Non-parametric methods – Tree and P-CFA – for the ecological evaluation and assessment of suitable aquatic habitats: A contribution to fish psychology

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Abstract

This study analyses multidimensional spawning habitat suitability of the fish species "Nase" (latin: *Chondrostoma nasus*). This is the first time non-parametric methods were used to better understand biotic habitat use in theory and practice. In particular, we tested (1) the Decision Tree technique, Chi-squared Automatic Interaction Detectors (CHAID), to identify specific habitat types and (2) Prediction-Configural Frequency Analysis (P-CFA) to test for statistical significance. The combination of both non-parametric methods, CHAID and P-CFA, enabled the identification, prediction and interpretation of most typical significant spawning habitats, and we were also able to determine non-typical habitat types, e.g., *types* in contrast to *antitypes*. The gradual combination of these two methods underlined three significant habitat types: shaded habitat, fine and coarse substrate habitat depending on high flow velocity. The study affirmed the importance for fish species of shading and riparian vegetation along river banks. In addition, this method provides a weighting of interactions between specific habitat characteristics. The results demonstrate that efficient river restoration requires re-establishing riparian vegetation as well as the open river continuum and hydro-morphological improvements to habitats.

Key words: River, fish, habitat, spawning, non-parametric analyses, Decision Tree technique (CHAID), Prediction-Configural Frequency Analysis (P-CFA)

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Introduction

This paper discusses Chi-squared Automatic Interaction Detectors (CHAID) Decision Tree technique and Prediction-Configural Frequency Analysis (P-CFA) as statistical methods for the search for typical and atypical habitat in applied limnology.

Natural rivers support a variety of needs, including fish and wildlife habitats, outdoor recreation, hydropower generation and flood protection. Existing water demands and projected increase in these demands have sometimes resulted in a conflict between the use of rivers as a source of water and energy, and their restoration and conservation as integrated ecosystems as well (Feld et al., 2011; Schinegger, Melcher, Trautwein & Schmutz, 2011).

Hydro-morphological modifications often underlie hydrological impacts in central and western European water bodies. Consequently to assess anthropogenic alterations on riverine systems, most attention is focused on morphological habitat attributes. It was recognized that functional processes in riverine environments depend on the interactions of many attributes like flow velocity or riparian vegetation (Melcher & Schmutz, 2010). Consequently a more sophisticated analytical toolset is required to quantify the biological consequences of impacted multi-metric environments and to assess fish habitat improvements in river restoration activities.

The fish species "Nase" (latin: *Chondrostoma nasus*) is one of the dominant cyprinid species in the barbel-zone of European rivers (Rakowitz, Berger, Kubecka, & Keckeis 2008). Knowledge of their spawning habitat requirements in rivers does much to explain their population biology. Moreover, knowledge of their habitat would be valuable when planning management schemes to mitigate and restore the effects of habitat impacts from river channelization, continuum disruption and impoundments. This paper analyses multidimensional spawning habitat-types of nase using as a case study the tributary of the Danube where the nase makes a spawning migration: the Pielach River in Lower Austria (Melcher & Schmutz, 2010).

Numerous habitat modeling studies have been undertaken over time in North America and Europe, mainly for salmonids, (e.g., Northcote, 1984; Shirvell, 1989; Wollebaek, Thue, & Heggenes, 2008; Moir & Pasternack, 2009, Melcher & Schmutz, 2010) using predominantly univariate habitat use and preference curves (i.e., functions). For a better identification and understanding of specific habitat requirements, multidimensional analyses (e.g., CHAID Tree) using environmental descriptors such as water flow velocity, water depth, substrate and cover are necessary.

Until now parametric methods such as classical variance, regression or discriminant (function) analyses (Ahmadi-Nedushan et al., 2006) have been the main statistical methods used for habitat modeling. Due to their specific statistical presumptions and requirements, their use is frequently limited in comparison to non-parametric methods. Non-parametric methods (e.g. CFA) are often used very successfully in different applied scientific disciplines such as sociology or psychology to identify "most typical" and "most atypical" behaviour; *types* in contrast to *antitypes* (von Eye, Spiel, & Wood, 1996; Netter, 1996).

