Oceanography Seminar

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"Exploring the Ocean Microbiome Using Metagenomic Sequencing: Tara Oceans and Beyond"

The presentation will discuss the use of metagenomic sequencing in microbial oceanography with a focus on the results of recent Tara Oceans expedition. Microbes are dominant drivers of biogeochemical processes, yet drawing a global picture of functional diversity, microbial community structure, and their ecological determinants remains a grand challenge. In the context of Tara Oceans 7.2 terabases of metagenomic sequencing data from 243 Tara Oceans samples from 68 locations in epipelagic and mesopelagic waters across the globe were analyzed. The data was used to generate an ocean microbial reference gene catalog with >40 million nonredundant and mostly novel gene sequences. In-depths analyses of this dataset found more than 35,000 species in the prokaryote-enriched samples, revealed a vertical stratification of these microbial communities and identified temperature rather than other environmental factors or geography as the main driver of epipelagic community composition. Further, the usefulness of such a dataset for independent applications in microbial oceanography will be discussed.

Thursday September 24, 2015 3:00 p.m. MSB 100