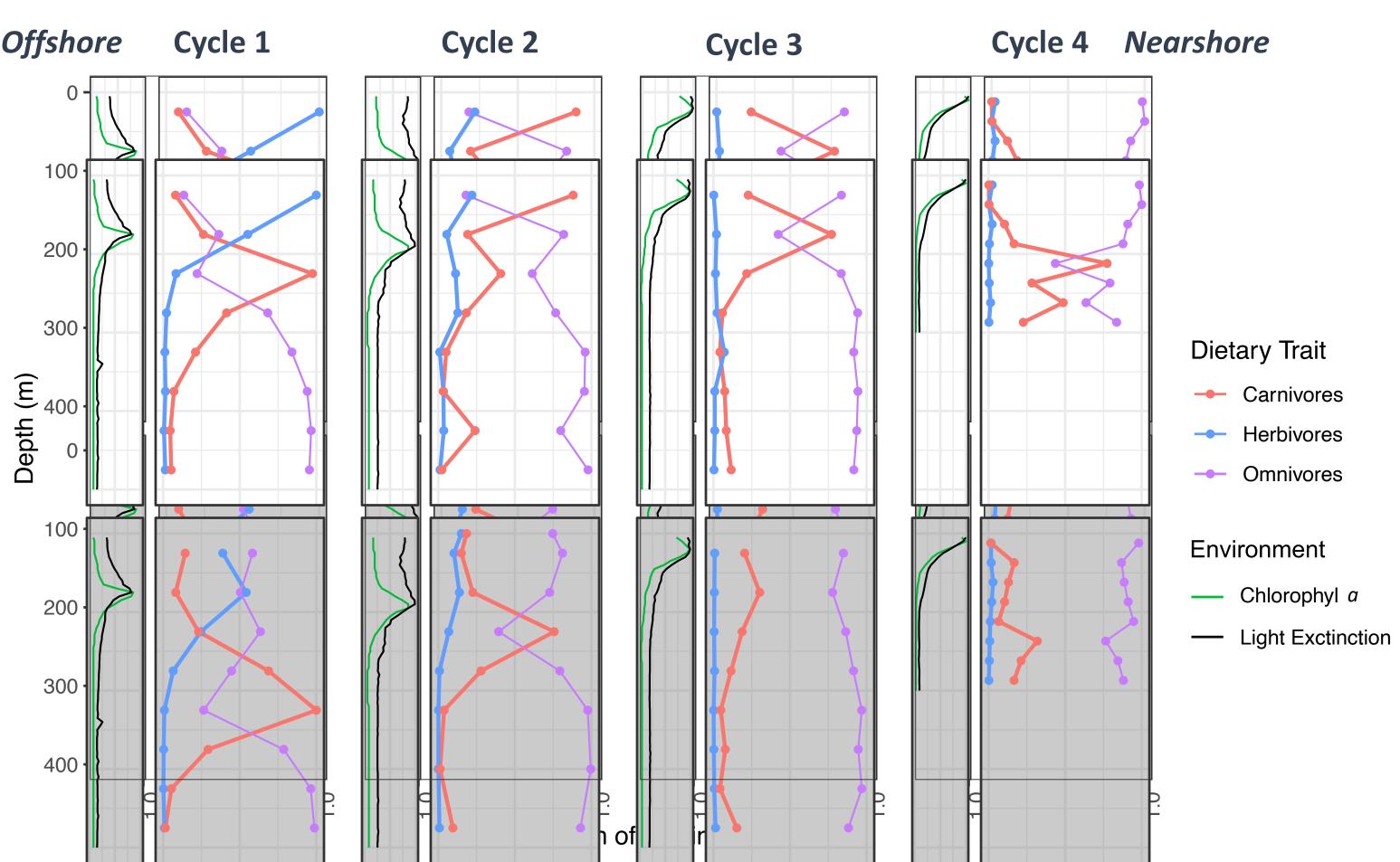
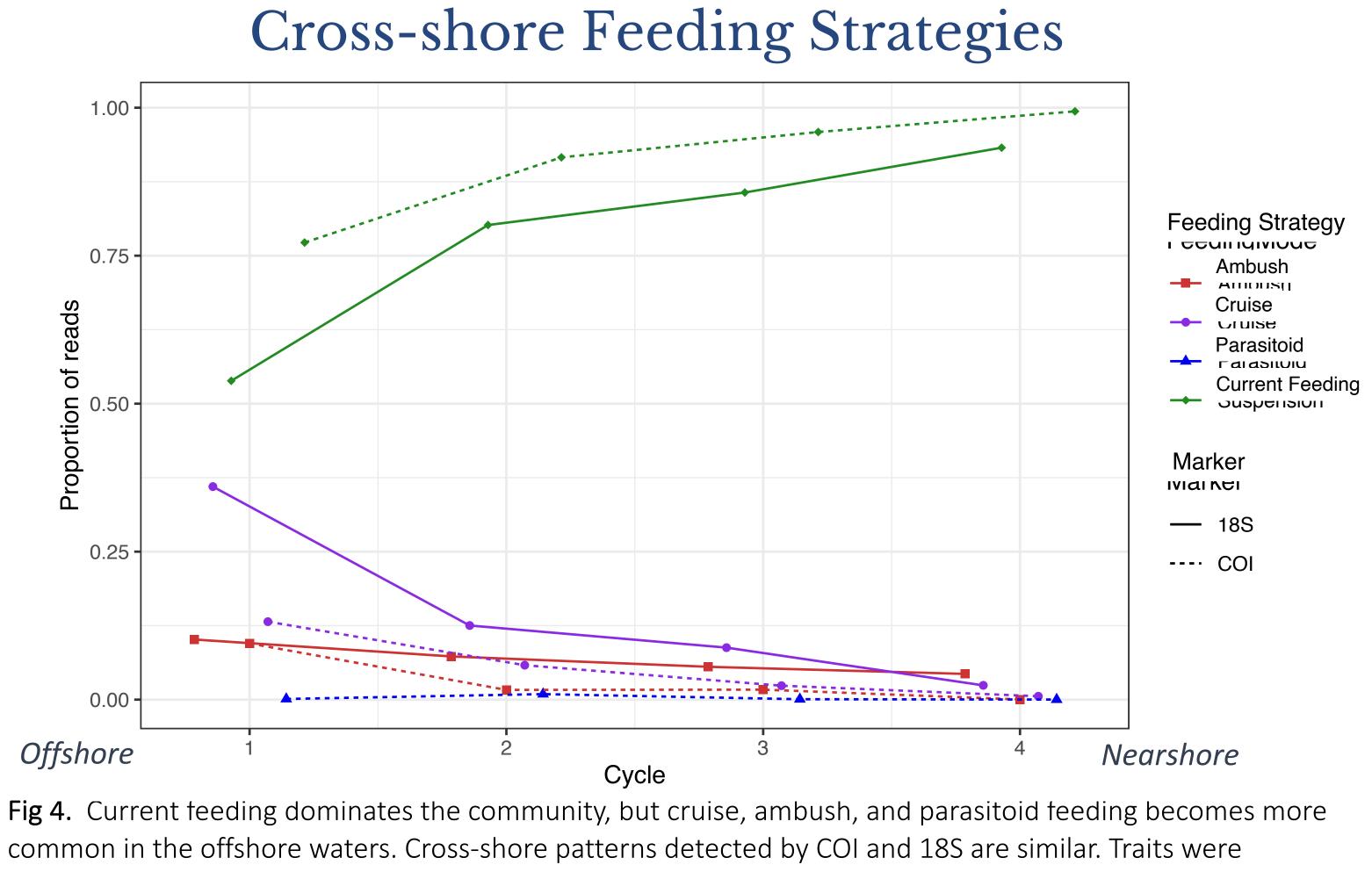


