THE ASSESSMENT OF ECOLOGICAL STATUS OF MEDITERRANEAN RIVERS BASED ON FISH COMMUNITIES USING A RECENTLY DEVELOPED PREDICTIVE METHOD

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INTRODUCTION

The use of predictive models is a widespread and powerful tool to asses the ecological status of river systems. This method provide ideal expected conditions (E) to be compared with those really observed (O). The deviation O/E represents a measure of the true ecological status of a particular site. This approach has been previously applied in several widely accepted formulations, such as the Index of Biotic Integrity or RIVPACS. Here, we present some preliminary results obtained from the adaptation of the recently developed ANNA (Assesment by Near Neighbour Analysis) predictive method (Linke, et al; 2005) to estimate the fish community in Mediterranean rivers. We predict the optimal community from a particular site directly from the community composition found in the environmentally nearest sites. So whatever intermediate artificial classification is avoided.

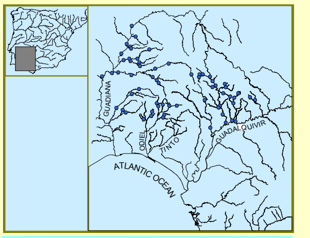

Fig. 1. Map of the study area. Sampled locations are in blue.

STUDY AREA AND DATA COLLECTION

The study was carried out in 3 south-western Iberian Peninsula basins (Guadiana, Guadalquivir and Odiel basins) with typical mediterranean regimen. Fish community was sampled by electrofishing. The sixty three studied sites were inhabited by 19 fish species. From them only the 6 most widespread native species were finally included in the analysis.

At the same time a total of 12 environmental variables, both at reach and basin scale, were measured from each sampled site. All of them were more or less free from human influence: stream order, basin surface, evapotranspiration, rainfall, air temperature, slope, source and mouth distance and relative position along the watercourse. With these data we developed the models to predict the expected communities not affected by anthropogenic influences.

THE MODEL

63 sites

Reference sites
(<5% abundance of exotic species)

"Perturbed" sites
(>5% abundance of exotic species)

1 Model construction (30 sites)

Matrix of presence-absence of species

was run trough a

Correspondence Analysis (CA)

Obtaining a

Ordination of sites in a three-dimensional space defined by the first three axes

were provided with meaning through

Pearson Correlation* + *Multiple regression

in order to

Choice of environmental variables as predictors

Table 1. Multiple regression models for each of the axes obtained in the Correspondence Analysis.

Axes	Multiple regression model	R^2	p
1	-0.37*ALTITUDE + 0.43*PRECIPITATION - 0.35*SLOPE - 1.277	0.42	<0.001
2	-0.47*TEMPERATURE - 0.37*DISTANCE TO SOURCE + 2.988	0.29	0.004
3	-0.5*DISTANCE TO SOURCE + 0.168	0.23	0.004

MODEL OPTIMISATION

To improve the predictive power of the model, two steps were followed

a) Evaluation of optimal *cut-off point to establish the presence-absence of species*

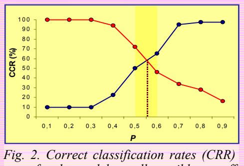

Fig. 2. Correct classification rates (CRR) for the model at all possible cut-off points at 0.1 intervals. The blue line represents presences and red absences.

b) Evaluation of optimal *number of neighbour localities to use as predictor*

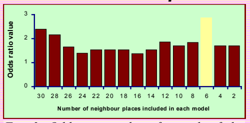

Fig. 3. Odds ratio values for each of the models obtained increasing the number of neighbour localities to predict de presence of species.

2 Model validation (15 sites)

Environmental variables

Through regression equations obtained above for each axes

Localization of a point in the three-dimensional space defined in the fish CA

Assessment of Euclidean distance to the 6 nearest points

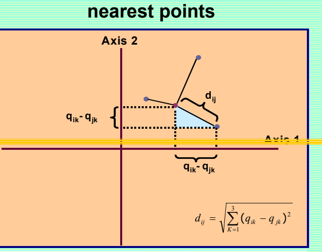

Fig. 4. Assessment of modified Euclidean distance from a reference point and the nearest neighbour ones. Total distance in the three-dimensional space is obtained combining the weights on the three axes by the formula showed in the down-right corner.

is transformed in probability of occurrence through

$$p = \frac{\sum_{i=1}^{n} X_i \frac{1}{\sqrt{d_{ij}}}}{\sum_{i=1}^{n} \frac{1}{\sqrt{d_{ij}}}}$$

Formula.1. Assessment of probability of presence for each specie in each point. $X_i=1$ if the specie is present at the neighbour locality and $X_i=0$ if it is absent.

Applying the optimal cut-off point obtained

Expected taxonomic composition derived from the nearest localities

Calculation of total 0/E for each species and plot all of them

If slope is not different from 1 and intercept not from 0

Model validated

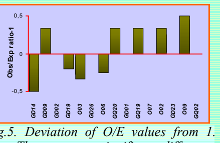

Fig.5. Deviation of O/E values from 1. There was no significant difference from 0 (t-student= 0.62, p>0.05). It is an additional prove of validation

3 Model application (18 sites)

Calculation of 0/E from observed and expected communities at perturbed sites

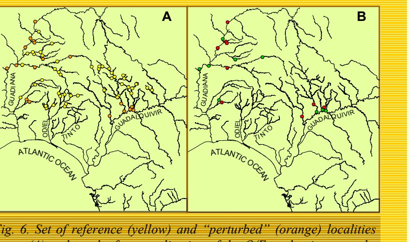

Fig. 6. Set of reference (yellow) and "perturbed" (orange) localities (A) and results from application of the O/E evaluation over the perturbed sites (B). Points in red show real perturbed places, while green point out not perturbed ones. The Q_{10} of E/O values from reference sites was taken as perturbation threshold.

The model was valid (slope of O/E plot not different from 1 and intercept not from 0). It showed that some localities initially considered as perturbed were not seriously affected by exotic degradation, since their species richness were not different from the expected (O/E values not different from 1).

The model optimisation showed the ideal cut-off point to consider the presences or absences of species and the optimal number of neighbour localities to include in the prediction to improve its efficiency.

A wide range of habitat types were accounted in the model construction, but the high abundance of exotic species, specially in downstream reaches, made difficult to obtain enough data from there. Additional studies are needed to solve this problem.

Only a few localities were badly perturbed (8/63). They appeared specially in middle-downstream reaches, where the more perturbed habitats allowed exotic species to establish permanent populations.

REFERENCE: Linke, S., Norris, R. H., Faith, D. P. & Stockwell D. (2005). *ANNA: A new prediction method for bioassessment programs*. FreshwaterBiology, 50: 147-158.