

## Data composition and taxonomic resolution in macroinvertebrate stream typology

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### Abstract

In the EU water framework directive (WFD) a typological framework is defined for assessing the ecological quality of water bodies in the future. The aim of this study was to test the effect of data composition and taxonomic resolution on this typology. The EU research projects AQEM and STAR provided 1660 samples of 48 stream types sampled all over the major geographical gradients in Europe. These stream types fit the WFD typological demands and fit to the major European geographic regions (ecoregions). The samples included gradients from reference conditions to samples with bad ecological quality. Despite standardisation, there were large differences between the participating countries concerning the number of taxa, the number of specimens, and the taxonomic resolution. The macroinvertebrate data were analysed by using detrended correspondence analysis (DCA). The distribution patterns using all samples, only reference samples, and only degraded samples showed that the use of species-level (or 'best available taxonomic' level) performed better at a practical (fine) scale in comparison to family-level. The analyses further showed that even the use of a standardised protocol can not easily overcome (i) differences in site conditions that force the researcher to deviate from the protocol as well as (ii) the experiences of the researcher(s) and (iii) the available taxonomic knowledge.

### Introduction

Can European stream types be based on orders or families while local stream types must be based on species-level identifications? Moog et al. (2004) concluded that a finer spatial resolution required a finer taxonomic resolution which is in concordance with the hierarchical approach described by Friswell et al. (1986). The strength and amount of detailed information that can be extracted from species-level data was already shown by several authors (e.g., Resh & Unzicker, 1975; Moog et al., 1997; Lenat & Resh, 2001). In stream or river assessment different taxonomic resolutions were used on different scales (e.g., Resh & McElravy, 1993; Verdonschot, 2000).

The European Commission recognised that the ecological status of water bodies should be determined compared to near-natural or reference conditions (European Commission, 2000). The water framework directive (WFD) approach of using reference conditions in assessment is in agreement with assessment approaches adopted in the USA (e.g., USEPA, 1996) and Australia (Davies, 2000). Communities are optimally developed under reference conditions (e.g., Karr & Chu, 1999). It is commonly accepted that human disturbance affects a stream ecosystem in such a way that communities become poor and look more alike (e.g., Wright et al., 1984; Verdonschot, 1990). Yet, would a stream typology become most explicit using only reference sites and species-level

identifications? In this study the amount of data of reference sites provided the opportunity to do analyses with such sites solely, and the question of taxonomic resolution could therefore be tackled.

Furthermore, the data composition was analysed to explore the variation to be expected in future assessment. The objectives of this study were:

- To explore the effects of variation in data composition on analyses results;
- To explore whether the stream typology depends on taxonomic resolution, whereby species-level (or ‘best available taxonomic level’) is compared to family-level at different scales;
- To explore whether the stream typology should be based on reference sites only or also on degraded sites.

## Methods

### *Data collection*

In the EU research project AQEM, in total 889 macroinvertebrate samples representing 29 stream types were taken in eight countries in 2000 and 2001. In the EU research project STAR, an additional 771 samples were taken in 13 countries in 2002 and 2003. The combined AQEM-STAR database composed 1660 samples representing 16 countries and 48 stream types (Table 1). All samples together cover the major geographical gradients in Europe. The AQEM site selection, sampling, sorting, and identification procedure was explained by Hering et al. (2004). The STAR samples were either processed according to a slightly adapted AQEM protocol (Furse et al., 2004) or according to several national sampling protocols: RIVPACS (Germany, Austria, Greece, and United Kingdom), IBE (Italy), IBGN (France), DSFI (Denmark), LVS 240 (Latvia), PERLA (Czech Republic), and the national protocols of Poland, Sweden, and Portugal.

Handnets were used in all methods. All samples were taken within a stream stretch of <500 m of the respective stream site. All samples were collected in at least two seasons, of which one was spring. The second sample was collected in summer or autumn, depending on the regional, geographical and climatological conditions. At the

STAR related sites replicate samples were taken. All samples were further processed in the same standardised way. Finally, different samples from the same site, either being replicates or taken using a different method, and samples taken in different seasons from the same site were kept in the analyses and treated as separate samples. Hereby, the variation caused by the different methods and seasons is accepted, because these differences will also be present when applying assessment in practical water management.

Identification took place to species-level when possible. In some areas, identification was limited to higher taxonomic levels due to a lack of taxonomic knowledge. Finally, all samples were combined into one European database.

### *Data composition*

Despite the sampling, sorting, and identification protocols agreed upon within the consortia, differences in sample size, sorted number of specimens, and levels of identification occurred. Therefore, for all data per country the number of samples, the total number of taxa, and the total number of individuals were compared to get an overview of this source of variation.