CFA was originally proposed by Lienert (1969), and was further developed by his collaborators (e.g., P-CFA; cf. von Eye, 1990; Lautsch & von Eye, 2003; von Eye, 2010). On this foundation our aim was to develop, optimize and establish these techniques to develop a practicable but accurate "habitat-type" assessment tool for water managers and stakeholders as well as to understand and evaluate the complexity of ecological interactions and as a consequence contribute to the improvement of the ecological status of rivers. Subsequently the aim of the study is to identify and analyse multidimensional habitat requirements testing the following methodological hypotheses: (1) the CHAID technique is an easy-to-handle tool for identification of specific habitat-type; and (2) the CFA increases the power to categorize selected habitat-types (profiles) as statistically and ecologically significant.

Method

The following habitat modeling method generally comprises four steps. Step 4 is used here in applied limnology for the first time:

Step 1: Selection of habitat parameters (descriptors);

Step 2: Sampling design in the field;

Step 3: Simple exploratory analyses – univariate frequency distribution;

Step 4: Multifactorial analyses:
      (4.1) CHAID – habitat types exploration;
      (4.2) P-CFA – habitat types confirmation.

Steps 1 and 2: During spring we conducted daily surveys of fish species' presence, number of individuals and habitat size. Habitat features, i.e., flow velocity, water depth, shading, cover, flow protection, type of structure, substrate and embeddedness were recorded at ten spawning grounds used by 1250 nase fish within one spawning season (Melcher & Schmutz, 2010).

Spawning took place in April at an average water temperature of 8.5° C, and the nase spawned in shoals on shallow gravel bars that are easy to identify from the river bank. A grid of equally-spaced points was laid over the spawning area (grid size 1 m², see Figure 1). Due to the very clear water and shallow habitats, it was possible to count spawning individuals by visual observations as described by Melcher and Schmutz (2010).

Additionally, we sampled representative sites with different morphological characteristics within the 35-km long study area to describe the entire available habitat in the Pielach River. We made point measurements interspersed at 2m intervals along 71 transects, resulting in 582 measurements. The principle of this point measurement method is graphically explained in Figure 1.
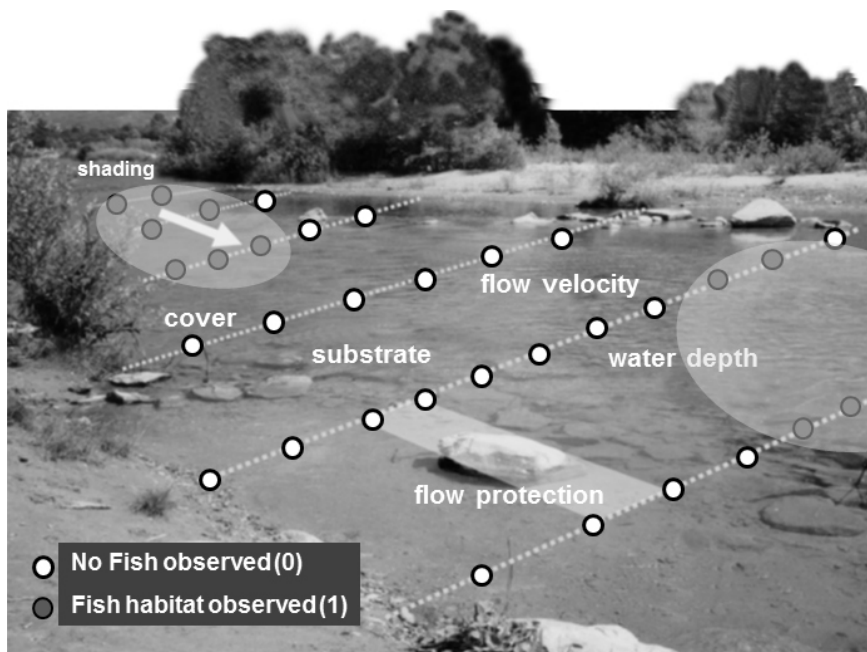
Figure 1:
Description of the sampling design (transects), whereas grey dots describe the habitat fish uses and white dots describe the available habitat (modified from Schneider, Noack & Gebler 2008)

