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POSTER – Estimation of the common dolphin (Delphinus delphis) mortality-at-age from strandings of a threatened population

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ESTIMATION OF THE COMMON DOLPHIN (*DELPHINUS DELPHIS*) MORTALITY-AT-AGE FROM STRANDINGS OF A THREATENED POPULATION.



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The short-beaked common dolphin (*Delphinus delphis*) is the most abundant small cetacean in the north eastern Atlantic and in some regions of its range, by-catch mortality is considered to be unsustainable. To help inform conservation measures and allow the quantification of the impact of by-catch, population models are needed to explore how the population will react under different scenarios. Mortality-at-age is one of the most important parameters necessaries to build a population model, but also one of the most difficult to estimate.

WHY WE NEED TO ESTIMATE DOLPHINS MORTALITY ?



SILER MODEL AND THE LACK OF THE FIRST AGE CLASSES

 Image: standed in galaxies

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<u>Study area:</u> map of Europe and detail of the position of Galicia, in the Northwest of Spain. Common dolphin is distributed in all Northeast Atlantic waters but higher abundance are fund from Portugal to the Southwest of Ireland and England along the Spanish and France coasts.

To estimate mortality-at-age from the stranded dolphins the most common way is to build a life table and apply a <u>Siler model</u> for the proportion of dead animals by age.

 $\mu_{(x)} = a_1 \exp(-b_1 x) + a_2 + a_3 \exp(b_3 x)$

Population structure is usually biased in the observer strandings, due to the <u>lack of the first age classes</u> in the samples. Therefore, is important to detect it and <u>remove these</u> ages from the sample or apply a correction factor.



<u>Bar plot:</u> Number of stranded dolphins by age (grey bars). Siler model prediction, fitted to the observed data (dashed line). Siler model prediction, fitted without first two age classes. <u>Inside the box</u>: Siler model fitted to all stranded animals (dotted line). Siler model fitted after removing the two first age classes (solid line). Points are the observed mortality at age.

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HELIGMAN - POLLARD MODEL DEALING WITH THE BY-CATCH







As in our case of study, some dolphin populations are under high levels of by-catch with affect different to the various age classes. We used an adaptation of the <u>Heligman-Pollard model</u> which allows to include an extra component representing by-catch.

$q_{(x)} = A^{(x+B)C} + (I + D \exp(-E (lnx-lnF))^2) + GH^x/(1+GH^x)$

Proportion of by-caught dolphins in the sample can be calculated and use as constraints to fit the whole model.



<u>Mortality model:</u> Heligman-Pollard mortality model (black line) fitted to the proportion of dolphins which die in each age (points) Mortalities related with the juveniles, senescences (dash line) and by-catch dolphins (doted line). <u>Inside the box:</u> Proportion of stranded dolphins with signs of by-catch by age range.

The three components Heligman-Pollard model allows to disentangle the by-catch mortality from the total mortality, and therefore, also the natural mortality. Know all kinds of mortalities to which a population is subject is critical to assess a species properly. This information allows to build population models and explore different scenarios and management plans.



Heligman-Pollard fitted to the proportion of dolphins which die in each age (points). After removing the two first ages from the analysis, a Bayesian framework was used to fit the model and calculate confidence interval. Using as constrains the proportion of by-caught animals to fit the second component. Natural mortality disentangle from the Heligman-Pollard model (doted line), by removing the second component from the total model. Differences between models are interpreted as the by-catch mortality of the population.





TESTING AND INTERPRETING THE RESULTS OF THE MODEL Leslie matrix are a simple way to explore population trends and test our results. We applied our mortalities estimates to an initial theoretical population and projected it throughout the years. In the figure, the population grows at a normal rate if only natural mortality is applied. But it will decrease fast with the actual total mortality (including bycatch). Total mortality showed here was calculated just for a fraction of the species distribution and therefore not applicable to the whole population. However, these mortalities can be included in complex population models exploring different management scenarios with the aim of the conservation of this species.



Abundance trends of a theoretical population without by-catch mortality (blue line) and including both kinds of mortalities (red line). The population here shown is highly threatened by by-catch, but for management purposes, this information should be included in a complex model for the whole distribution area since these levels of by-catch only reflect a portion of its distribution range.