### *Taxonomic adjustment*

For several reasons taxonomic resolution within and between samples differed. This can be because of damaged specimens, lack of taxonomic knowledge in certain areas of Europe, lack of certain life stages, or lack of certain taxonomic groups in general. Therefore, taxonomic adjustment was needed to assure unambiguous data processing. Differences in taxonomic resolution could otherwise later prove to be the cause of differences between sample groupings in typology. To study the influence of taxonomic resolution on the analyses results, two datasets were extracted. The first dataset is based on the best available taxonomic level possible. To reach the best available taxonomic resolution a weighed taxonomic adjustment was applied according to the criteria described by Vlek et al. (2004). This dataset is indicated as ‘species data’. The second dataset is composed of the family-level as best achievable level, and is indicated as ‘family data’. Therefore, all taxa

Table 1. Stream type code and name

Code	Name
A01	Small to medium-sized streams in the Hungarian Plains
A02	Medium-sized, calcareous streams in the Alps
A03	Small, siliceous streams in the Alps
A04	Medium-sized, siliceous streams in the Bohemian Massif
A05	Small, shallow streams in the Central sub-alpine Mountains
A06	Small, crystalline streams of the ridges of the Central Alps
C04	Small, shallow, siliceous, mountain streams in the Carpathians
C05	Small streams in the Central sub-alpine Mountains
C14	Medium-sized, siliceous streams in the Central sub-alpine Mountains
C15	Small, calcareous streams in the Carpathians
C16	Small to medium-sized, calcareous streams in Carpathians
D01	Small, sand-bottom streams in the German Lowlands
D02	Small, organic type brooks in the German Lowlands
D03	Medium-sized, sand-bottom streams in the German Lowlands
D04	Small streams in the Central and Western Mountains (Germany)
D05	Medium-sized streams in the Central Mountains (Germany)
D06	Small, Buntsandstein streams in the Central Mountains (Germany)
F08	Small, shallow to medium-sized, headwater streams in the Western sub-alpine Mountains (Eastern France)
H01	Small to large, siliceous streams in North-Eastern Greece
H02	Small to large streams in Central and North Greece
H03	Small to large, calcareous streams in Western Greece
H04	Small, calcareous streams in the Hellenic Western Balkans (Greece)
H05	Small, siliceous streams in the Eastern Balkans and Hellenic Western Balkans (Greece)
H06	Small, siliceous streams on the Aegean Islands
H07	Medium-sized, calcareous streams in Hellenic Western Balkans (Southern Greece)
I05	Small streams in the southern calcareous Alps
I06	Small, calcareous streams in the Central Apennines
I22	Small, siliceous, source streams in the Po valley
I23	Small to medium-sized, lower mountain, siliceous streams in the Northern Apennines
I24	Small to medium-sized, lower mountain, siliceous streams in the Apennines (Southern Italy)
K02	Small to medium-sized, siliceous, lowland streams in the Central Lowlands
L02	Medium-sized, siliceous, lowland rivers in the Baltic Province
N13	Small, siliceous, sand-bottom streams in the Dutch Lowlands
N14	Small to medium-sized, organic and siliceous, sand-bottom streams in the Dutch Lowlands
O02	Medium-sized, siliceous, lowland streams in the Central and Eastern Lowlands
P01	Small, lower mountain streams in Southern Portugal
P02	Small to medium-sized, lowland streams in Southern Portugal
P03	Medium-sized, lowland streams in Southern Portugal
P04	Medium-sized, lower mountain streams in Southern Portugal
S01	Small to medium-sized, lowland streams in Northern Sweden
S02	Small to medium-sized, medium-altitude streams in Northern Sweden
S03	Small to medium-sized, medium-altitude streams in the Boreal Highlands
S04	Small, high-altitude streams in the Boreal Highlands
S05	Small and medium-sized, lowland streams in the Swedish Lowlands and Northern Sweden

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Table 1. (Continued)

Code	Name
S06	Small to large, lowland and calcareous streams in the Swedish Lowlands and Northern Sweden
U15	Small to medium-sized, shallow, lowland streams in England
U23	Small to medium-sized, lowland streams in England
V01	Small, mountain streams in the East and West Carpathians

below family-level (e.g., species or genus level) were adjusted to their respective family, and all familial and higher taxonomic units (e.g., suborder or order) were kept as such. Both adjustments were done for the total database.

#### Data analyses

After taxonomic adjustment the macroinvertebrate abundances of each sample were transformed [ $^2\log(x+1)$ ] (Preston, 1962; Verdonschot, 1990).

The multimetric AQEM assessment system (Hering et al., 2004) was used to classify all AQEM samples into an Ecological Quality Class ranging from 5 (high quality) to 1 (bad quality). For all STAR samples only a pre-classification was available assigning the samples to the same quality classes based on the expert knowledge and abiotic field measurements. For data analysis three datasets were compiled: (i) 'all samples'; 1660 samples, (ii) 'reference samples'; 876 samples including only samples with an ecological quality classification good (class 4) and high (class 5), and (iii) 'degraded samples'; 784 samples including only samples with an ecological quality classification moderate (class 3), poor (class 2), and bad (class 1). The inclusion of class 4 (good) in the group of reference samples was done because (i) the quality deviation from the reference is only slight, and (ii) to obtain enough samples for reliable analyses.

Ordination was designed for data analysis in community ecology. Used in an explorative way it shows an ordination diagram that optimally displays how community composition varies (ter Braak & Šmilauer, 2002). In order to analyse the macroinvertebrate species composition in relation to stream type, detrended correspondence analysis (DCA) was used. DCA is an indirect ordination technique and part of the program

CANOCO for Windows, version 4.2 (ter Braak & Šmilauer, 2002). In DCA, the samples are patterned in a multidimensional space based on their taxonomic composition.

