Central Adriatic Sea (Sala et al. 2007). Due to the high cost of such trials we chose to use sea trials carried out at two different bottom depths at which two different towing speeds were tested (named WL450 and WL200 the first and the second cruise respectively). Then we applied the computer-based simulation program to make a preliminary comparison with experimental results collected. In order to set up the model it is first necessary to characterize the net resistance and the horizontal net opening for this particular gear (see PREMECS-II 2006; Sala et al. 2007). As a starting point we have compared the horizontal door spread and the total gear drag with experimental data (see Figure 1). Preliminary results of the model suggest a correlation with general behaviour of experimental data. The model results reacted in a similar way when the warp lenght/depth or towing speed was changed. We found the average relative difference to be less than 11% between model results and experimental data. The

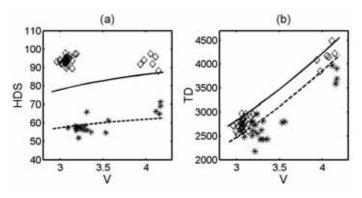


Figure 1: Horizontal door spread HDS (m) and total drag TD (kg) as a function of towing speed V (kn). Solid line/dashed line from results of the model and diamonds/stars from experimental data (WL450/WL200 resp.).

principal sources of discrepancies in our opinion are the model assumptions and the use of a different trawl door.

In summary, we have shown the potential of the model to analyze a bottom trawl fishing gear. A relevant feature of the model is that it skips a detailed simulation of the net and hence provide approximate results at negligible computational cost. The model results obtained are considered satisfactory, and we think that at present computer simulation methods for fishing dynamics can estimate fishing net shape configurations and loads in as much detail as flume tank tests. We are aware, however, that further comparison with data is necessary before reaching definitive conclusions.

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INSTRUMENTATION VIEWPOINT

# LINKING SHAPE, TAXONOMY AND FUNCTION IN TELEOST FISH: A MACHINE LEARNING APPROACH

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## 1. Introduction

Teleosts, with an estimated 23,600 extant species [1], are the most diverse group of vertebrates. Teleosts have a great taxonomic diversity which is accompanied by a wide variety of morphological patterns and adaptations to different freshwater, brackish, and marine habitats all over the world [2]. The form constrains the use of resources through performance of important tasks and resource availability helps in constructing the form. This occurs via the evolution by determining which tasks are the most important for the increase of the fitness [3]. A method to predict the habitat use based solely on the fish morphology may be based on the ecomorphological approach [4]. To overcome sparse or absent habitat use information in determining suitable habitat criteria, especially for rare fishes or communities, a statistical approach can be used to obtain a generalized model that share similar morphological, physiological and behavioural constraints. The aim of this study is to find a model to predict ecology and phylogeny of Teleosts only from their external body shape. Finally, a sensitivity analysis of the neural network model was conducted to evaluate the relative importance of each predictive variable.

#### 2. Results and Discussion

The morphological traits of 1203 selected species were analysed

with two types of statistical comparative and quantitative analysis: the geometric morphometry and the artificial neural networks (ANN) (Multilayer Perceptron). The ANN training was performed using the most common training algorithm, i.e. the error back-propagation algorithm. The best architecture of the ANN was empirically defined after a set of test runs in which different numbers of hidden layers nodes were used. The final ANNs, had 38+n input nodes (19 x y landmarks coordinates + n grouping variables), 20 nodes in the hidden layer and n output nodes (n grouping variables) [5]. For each species a total number of 19 landmarks were identified (Fig. 1) as reported by Costa and Cataudella (2006). Landmarks are defined as homologous points which bear information on the geometry of biological forms [6]. Points were digitized using the software TPSdig [7] applied to the left side of each specimen.

Results on the relationship between body shape and phylogeny show their co-variation according to morpho-functional aspects described by Webb [8]. ANN sensitivity analysis on the taxonomical order suggests that this variable is especially influenced by the relative position of three morphological characters: the pectoral, the dorsal and the anal fins (Fig.2).



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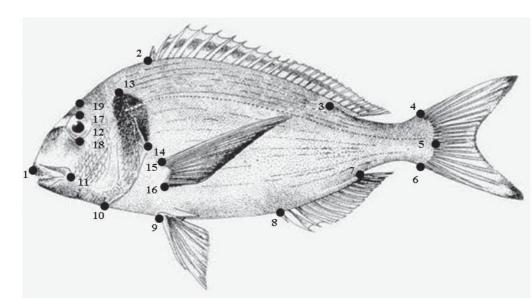


Figure 1: Landmark's pattern.

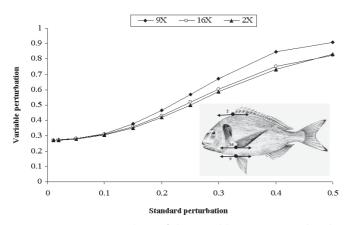


Figure 2: Sensitivity analysis of the variable "Taxonomical Order" with the three most perturbed landmarks (Sparus aurata in the example).

Body shape differences between groups were visualized and described through the deformation grids (splines). Figure 3 shows the splines of the extreme values of CAN1 of Canonical Variates Analysis (CVA) of the Ecology variable The spline of the negative side of CAN1 axis (left side of Fig.3) corresponds to a pelagic fish: this shape has a narrower and longer body, a larger mouth gap and a longer and narrower caudal peduncle. The spline of the positive side of CAN1 (right side of Fig.3) corresponds to a reef-associated fish with a shorter body, a narrower mouth gap and a shorter caudal peduncle.

#### 3. Conclusions

This study suggests: 1) the use of new tools to understand phylogenetic relationships of Teleosts based on a morpho-functional approach. 2) at a larger scale a non phylogenetically based relationships between shape and ecology in Teleosts. Among the potential applications of this study the most promising is probably the automatic recognition of fish shapes in filed conditions, e.g. for monitoring fish assemblage composition.

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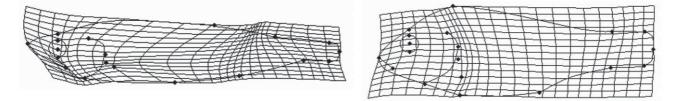


Figure 3: Splines of the extreme values of CAN1 of the CVA on the Ecology variable. On the left side: spline relative to the negative part of CAN1. On the right side: spline relative to the positive part of CAN1.

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