Leveraging microbial structure data to inform traits-based modeling, an approach based on microbial community segmentation.

I. Introduction
Numerical modeling is a critical method for understanding ecosystem processes. However, current approaches are typically not informed by microbial diversity data due to its high dimensionality. This creates a discrepancy between the observed and modeled biological complexity that over-simplifies the dynamics and function of the microbial communities in marine ecosystems. Here we describe a strategy for incorporation of microbial community structure data in the Regional Test-bed Model, a 1-D data assimilative ecosystem model with parameters optimized for the pelagic western Antarctic Peninsula (WAP) near Palmer Station.

II. Segmentation of Microbial Community Structure
Bowman et al. (2017) introduced a technique to “segment” the microbial community into functionally coherent units ("modes") that can be described by a single categorical variable. This categorical variable reflects the key genetic traits of the microbial community. An analysis of 16S rRNA gene data from a 5-year time-series from the WAP was described by 8 recurrent modes in the bacterial community. Each point in the time series is associated with a specific mode based on microbial community relative abundance. Estimates of genome parameters estimated for each mode showed a discrepancy between the observed and modeled biological complexity that over-simplifies ecosystem processes.

III. Palmer Regional Test-bed Model (Kim et al. in preparation)
1-Dimensional data assimilative marine ecosystem model which utilizes a variational adjoint scheme (Lawson et al. 1995) to optimize biological model parameters. Built from existing regional test-bed models from other long term time series (Luo et al. 2010, Friedrichs et al. 2006).

IV. Unifying trait-based microbial community segmentation and numerical modeling
Each community mode has its own functional genetic traits from which we can make reasonable estimates of model parameters.

- Maximum BA growth rate
- BA active respiration rate vs. Production
- Bacteria extra semi labile DOC excretion rate
- BA inorganic nutrients regeneration rate
- BA refractory DOC production rate
- BA selection strength on SDOM
- BA basal respiration rate - min/max
- BA mortality rate
- Half-saturation density of BA for grazing

Using a model hind-cast of the time series, we can compare data assimilation parameter estimates with estimates from observed mode.

V. Conclusion
By reducing the dimensionality of microbial diversity data to enable a correlation between community structure and function we are able to better incorporate microbial dynamics into predictive models. Ultimately, we expect this approach to improve the fidelity of traits-based ecosystem models, leading to a better understanding of complex ecosystem processes.