The options chosen in CANOCO will influence the result of the DCA ordination. In this study the following options were selected (ter Braak & Šmilauer, 2002):

- detrending by 2nd order polynomials to reduce the 'arch' effect;
- downweighting of rare species which reduces the influence of rare species and stresses the importance of more common ones in the analysis;
- inter-sample distance that optimises the position of the samples in the ordination diagram;
- Hill's scaling to allow for long gradients the sample distances to represent turn over distances.

To establish the percentage of overlap between groups of samples a new approach was used. Using more 'classical' clustering techniques such as hierarchical agglomerative clustering a number of reproducible but more or less subjective choices within the program to be made by the user decide the results of the classification. The technique chosen is based on the interpretation of the DCA ordination diagram by counting the number of samples present in adjacent groups. Therefore, within the resulting ordination diagram, which included the first and second ordination axes, the samples were labelled according to stream type. The overlap between stream types was established by drawing contour lines around the types and summing up all the overlapping samples. The position of the contour line was the result of an iterative process of repositioning the line and counting the overlap until a minimum overlap was reached. Overlapping stream types were grouped into larger groups, if more than 25% of the

samples were positioned within the other type or group, and next the overlap between these new established groups was calculated again by summing up all the remaining overlapping samples. The groups with an overlap < 25% of the samples were identified as an identifiable group. Each group was considered to represent a recognisable typological unit, and a next DCA run was performed for this respective group to identify groups within. This process was repeated until no groups could further be disentangled or the level of stream type as recognisable group was reached. Starting with the whole database, the groups recognised in the first ordination were considered to represent the highest hierarchical units and are considered the major groups in Europe, the further the ‘peeling off’ was done the lower hierarchical position a group represented: groups, sub-groups, and stream types, respectively.

The calculation of the overlap was restricted to axes one and two, as in each run only two to three major groups were separated. DCA plots the major grouping of samples along the first and the second major grouping along the second axis (ter Braak & Šmilauer, 2002). The DCA analyses were repeated for all six datasets; ‘all samples’, ‘reference samples’ and ‘degraded samples’; each as ‘species data’ and ‘family data’.

## Results

### *Data composition*

The number of samples, taxa, and adjusted taxa, and percentage of adjusted taxa differed strongly between countries (Table 2), partly due to the fact that some partners were in both the AQEM and STAR project and some partners were not. Denmark and France had the lowest numbers of samples (34 and 36, respectively) and Germany had the highest number of samples (279) taken. Germany also had the highest total number of taxa (912) collected, and both Austria and the Netherlands also collected high numbers of taxa. The overall lowest numbers of taxa were collected by France (224) and Denmark (237), though this is related to their low number of samples.

Differences in number of samples taken by each country will affect the distribution of samples over

Table 2. The number of samples, taxa, ‘species’ adjusted taxa, and percentage of ‘species’ adjusted taxa per country

Country	Number of samples	Number of taxa	Number of taxa left after adjustment	% Taxa left after adjustment
Austria	169	868	160	18
Czech Republic	146	717	172	24
Denmark	34	237	97	41
France	36	224	118	53
Germany	279	912	231	25
Greece	152	595	198	33
Italy	133	422	152	36
Latvia	93	450	132	29
Netherlands	156	885	215	24
Poland	64	515	158	31
Portugal	71	416	160	38
Slovak Republic	48	375	97	26
Sweden	217	352	130	37
United Kingdom	62	388	136	35

stream types and thus influences the analyses. For example, only 24 samples were taken in the Hungarian plains vs. 93 in the Baltic province. Furthermore, the lower the number of samples taken in a geographical area the lower the number of taxa collected is. This skew distribution of data must be taken into account interpreting the results.

### *Taxonomic adjustment*

After taxonomic adjustment, Germany still showed the highest number of taxa (231) together with the Netherlands (215 taxa). The Slovak Republic and Denmark collected least numbers of taxa (both 97 taxa). On average per sample Austria collected most taxa before adjustment and Latvia after, while Greece collected lowest average number of taxa before as well as after adjustment.

The loss of taxa due to taxonomic adjustment was lowest in France and highest in Austria (Fig. 1). Also the Czech Republic and the Netherlands lost more than 50% of the average number of taxa per sample after adjustment.

The loss of individuals through adjustment was negligible (Table 3). Only Greece and Italy lost