For our analyses we measured and used the following 10 habitat variables: water depth, mean and bottom flow velocity, shading, cover, flow protection, broken water surface, overhanging riparian vegetation, embeddedness of the substrate and dominant substrate (see Table 1). The later one was well-defined by six categories (pelal - psammal < 2, akal 2-20, microlithal 20-63, mesolithal 63-200, macrolithal 200-400, megalithal > 400 mm).

Step 3: Exploratory analyses – the univariate frequency distribution (use curves) for this case study was described by Melcher and Schmutz in 2010. Available habitat, suitability and preference curves were developed for each habitat variable using frequency-of-use graphs (Raleigh, Zuckerman & Nelson, 1986) as Normalized Probability Density Functions ranging from 0 to 1.

Step 4 includes multivariate analyses using (1) CHAID and (2) P-CFA. All statistical analyses were made with IBM SPSS. For our specific habitat selection process we tried to find a method that identified the most important, yet straightforward, descriptive variables to interpret fish habitat types and consequently their habitat preferences. It was also necessary to identify the class threshold at an optimum for significant linear variables. Tree analysis allows identification of homogeneous groups and makes it easy to define

Table 1:
Description of potential environmental parameters

Variables	Unit	Characteristic
Dependend variable		
Occurrence of nase fish spawning habitat	yes, no	binary (0, 1)
Independent variables		
Velocity mean (v - mean)	cm/s	linear
Velocity bottom	cm/s	linear
Water depth	cm	linear
Subatrate	6 categories	ordinal
Presence of embeddedness	yes, no	binary (0, 1)
Cover	yes, no	binary (0, 1)
Flow protection	yes, no	binary (0, 1)
Shading	yes, no	binary (0, 1)
Overhanging riparian vegetation	yes, no	binary (0, 1)
Broken water surface	yes, no	binary (0, 1)

rules for making predictions about habitat selection. It classifies cases into groups or predicts values of a dependent variable (i.e., fish habitat occurrence) based on values of independent environmental variables. The procedure provides validation tools for exploratory and confirmatory classification analysis (SPSS Inc., 2010b).

The analyses were supported using the CHAID method for graphical Decision Trees (Kass, 1980; Hawkins & Kass, 1982; Magidson, 1994). The acronym CHAID means Chi-squared Automatic Interaction Detector and refers to the graphically-oriented non-linear discriminant analysis method to winnow the number of variables down to only the most significant ones. CHAID performs a stepwise bivariate analysis for each situation with many chi-square tests. As the dependent variable, fish habitat occurrence is defined as nominal (0, 1); all calculations are based on the crosstab analysis.

Goodness-of-fit statistics of the selected models are explained in classification tables. The main result shows a graph Tree with different number of branches in a hierarchical order. Each branch is defined by a node and its identification number (Node ID). In the first step all independent variables were cross-classified with the dependant variable and tested for their significance. In the following steps all other independent variables were classified if they were significant. With the help of the CHAID method it is possible to show interactions between independent variables to identify specific fish habitats. Finally, it was necessary to test the statistical significance of these "significant" habitats while considering interactions between the described parameters. One approach to this is the P-CFA as described by G.A. Lienert and published later by Lautsch and von Eye (2003) and von Eye in 2010. In principle a two dimensional cross-table ($i = 2$; $j = 8$) is used with the following two dimensions: Node ID and fish habitat occurrence (see Figure 2 and Table 3). The assumption of total independence of both dimensions is tested for all

2 by 8 cells of the cross-table. The normally-distributed test statistic is calculated based on adjusted (standardized) residuals (z_{ij}):

$$zij = \frac{(o_{ij} - e_{ij})}{\sqrt{e_{ij}\left(1 - \dfrac{c_j}{N}\right)\left(1 - \dfrac{r_j}{N}\right)}} \tag{1}$$

for o_{ij} = observed frequencies, e_{ij} = excepted frequencies, r_i = i^{th} column subtotal, c_j = j^{th} row subtotal and N = grand total (see: Bishop, Fienberg & Holland, 1975; Haberman, 1978; Goodman, 1979; SPSS Inc., 2010a).