Fig 3. Carnivorous zooplankton shift to deeper depths in more stratified offshore waters. Offshore, herbivorous zooplankton vertical distributions become closely associated with the chlorophyll maximum. Traits were assigned to DNA sequences based on taxonomy.



assigned to DNA sequences based on taxonomy, following Kiorboe (2011).

### Acknowledgements

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## References biotechnology 37.8 (2019): 852-857

- (2010): 285-303

- and Evolution 4.6 (2013): 558-565.





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Bolyen, Evan, et al. "Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2." Nature

Callahan, Benjamin J., et al. "DADA2: high-resolution sample inference from Illumina amplicon data." Nature methods 13.7 (2016) Gorsky, Gaby, et al. "Digital zooplankton image analysis using the ZooScan integrated system." Journal of plankton research 32.3

(iørboe, Thomas. "How zooplankton feed: mechanisms, traits and trade-offs." Biological reviews 86.2 (2011): 311-339. eray, Matthieu, et al. "A new versatile primer set targeting a short fragment of the mitochondrial COI region for metabarcoding. metazoan diversity: application for characterizing coral reef fish gut contents." Frontiers in zoology 10.1 (2013): 34. Matthews, Stephanie A., Erica Goetze, and Mark D. Ohman. "Recommendations for interpreting zooplankton metabarcoding and integrating molecular methods with morphological analyses." ICES Journal of Marine Science 78.9 (2021): 3387-3396. Sommer, Stephanie A., et al. "Vertical gradients in species richness and community composition across the twilight zone in the North Pacific Subtropical Gyre." Molecular ecology 26.21 (2017): 6136-6156 Zhan, Aibin, et al. "High sensitivity of 454 pyrosequencing for detection of rare species in aquatic communities." Methods in Ecology