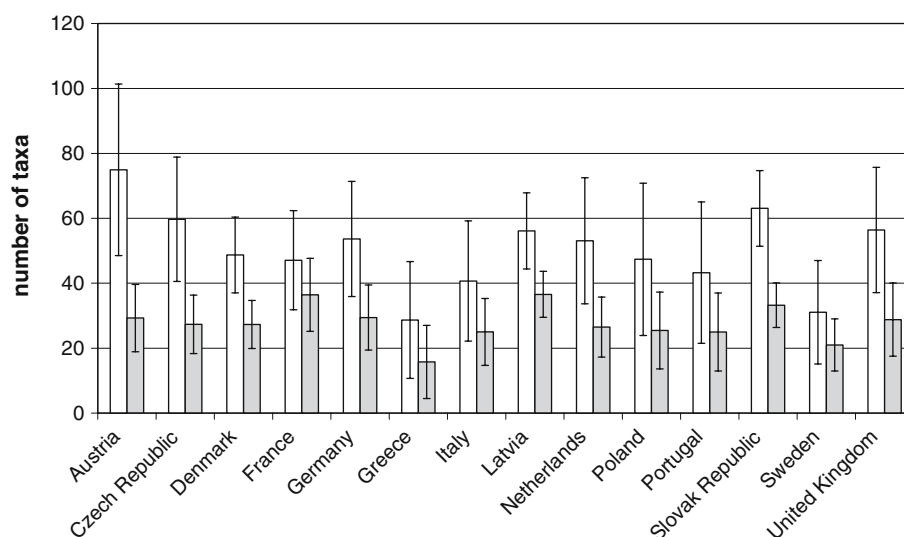


Figure 1. Average number of taxa (white bar) and adjusted taxa (grey bar) per sample per country (standard deviation indicated).

38% and 11%, respectively, of their numbers of individuals due to specimens only identified to very high taxonomic levels which were deleted in taxonomic adjustment. The differences in average number of individuals per sample between countries were very large (Fig. 2). The lowest number was less than 2% of the highest. Furthermore, the standard deviation was large in all countries. So, the one country on average per sample collected

50 times more specimens in comparison to the other.

In general, the loss of species due to taxonomic adjustment was very high (Table 4). Many species and combinations of species were assigned to the genus-level and family-level.

All major taxonomic groups were strongly reduced in number of taxa after adjustment (Table 5). Major losses occurred in the Chironomidae, but also the numbers of Hydrachnidia, Megaloptera, Plecoptera, and Coleoptera taxa were strongly reduced. Gastropoda seemed to be best known throughout Europe and the decrease of the number of taxa was restricted to 61%.

Table 3. The total number of individuals for raw and 'species' adjusted taxa data per country

Country	Raw	Adjusted	% Loss
Austria	1520784	1503759	1.12
Czech Republic	621715	618294	0.55
Denmark	183711	182466	0.68
France	360518	358886	0.45
Germany	546684	532279	2.63
Greece	38984	24316	37.63
Italy	568866	507013	10.87
Latvia	414679	404294	2.50
Netherlands	450035	441351	1.93
Poland	227760	220340	3.26
Portugal	294708	288746	2.02
Slovak Republic	149289	144296	3.34
Sweden	220496	219266	0.56
United Kingdom	570897	569158	0.30

#### *Reference or degraded samples and taxonomic resolution*

The full typological analyses are described by Verdonschot (2006). This manuscript focuses on the importance of taxonomic resolution. The hierarchical grouping of European (groups of) stream types is listed in Table 6 and reflects the full typological analyses. The number of samples per major group, group, sub-group of stream types, and stream types is indicated for all samples, reference samples and degraded samples, respectively (Table 6). The differences of number of samples for all groups must be taken into account interpreting the further analyses. The overlap between

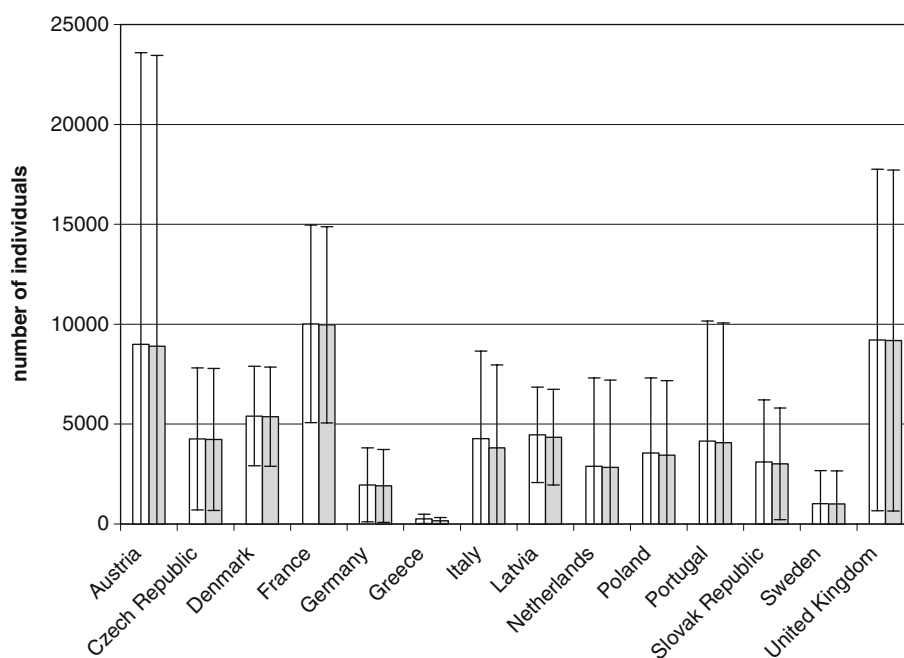


Figure 2. Average number of individuals for raw data (white bar) and adjusted data (grey bar) per country (positive standard deviation indicated).