Whereas the level of significance is defined as:

$$z_{a=0.05;\ one\ sided} = 1.65 \tag{2}$$

Finally positive $z_{ij} > 1.65$ cells (configural) are assumed and interpreted as significant habitat types (T) and negative $z_{ij} <= -1.65$ configurals as significant (habitat-) antitypes (AT).

The Bonferroni α-adjustment (Bonferroni, 1935; Shaffer, 1995; Abdi, 2007) is given as:

$$a* = \frac{a}{t} \tag{3}$$

for t = number of cells (i.e., t = 2 x 8 = 16 cells); this means for Table 3: α* = 0.05 / 16 = 0.003125.

The adjusted level of significance is: $z_{a*=0.003125;\ one\ sided} = 2.73$.

Results

Using CHAID it was possible to show evidence of statistical significance for three variables out of nine that were sufficiently accurate to identify one or more different habitat types. The variables are flow velocity, shading and substrate.

As shown in Figure 2, three different fish spawning habitats can be determined in an exploratory fashion by the absolute dominance of nase occurrence , i.e., nodes 9, 10 and 11. Overall 94.4 % of the model can be explained (see Table 2).

Looking at the results in detail, we note that the independent variable of mean flow velocity (v-mean) had the highest explanatory rate, e.g. level one. Additionally the optimal classified thresholds are given in four velocity classes (in cm/s): [<=39], [39-69], [69-82], [>82]. The classes are coded by the nodes 1, 2, 3, 4. Following the hierarchical Tree analyses all nodes end in a new branch except for node 1, the flow velocity class between equal and less than 39 cm/s. The nodes at level two were built using the variables
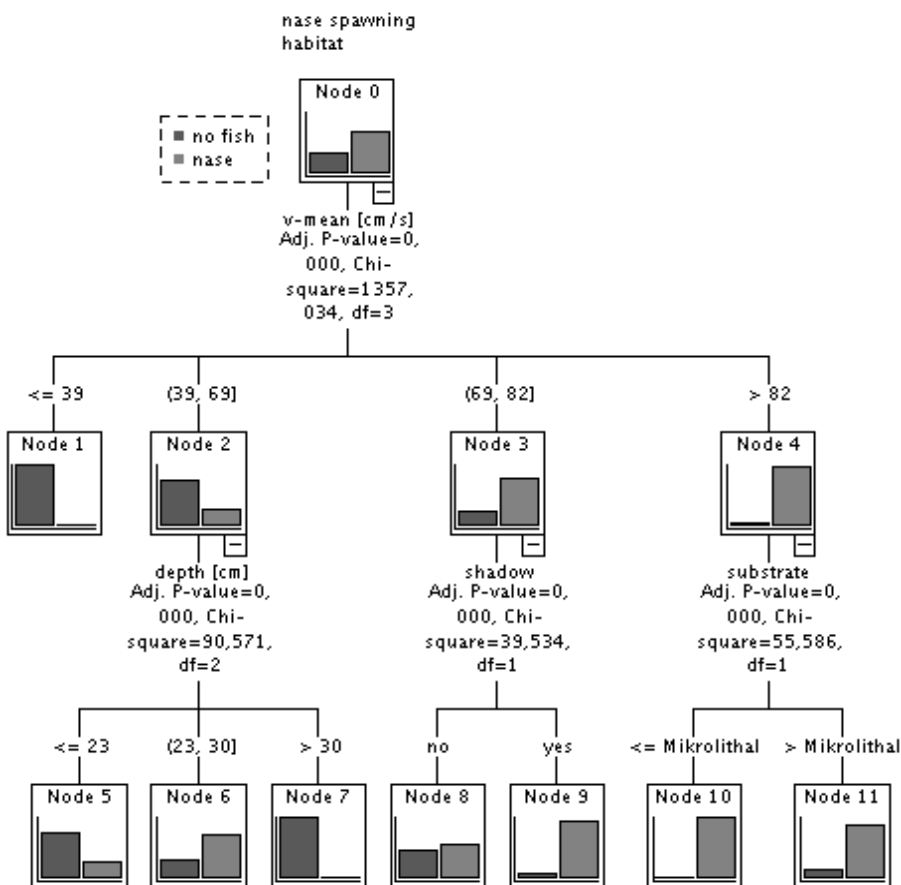
Figure 2:
CHAID Tree for nase spawning habitat type identification (green: fish habitat used "nase",
blue or left bars: available habitat "no fish")

