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Using co-correspondence analysis (CoCA) to compare biodiversity patterns detected by two seafloor sampling methods

Long-term monitoring of marine benthic communities provides data that are essential for effective marine management. However, monitoring is limited by the difficulty and expense of sampling deep seafloor areas comprehensively enough to represent the whole benthic community. This has led to the development of a wide array of seafloor sampling methods. Consequently, the integration and prioritisation of data collected using different methods remains an area of concern. Demersal research trawling and grab sampling are two methods employed to sample the marine benthos, targeting different habitats and fauna, at different scales and with different sampling efficiencies. The aim of this study is to determine whether these two sampling methods detect different taxonomic and functional diversity patterns. This was explored using research trawl and grab datasets collected from twenty-four pairs of offshore stations within the Southern Benguela Shelf ecoregion on the west coast of South Africa (70 – 600 m) between the years 2009 and 2020. Symmetric co-correspondence analysis (sCoCA) was used to test for patterns among infaunal (collected by grab) and epifaunal (collected by demersal trawl) communities and functional trait assemblages. sCoCA found infaunal assemblage patterns to be highly correlated with epifaunal assemblage patterns across the study area using both taxonomic and traits-based approaches. The predictive form (pCoCA) was used to determine whether taxonomic diversity is an adequate surrogate for functional diversity in the marine benthos. These findings should be considered when including different biological datasets into ecosystem classification and long-term monitoring.