the groups of stream types was analysed and calculated for the reference samples based on family-level data as well as for the datasets of all samples and degraded samples using species-level or family-level data. Because the number of samples per group differed, the percentage overlap was calculated for each dataset and both species-level

Table 4. The number of taxa per taxonomic level before (raw taxa data) and after taxonomic adjustment ('species' adjusted)

Taxonomic level	Raw taxa data	'Species' adjusted taxa data
Phylum	2	3
Class	9	153
Order/suborder	38	38
Family	270	1170
Subfamily/tribus	56	10
Genus/subgenus	707	1377
Species group/aggregate /combination	214	3
Species	1851	188
Subspecies	72	6
Deleted taxa	0	271
Total	3219	3219

and for family-level data (Table 7). Certain groups do show a much higher percentage of overlap than others. For example, the highest percentage of overlap is between Mediterranean and Lowlands for family-level data of degraded sites (64%). Degraded sites tend to have a poorer taxa composition, and the slope, current and substrate composition of sites within the Lowlands and the Mediterranean is mutual more alike and differs from the Mountains. On the other hand, the overlap within sub-groups and stream types is often 0%.

As an example the DCA ordination diagrams for species-level and family-level data of reference samples of all stream types at the European level are shown in Figures 3 and 4. The overlap between the major groups Mountains, Mediterranean and Lowlands for species-level data of reference samples differs strongly. Only 0.8% of the samples belonging to the Mountains or the Lowlands is projected within the Mediterranean, while on the other hand 15.2% and 26.3% of the Mediterranean samples is situated within the Mountains and Lowlands, respectively. On average there is an overlap of 15.1% (Table 7). For family-level data this overlap is larger (20.2%). This

Table 5. The number of taxa before and after taxonomic 'species' adjustment, and percentage left after 'species' adjustment per major macroinvertebrate taxonomic group

Group	Number of taxa		% Taxa left after adjustment
	Raw	Adjusted	
Aranea	1	1	100
Bivalvia	37	8	22
Chironomidae	478	1	0.2
Coelenterata	2	0	0
Coleoptera	407	79	19
Collembola	1	0	0
Crustacea	53	17	32
Diptera	296	58	20
Ephemeroptera	215	34	16
Gastropoda	97	38	39
Heteroptera	87	24	28
Hirudinea	49	15	31
Hydrachnida	8	1	13
Lepidoptera	10	0	0
Megaloptera	8	1	13
Mermithidae	1	0	0
Nematoda	1	0	0
Nematomorpha	3	1	33
Odonata	92	27	29
Oligochaeta	117	1	1
Planipennia	5	0	0
Plecoptera	142	26	18
Trichoptera	352	70	20
Turbellaria	23	1	4

larger overlap can be seen comparing Figures 3 and 4.

## Discussion

### *Data composition*

Although, both the AQEM and the STAR project used a standardised protocol for sampling, sorting and identification of samples (Hering et al., 2004; Furse et al., 2006) the analyses of the composition of the data used in this study showed a wide spread in number of samples, number of taxa, number of specimens, and taxonomic level achieved through identification amongst participating countries. Verdonschot & Nijboer (2004) already listed some arguments that could explain these differences:

differences in taxonomic knowledge, differences in natural population densities, changes of taxon diversity along geographical and altitudinal gradients, and local environmental differences that affected sampling efficiency or forced changes to the protocol. The data showed that all these arguments could also be valid for the STAR and national sampling procedures. The experience of the AQEM project results on the level of standardisation achievable was the same in the follow-up project STAR. The local environmental conditions and the researchers training and experience set the limits for a European wide standardisation.

As ordination is a robust technique, major patterns are shown and such patterns strongly depend on the number of comparable samples present. The differences in number of samples per country and per (groups of) stream type(s) affected the ordination results. Some major groups were represented by much more samples than others, like Mountains (645) and Lowlands (798) vs. Mediterranean (217). Furthermore, as standardisation showed its limitations, the average number of taxa and individuals strongly differed between countries and (groups of) stream type(s) and this affects ordination. As a consequence, some groupings or divisions of stream types will have been influenced by these differences in data composition.

### *Taxonomic adjustment*

The species is the basic unit that carries features related to its ecological requirements (Resh & Unzicker, 1975; Stubauer & Moog, 2000). Higher taxonomical units, like genus, family or order are aggregates of different species. This aggregation is commonly based on morphological characteristics (especially of the reproductive organs). This implies that species within a higher taxonomical unit can carry different ecological features (Moog, 1995). The consequence is that higher taxonomical units will show wider varieties in ecological response and thus have wider distribution ranges. Taxonomical adjustment, especially in this data set, led to a number of groupings of taxa to higher taxonomical levels. Adjustment to higher taxonomical level automatically implies loss of ecological information (Nijboer & Verdonschot, 2000; Nijboer & Schmidt-Kloiber, 2004; Schmidt-Kloiber & Nijboer, 2004), because the most refined



Table 6. Hierarchical grouping of European (groups of) stream types for Europe. Number of samples per group/type indicated for all samples, reference samples and degraded samples, respectively