Table 2:
Classification table for the exhaustive CHAID Tree model (dependent variable nase spawning
habitat)

Observed	Predicted		
	0 no fish habitat	1 nase	Percent correct
0 no fish habitat	489	93	84.0 %
1 nase	10	1240	99.2 %
Overall percentage	27.2 %	72.8 %	94.4 %

water depth, shading and substrate (i.e., micro- versus mesolithal). A total of four variables were used to explain a nase spawning habitat. The original variables used are reduced by more than 50 %.

Following the Tree from node 0 down to node 11 it is possible to determine nodes with a high proportion of fish nase occurrence (see green bars on the left side of Figure 2), but also nodes with a low density of nases. Obviously eight different routes/paths or so called profiles could be visually distinguished:

Profile 1 [node 0 - node 3 - node 8]: v-mean [69-82] and shadow [no];

Profile 2 [node 0 - node 3 - node 9]: v-mean [69-82] and shadow [yes];

Profile 3 [node 0 - node 4 - node 10]: v-mean [>83] and substrate [<=microlithal];

Profile 4 [node 0 - node 4 - node 11]: v-mean [>83] and substrate [>microlithal];

Profile 5 [node 0 - node 1]: v-mean [<39];

Profile 6 [node 0 - node 2 - node 5]: v-mean [39-69] and water depth [<=23];

Profile 7 [node 0 - node 2 - node 6]: v-mean [39-69] and water depth [23-30];

Profile 8 [node 0 - node 2 - node 7]: v-mean [39-69] and water depth [>30].

Each of these profiles describes a specific fish habitat that is either "typical", i.e., high abundance of the fish species, or "not-so-typical" (Profiles 5 to 8), i.e., a lower occurrence of the target species.

For the final assessment of significant fish habitat types we used the P-CFA. To run the P-CFA it was necessary to define a cross-table by using the profiles described above (see Table 3).

The most important step in our method is the application of P-CFA to determine all significant "types" and "antitypes" (see Table 3). Positive $z_{ij} > 1.65$ cells (configural) are interpreted as „typical" and negative $z_{ij} <= -1.65$ as "atypical". Finally the three profiles 2, 3, and 4 with their final nodes 9, 10, and 11 could be identified as significant fish habitat types. In contrast, profiles with their final nodes 1, 5, 7, and 8 are significant antitypes. The Bonferroni adjustment garantees the original significance level and corrects for the alpha inflation. The only profile that looses its significance through the Bonferroni adjustment is Profile 1.

Discussion

In this paper we test the applicability of the CHAID Tree technique and P-CFA, two non-parametric methods, in applied limnology, particularly for the evaluation and assessment of suitable aquatic habitats. The rheophilic cyprinid fish species nase, which we use here as a target species, was once one of the dominant key species in several mid-sized and larger European rivers (Schiemer & Waidbacher, 1992). Due to its life-history

Table 3:
Cross-tabulation (2 columns by 8 rows = 16 cells) after P-CFA and their adjusted residuals (z) to determine types (T) and antitypes (AT) fish spawning habitat profiles. T° and AT° are not significant after Bonferroni Adjustment.

