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Paleometagenomic network analysis of ancient DNA from Bering Sea sediments to examine past ecological communities

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Understanding marine ecological systems is a challenging task that requires probing of different comparable states and comprehensive time series analysis. In this approach, we analyze sedimentary ancient DNA recovered from marine sediments which function as an extensive archive of past biota, as they conserve snapshots of the ecological community from the time of its DNA deposition. We examine metagenomic shotgun data from 22 samples as a time series ranging 124 kyrs from a probed sediment core recovered from the Shirshov Ridge in the Bering Sea basin to explore the possibilities of paleometagenomic network analyses. Looking at the presence and abundance of different taxa inhabiting the ocean at certain periods and climatic conditions including (1) the last interglacial (Eemian), (2) the last glacial period, and (3) the modern interglacial (Holocene), we reconstruct and analyze ecological networks and inspect how they have changed and adapted over time. Moreover, by developing extensive network analysis methods including species interaction enrichment and comparable simulation models we evaluate the viability of identifying complex connections and relationships between organisms, as well as the influence of reconstructed environmental factors. Our analysis establishes an initial pipeline for paleometagenomic network analyses and enables further research, e.g. network comparison of multiple marine sites to better understand past ecological mechanisms.