Europe	major group	group	sub-group	stream type	number of samples										
					all	reference degraded									
Mountains	all samples				1660	876	784								
					Northern European Mountains		no further grouping of S01 and S02	645	339	306					
								120	68	52					
					Boreal Highlands			60	40	20					
								60	28	32					
					Central European Mountains			S03	30	22	8				
								S04	30	6	24				
								441	224	217					
					Central Alps		Central European Mountains (medium-sized)		64	29	35				
								C14	24	14	10				
								D05	40	15	25				
								no further grouping of A04, A05, A06, C04, C05, C15, C16, D04, D06, V01	377	195	182				
								84	47	37					
					Mediterranean	all samples				217	128	89			
										Central and Eastern Mediterranean			159	92	67
Greece (Medit.)	80	53	27												
Central Apennines			34	18						16					
			I06	45						21	24				
Northern Apennines			I23	23						11	12				
			I24	22						10	12				
Western Mediterranean			P04	58						36	22				
			S-Portugal (medium-sized)	32						20	12				
			S-Portugal (small)	26						16	10				
Lowlands	all samples									798	409	389			
										Central and Southern Lowlands			572	257	315
													A01	24	11
										Hungarian Plain		no further grouping of H04, H05, H06 and H07	72	43	29
													Hellenic Balkans	476	203
					Central European Lowlands		no further grouping of D01, D02, D03, I22, K02, N13, N14, O02, P03, U15, U23	226	152	74					
								226	152	74					
					Northern Lowlands		no further grouping of S05 and S06	97	61	36					
								L02	93	71	22				
								Western sub-alpine Mountains	36	20	16				

Table 7. Percentage of overlap between (groups of) stream types using all samples, reference samples and degraded samples at both species and family-level

Source group	Overlap with	All samples		Reference		Degraded	
		Species data	Family data	Species data	Family data	Species data	Family data
<i>Major groups</i>							
Mediterranean	Mountains	15.2	8.3	15.6	18.0	3.4	2.2
Mediterranean	Lowlands	26.3	31.3	13.3	8.6	60.7	64.0
Lowlands	Mountains	8.0	8.6	10.0	15.4	2.3	3.3
Lowlands	Mediterranean	0.8	3.5	1.2	7.1	1.0	2.8
Mountains	Mediterranean	0.8	1.4	5.3	5.3	8.8	7.5
Mountains	Lowlands	13.2	22.3	9.1	9.4	8.2	8.8
	<i>Overall overlap</i>	15.1	20.2	15.1	20.1	15.6	17.0
<i>Groups</i>							
Mountains							
Northern European Mountains	Central European Mountains	0.8	18.3	1.5	5.9	17.3	26.9
Northern European Mountains	Central Alps	0.8	1.7	0.0	0.0	3.8	9.6
Central European Mountains	Central Alps	0.2	0.0	0.9	0.9	0.0	0.0
Central European Mountains	Northern European Mountains	0.5	1.4	0.4	0.4	0.9	0.0
Central Alps	Northern European Mountains	1.2	8.3	0.0	0.0	10.8	5.4
Central Alps	Central European Mountains	8.3	2.4	4.3	2.1	10.8	5.4
	<i>Overall overlap</i>	2.0	6.0	1.8	2.4	6.9	7.5
Lowlands							
Lowlands	Northern Lowlands	5.2	8.2	8.2	12.1	2.9	4.4
Northern Lowlands	Lowlands	15.0	22.6	7.9	11.2	41.9	47.3
	<i>Overall overlap</i>	8.0	12.3	3.8	11.7	4.6	12.6
Mediterranean							
Central and Eastern Mediterranean	Western Mediterranean	0.6	6.3	1.1	3.3	3.0	6.0
Western Mediterranean	Central and Eastern Mediterranean	0.0	13.8	0.0	19.4	0.0	4.5
	<i>Overall overlap</i>	0.5	8.3	0.1	7.8	0.2	5.6
<i>Sub-groups</i>							
Northern European Mountains							
N-Sweden	Boreal Highlands	3.3	5.0	10.0	7.5	25.0	25.0
Boreal Highlands	N-Sweden	10.0	10.0	7.1	7.1	6.3	6.3
	<i>Overall overlap</i>	6.7	7.5	8.8	7.4	13.5	13.5



Table 7. (Continued)

Source group	Overlap with	All samples		Reference		Degraded	
		Species data	Family data	Species data	Family data	Species data	Family data
Plains	Hungarian Plain	0.2	0.2	0.5	0.0	1.1	2.9
Plains	Hellenic Balkans	3.2	3.6	1.0	0.5	6.6	2.2
	<i>Overall overlap</i>	8.0	7.5	1.9	3.5	11.4	8.6
<i>Stream types</i>							
<b>Central Alps</b>							
A02	A03	3.8	3.8	0.0	0.0	8.3	0.0
A02	I05	0.0	0.0	0.0	0.0	0.0	0.0
A03	A02	0.0	3.8	0.0	7.7	7.7	7.7
A03	I05	0.0	0.0	0.0	0.0	0.0	0.0
I05	A02	0.0	0.0	0.0	0.0	0.0	0.0
I05	A03	0.0	0.0	0.0	0.0	0.0	0.0
	<i>Overall overlap</i>	1.2	2.4	0.0	2.1	5.4	2.7
<b>Boreal Highlands</b>							
S03	S04	6.7	6.7	0.0	4.5	0.0	12.5
S04	S03	3.3	0.0	0.0	0.0	0.0	0.0
	<i>Overall overlap</i>	5.0	0.0	0.0	3.6	0.0	3.1
<b>Central European Mountains (medium-sized)</b>							
C14	D05	8.3	8.3	14.3	0.0	0.0	0.0
D05	C14	10.0	0.0	0.0	0.0	8.0	0.0
	<i>Overall overlap</i>	9.4	3.1	6.9	0.0	5.7	0.0
<b>Northern Apennines</b>							
I23	I24	4.3	0.0	0.0	0.0	0.0	0.0
I24	I23	4.5	0.0	0.0	0.0	16.7	0.0
	<i>Overall overlap</i>	4.4	0.0	0.0	0.0	8.3	0.0