Profile	Node ID		0 no fish habitat		1 nase spawning habitat		Total
1	0 - 3 - 8	n	33		39		72
		z	2.6	T°	-2.6	AT°	
2	0 - 3 - 9	n	7		103		110
		z	-5.9	AT	5.9	T	
3	0 - 4 - 10	n	17		928		945
		z	-28.4	AT	28.4	T	
4	0 - 4 - 11	n	21		133		154
		z	-5.0	AT	5.0	T	
5	0 - 1	n	366		0		366
		z	31.3	T	-31.3	AT	
6	0 - 2 - 5	n	26		10		36
		z	5.3	T	-5.3	AT	
7	0 - 2 - 6	n	15		37		52
		z	-0.5	n.s.	0.5	n.s.	
8	0 - 2 - 7	n	97		0		97
		z	14.8	T	-14.8	AT	
Total		n	582		1250		1832

pattern and habitat requirements the nase is an ideal indicator to assess the ecological quality and integrity of riverine systems (Keckeis, Frankiewicz & Schiemer, 1996; Hauer, Unfer, Schmutz & Habersack, 2007). Recent European wide studies showed that nase are very rare nowadays (Melcher, Schmutz, Haidvogl & Moder, 2007). The main reason for that is loss of habitat because of increasing hydro-morphological pressures, mainly channelization, flood protection and construction of migration barriers like hydro power plants (Souchon et al., 2008). Therefore, this mandate to restore rivers requires that we find appropriate and easy-to-understand methods for helping our running waters to become healthy again.

By combining the two methods of CHAID and P-CFA it was possible to show interactions between independent environmental parameters that help to identify and evaluate specific habitat preferences. Information on habitat-types that fish do not prefer and avoid is very important and useful for river restoration. In practice this facilitates discussions with water managers, on the one hand, as to the specifics of what river restoration requires. On the other hand this information permits us to explain what measurements are wrong from the fish's perspective. In our example, this means that all river reaches having a water flow velocity below 70 cm/s are not suitable at all, but higher velocities, course substrate and shading would be the optimum requirements for a successful spawning of the endangered fish species nase.

The results of this study also show, that this approach is, in general, statistically feasible for applied limnology. In contrast to other modelling techniques, like Logistic Regression (see Melcher, 1999; Melcher 2009), it was possible for the first time to distinguish between different significant habitat-types and habitat-antitypes.

The stepwise Logistic Regression used in Melcher (1999), resulted in selection of five variables, instead of four, as determined by our methods in this paper, e.g., CHAID. With an explained variance of 96%, the Logistic Regression was able to predict fish habitat at a rate 1.6% greater than the Tree method. Based on the stepwise procedure of logistic regression, we obtained a hierarchical ranking of the significant variables: 1 depth, 2 velocity, 3 shading, 4 substrate and 5 cover. This information provided by Logistic Regression appears to explain more but is difficult to use for management decision because it is harder to interpret their interactional effects (saturated model). The Tree method provides a meaningful and visually-intuitive description of the differences between specific habitats using profiles. The result is an economical and easily interpretable interaction model. This is a fundamental advantage of the CHAID technique compared to Logistic Regression.

For our methodological Step 4.1 (CHAID) IBM SPSS provides the option to run a cross-validation automatically. The Tree results were cross validated by splitting the entire data set into a training and test data set. With this additional method we are able to compare our results described above (see Figure 3) and estimate how accurately our predictive model would perform in practice. This means partitioning our total sample into 50% to 50 % complementary subsets, performing the Tree technique on one subset (training data), and validating the analysis on the other subset (test data) for their "statistical significance." In general cross-validation is important in guarding against testing hypotheses suggested by the data, especially where further samples are costly or difficult to collect. Such sampling challenges can be especially acute in applied limnology, where the sampling performance and success depends a lot on daily fish behaviour, water temperature, water level and the weather in general, to mention some of the environmental parameters.

