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Design-based and model-based estimations of distribution and abundance of dolphin populations in Gulf of Corinth, Hellas

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Abstract. In recent years a major scientific effort has been focused on the protection of marine mammals. Gulf of Corinth is part of the Natura 2000 network (GR2530007) since 2016, with Special Areas of Conservation and constitutes an important habitat for striped dolphin (*Stenella coeruleoalba*), bottlenose dolphin (*Tursiops truncatus*) and short-beaked common dolphin (*Delphinus delphis*). Dedicated shipboard transect line surveys were designed and based in Conventional Distance Sampling and were implemented seasonally during 2018-2019, using passive acoustic and visual techniques, combined with related data derived from 2005-2006 field surveys. Estimation of distribution and abundance of dolphins' population with a design-based approach using factors such as weather conditions and cluster sizes surprisingly revealed the total absence of *Delphinus delphis* from the studied area. Density Surface Models (DSM) were used to model these adjusted counts based on a formula involving environmental covariates (depth, surface temperature), in order to investigate the response of populations to biotic and abiotic covariates. Model-based approach for mapping the spatial distribution of animal species clusters can be a useful management tool in establishing protected areas, as well as in communicating monitoring data with non-experts.

Keywords: Delphinids, Gulf of Corinth, Distance Sampling, Density Surface Models

1. Introduction

Systematic surveys for monitoring marine mammals in the field are an irreplaceable way of collecting valuable and reliable data of abundance and distribution patterns of a species. Eastern Mediterranean consists an area which the importance of monitoring marine mammals is underlined due to species subpopulation patterns (Gkafas et al. 2017) particularly in common dolphins which facing eradication in local scales (Santostasi et al. 2018). Golf of Corinth at the eastern Mediterranean consists of such a hot spot with extensive monitoring so far (Bearzi et al. 2011) underlying the importance of our ongoing monitoring scheme of abundance and distribution of the local delphinids.

2. Material and Methods

2.1. Data Collection

Data was collected during dedicated shipboard surveys from December 2018 to April 2019 in Gulf of Corinth. For the survey design automated survey algorithms in the software Distance 7.1 (Thomas et al. 2010) were used, in order to create survey architecture with 18 transect lines. The algorithm of equal-spaced zigzags was used with the assumption of constant coverage probability, in order to reduce off effort transitions between transect lines (Strindberg and Buckland 2004). For all surveys, a 14 m catamaran boat with diesel engine was used. All observations and GPS geographic information were recorded every 10 secs and stored in a database using Logger 2010 software (IWFA).

2.2. Data Analysis

Data from our designed based approach were analyzed with multiple covariates distance sampling approach in Distance 7.2. Detection function was modeled with covariates of group size and sea state (Beaufort scale) and model selection was guided by Akaike's Information Criterion (AIC). Additional data from three non-designed surveys were added in Model-based approach. Density surface modeling (DSM) was fitted in R "dsm" package (Miller et al. 2013). A generalized additive model was constructed per segment counts as the response with covariates such as latitude, longitude, depth (GEBCO08) and annual surface temperature (MODISA).

3. Results

The shipboard surveys covered a total of 1,040 km on effort focused primarily on Delphinids. During the surveys 20 clusters with an average of 7.4 animals was recorded. Two species were visually detected and recognized at the species level; the bottlenose dolphin (*T. truncatus*) and the striped dolphin (*S. coeruleoalba*), in contrast with common dolphins (*D. delphis*) which could not be detected. The best fit model, as determined by AIC, was the hazard-rate key function with no adjustment terms and cluster size as a covariate. For density modeling a gridded data set was created, containing a value in every grid cell for each explanatory variable in the model. The selected model included the following explanatory terms: s(x, y) + s(SST) (Fig. 1) based on the deviance explained. The explanatory power of the model was positive, with an adjusted R-square score for the model of 0.037, and deviance explained of 82.7%. A square grid size of 4 km on a side was chosen for concluding prediction (Fig. 2)

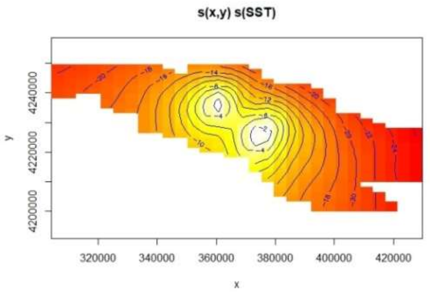

Figure 1. Plot of the bivariate smooth of x and y with additional covariate SST.

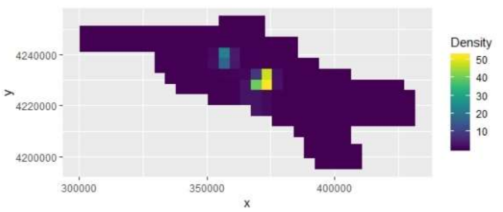

Figure 2. Spatial prediction of the best fit model.

4. Discussion and conclusions

GAM-based models enable estimation of the number of animals in a spatially flexible way in order to combine different surveys to detect changes in distribution and abundance. The smooth density surface model predicted for Delphinidae could be used in a variety of ways, providing that they accurately reflect mean animal distribution during the survey. Such a pattern may be explained in various ways where many species co-occur and interact. A better understanding of how communities are organized would be useful with respect to environmental changes; e.g. global warming. However, predictable patterns within most natural niches are comprised of distribution of species abundance. In our model higher densities of the species in question have been predicted in the central of Gulf of Corinth, suggesting a species higher abundance in restricted areas compared to their geographic distribution (Bearzi et al. 2016). Indeed, comparing species abundance can be challenging due to the fact that species communities often comprise many different aspects of abundance profiles, such as predation (Hoelzel 2009), social structure (Natoli et al. 2008), kinship associations, demographic dynamics (Gkafas et al. 2017) and evolutionary forces. On top of that, different environments could drive different population structure in a widely distributed species in a given area (Moura et al. 2012).

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