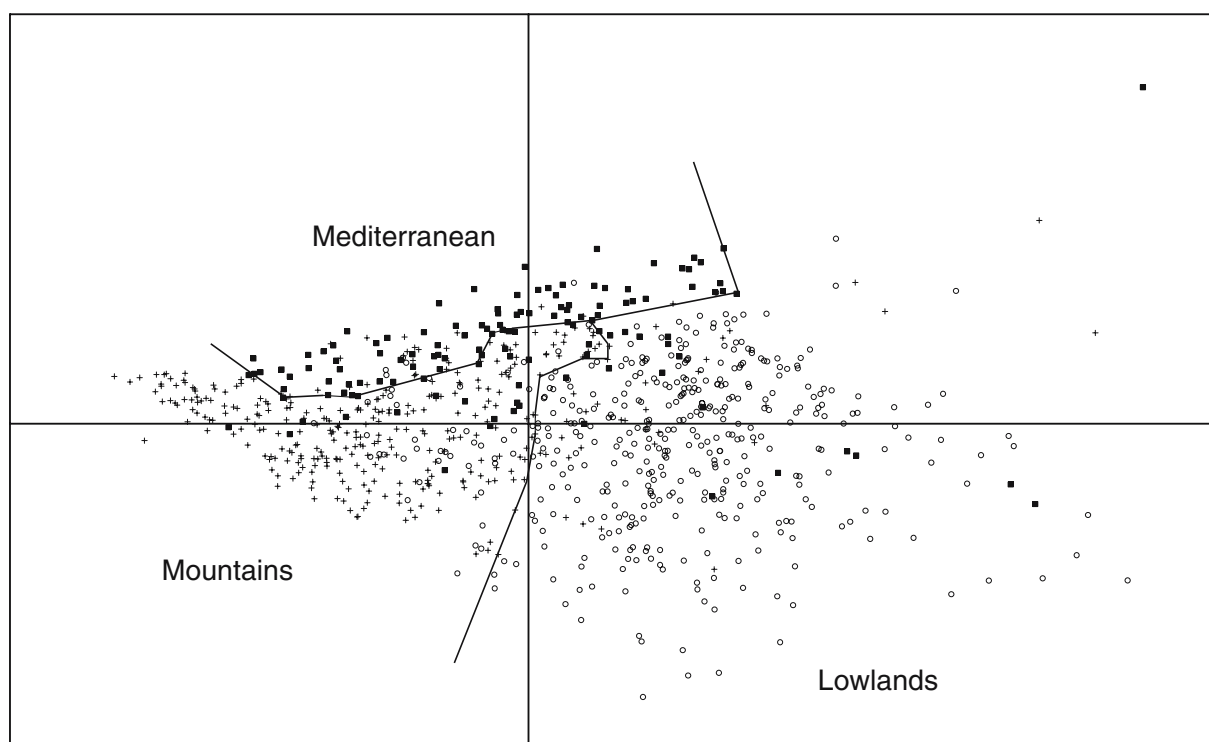


Figure 3. DCA ordination diagram of the axis 1 (horizontal; eigenvalues: 0.23) and 2 (vertical; eigenvalues: 0.13) of the (groups of) stream types within Europe based on species level data of reference samples.

level of information is the ecological response of the species. Even in the ‘species data’ part of this study, quite a large amount of information got lost since adjustment forced in a number of cases an up-scaling of the respective taxonomical level. On the other hand, to keep samples comparable all over Europe and to perform a balanced analysis, adjustment was needed. In conclusion, the need for standardising taxonomic levels to be achieved in European assessment projects is crucial. Areas in Europe where taxonomy is less developed should get and give more attention to improve taxonomic knowledge. In general, taxonomy is the fundament of ecological research and in practical applications. Therefore, also water management and water policy makers should become aware of the importance of a well established knowledge of taxonomy all over Europe.

#### *Taxonomic resolution*

First, it was tested whether the use of reference sites would give better results. Indeed, the refer-

ence samples performed best and were most optimally separated. This supports the hypothesis that human stress diminishes the natural differences between stream communities.