Again we find three significant habitat-types, mainly described by a mean velocity higher than approximately 72 cm/s and the importance of the occurrence of shading. One type (node 0-4-9) shows less relevance of shading; as was shown by our original model. One reason for that could be a specific interaction between the environmental parameters shading and substrate. The overall classification (probability assignment) of the model was with 94.7 % and 94.0 % nearly the same for both subsamples (i.e., training and test) (see Table 4).

The CHAID Tree results describe specific fish habitat on micro- and meso scale, similar to other studies (Ovidio & Phillipart, 2008; Melcher & Schmutz, 2010). By combining the CHAID results with the P-CFA, the importance of flow velocity and shading was clearly demonstrated by defining significant typical habitat-types but also significant habitat-antitypes. To the authors' opinion the habitat assessment method explained in this paper is not only applicable to other fish species and their life stages but also to other biological quality elements (e.g., benthic invertebrates, makrophytes, amphibians, birds
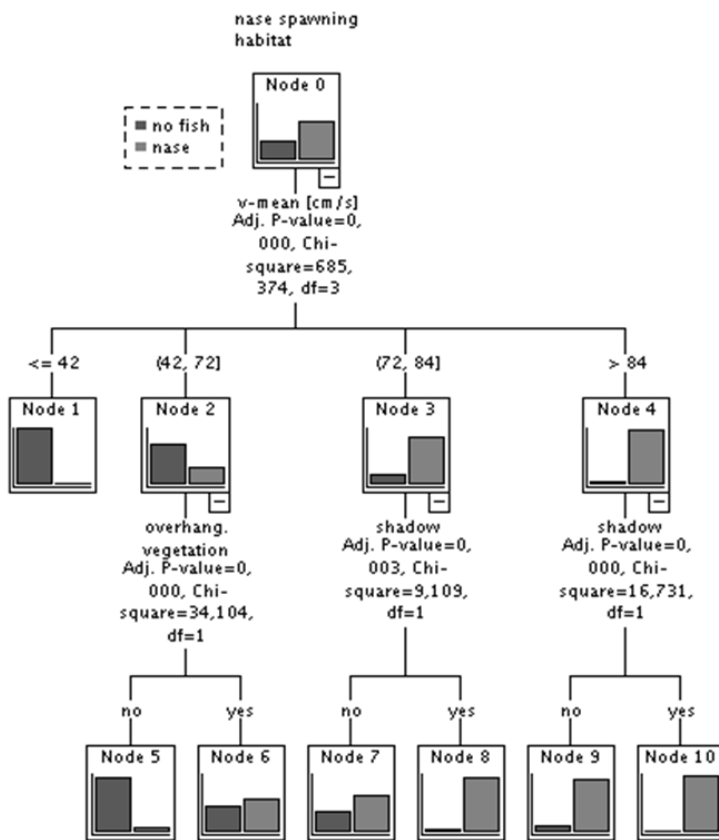
Figure 3:
Results of the Cross-validation: CHAID Tree for nase spawning habitat types (test sample)
identification (green: occurrence of fish habitat "nase", blue or left bars: available habitat "no
fish")

Table 4:
Cross-validation classification table for the exhaustive CHAID Tree model (dependent
variable nase spawning habitat) for training and test dataset

Sample	Observed	Predicted		
		0 no fish habitat	1 nase	Percent correct
Training	0 no fish habitat	231	45	83.7 %
	1 nase	4	636	99.2 %
	Overall percentage	25.7 %	74.3 %	94.7 %
Test	0 no fish habitat	254	52	83.0 %
	1 nase	3	607	99.5 %
	Overall percentage	28.1 %	71.9 %	94.0 %

etc.) and ecosystems. As most European rivers are affected by a long list of pressures (Schinegger, Melcher, Trautwein & Schmutz, 2011) river restoration strategies have to consider integrated approaches that cover both traditional technical methods and essential habitat improvement based on biological knowledge. The combined Tree and P-CFA technique will be very helpful to assist future decision-making processes for water managers and stake holders when restoring habitats in waters.

Acknowledgements

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