11/30/2021

Dear Editorial Board.

This letter accompanies the manuscript, “Environmental DNA provides quantitative estimates of Pacific hake abundance and distribution in the open ocean” which we wish to submit for consideration as a new research article to Proceedings of the Royal Society B under the new category of Biological Applications.

Understanding spatio-temporal patterns of species abundance and distribution are vital for conserving and managing natural ecosystems. Quantifying abundance can be a complex and expensive task and increasingly new technologies like environmental DNA (eDNA) are advocated as inexpensive and efficient means to improve estimates of abundance of wild populations. However, there are persistent questions about the validity of using eDNA a quantitative measure of abundance and limited methodologies for translating eDNA observations into abundances indices that can be used in practice. In this study, we present results from a very large open ocean survey of a commercially and ecologically important species, Pacific hake (*Merluccius productus*), and show how eDNA can provide estimates of distribution and abundance for hake that correspond very closely with results from traditional acoustic-trawl sampling. Our methods reveal that with relatively limited eDNA sampling – based on hundreds of sampling stations as opposed to thousands of kilometers of acoustic surveys – can provide estimates of abundance that have similar precision to the existing acoustic surveys yet use only a fraction of the effort. Furthermore, we show how information derived from eDNA can be turned into indices that are very similar to information currently used in management models. Our results provide strong support for the expanded use of eDNA as a general, inexpensive, and quantitative survey tool to support the conservation and management of marine species.

Sincerely,

A.O. Shelton for the co-authors