The need to establish reference conditions for typology and classification purposes is one, but the biotic parameters to express these conditions are as important. This study demonstrated that the use of species vs. family-level data changed the results. The use of the family-level data led to a less distinct separation of reference sites. This implies that the description of reference conditions must be based on species-level data (‘best achievable taxonomic level’). But this conclusion reaches further. It also demands two other improvements in the current approaches, one that deals with the use of metrics and the autecological information within, and one with the question what is ‘best achievable’ in identification. The second is related to the former plea of improvement of taxonomy in European research. The first touches the multi-metrics approach in its fundament. In Europe, at the moment there is a very strong tendency to use

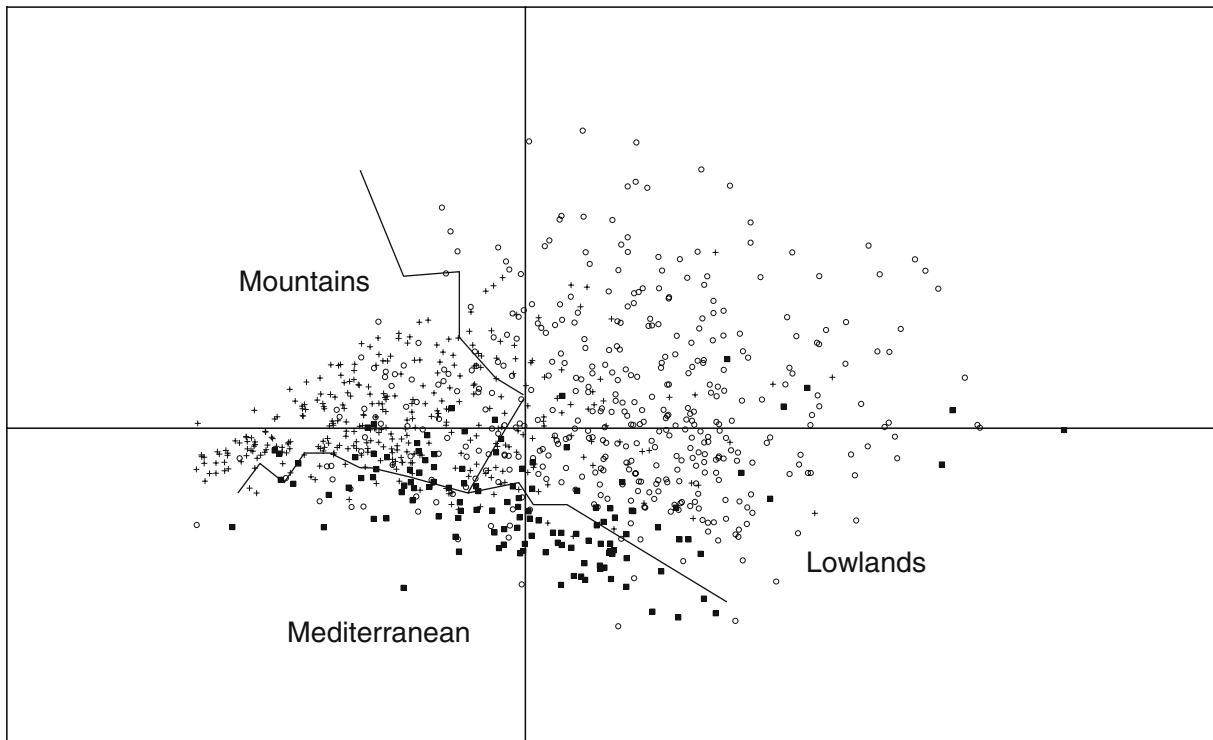


Figure 4. DCA ordination diagram of the axis 1 (horizontal; eigenvalues: 0.18) and 2 (vertical; eigenvalues: 0.10) of the (groups of) stream types within Europe based on family level data of reference samples.

multimetrics in assessment (Hering et al., 2004). The AQEM research project tested over one hundred metrics and came up with a list of 18 suitable core metrics (Hering et al., 2004). Most of these metrics are based on the use of autecological information, often at high taxonomic (family) level. It was shown that the use of family-level data resulted in a lower resolution thus smaller differences between stream types. Families aggregate information of individual species and thus generalise information. Testing the use of family-level data already showed poorer results (Lenat & Resh, 2001; Schmidt-Kloiber & Nijboer, 2004). Using multimetrics means approaching communities by their individual taxonomic features. Each taxon that is included in the respective metric is used as an indicator. But most metrics are (i) dependent on the autecological, often family-level, information, and (ii) restricted to inclusion of a limited number of taxa. A metric extracts only part of the information of the community and expresses it into a value, the ecological quality class. The alternative is the community approach. The classification is

herein based on the use of the community as a whole (e.g., Wright et al., 1999). From community descriptions further information on the ecology of the composing species can be extracted and used in metrics. This improves the metrics as well as the supporting autecological information. The multi-metric and community approach are both complementary ecological tools and can strengthen each other.

## Conclusions

The conclusion of this study were:

- Human stress diminishes the natural differences between stream communities and typologies should therefore be based on reference conditions.
- Stream typology depends on the taxonomic resolution, the finer the resolution the more distinctive the types become.

- Species (or ‘best available’) taxonomic level performed better at a practical (fine) scale in comparison to family-level.
- Even a standardised protocol can not easily overcome (i) local differences in site conditions that cause deviations from the protocol as well as (ii) the experience of the researcher(s).

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