TABORD, A PROGRAM FOR STRUCTURING PHYTOSOCIOLOGICAL TABLES*.**

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Introduction

Since Benninghoff & Southworth (1964) published an abstract of their computer program for ordering phytosociological tables according to the Braun-Blanquet (1964) method along the lines developed by R. Tüxen and collaborators in the 1930's (which were first described in detail by Ellenberg 1956, see also Mueller-Dombois & Ellenberg 1974), many similar programs have been devised. They have been briefly reviewed by Westhoff & van der Maarel (1973), who distinguished two types of program: a. for tables with comparatively many relevés and few species, b, for tables with comparatively few relevés and many species. The Type a programs concentrate on finding groups of species with a similar distribution within the table which can be used in finding species/relevé blocks. Typical examples are the programs by Moore (1973, Moore et al. 1970), Ceska & Roemer (1971) and Stockinger & Holzner (1972, see Holzner, Werger & Ellenbroek 1978).

The *Type b*-programs concentrate on relevé grouping on the basis of mutual (dis) similarity values and produce tables with the relevé groups ordered according to their group (dis) similarities. A typical example is the program by Spatz (1972, Spatz & Siegmund 1973, see also Mueller-Dombois & Ellenberg 1974).

In both types of program the objective is to impose a *diagonal structure* on the table, i.e. to obtain a sequence of relevé groups from left to right and one of species groups (as they differentiate the relevé groups) from top to bottom so that the species relevé blocks occur from left top to bottom right.

Thus most table rearrangement programs are essentially concerned with both releves and species. This twofold approach is also characteristic for the traditional manual ordering of phytosociological tables according to Braun-Blanquet and Tüxen, with the difference, of course, that usually only small tables are sorted by hand. There would be much value in a computer program approaching a table in two directions. The two-parameter *inosculate* method of Dale (Dale & Anderson 1973, Dale & Webb 1975) may be a good start, but no results on phytosociological tables are available yet.

In most of the programs referred to, a finishing touch by the investigator is needed, which mainly consists of changing the position of species. In some programs, this final step is incorporated in an additional program.

Since the 1973 review, entirely new programs have not become known to us, but most of the existing programs have been refined and further improved (see Westhoff & van der Maarel 1978 and van der Maarel, Orlóci & Pignatti 1976 for references). Dale & Quadraccia (1973) introduced an interactive tabular sorting program with a graphic display. Clearly, the automized final rearrangement of a table will usually both improve its structure and diminish errors.

^{*} Nomenclature of salt marsh species follows Lausi, Kortekaas & Beeftink (1978); for names of Arrhenatheretum species see Oberdorfer (1970): Pflanzensoziologische Exkursionsflora für Süddeutschland, 3. Aufl., Ulmer, Stuttgart.

^{**} Contribution from the Working Group for Data-Processing in Phytosociology, International Society for Vegetation Science. *** The program has been tried and discussed by students and colleagues in our Department. We thank them for their help, particularly Drs. Wil Kortekaas and Drs. Willem Schenk. The first author introduced the program and prepared a draft of the manuscript at the Department of Plant Ecology, University of Lund, during his stays there from 1975–1977 under a grant of the Swedish Natural Science Research Council (NFR-B252605). The invitation of Prof. Nils Malmer for the visits to his department and the discussions of results from TABORD with fil. kand. Stefan Persson, fil. kand. Sven Jensén and fil. mag. Čarin Tyler are gratefully acknowledged. Meanwhile Persson (1977) completed a manual on TABORD in Swedish. Finally we thank Prof. László Orlóci for his comments on the manuscript.

Our program was initially developed in 1970 for the Working Group for Data-Processing. Janssen (1972) published the essentials of the program and a first application, whereafter Janssen and van der Maarel made the program available for external use under the name TABORD in 1972. This version has been supplied to many users and regularly improved on in various details, mainly by Louppen.

TABORD structures comparatively large phytosociological tables, i.e. with many relevés and many species, which is considered a major advantage in phytosociological data-processing (van der Maarel 1974, van der Maarel, Orlóci & Pignatti 1976). TABORD differs in approach from most of the existing programs which are not adapted to such large tables, either because they require too much computer storage and time, or because the finishing manual work is too complicated. TABORD is written in FORTRAN IV. A listing on punchcards is available on request.

Description of TABORD

TABORD is essentially a clustering procedure based on relevé similarity, combined with a procedure for obtaining a diagonal structure of clusters in the table. The program includes the following steps:

Establishment of initial clusters

The procedure starts with the establishment of a number of initial clusters. Usually the investigator has at least some idea about the floristic structure of the relevé set to be clustered and tabularized. Therefore the procedure normally starts with the formation of initial clusters by the investigator. If there is no such preconception or if one wishes to avoid any personal influence on the clustering process by subjective choices at the beginning, the program generates initial clusters automatically, by assigning relevé 1 to cluster 1, rel. 2 to cl. 2, etc., up to the *k*-th relevé, if the number of initial clusters is chosen k; rel. k+1 is assigned to cl. 1, etc. up to the last relevé.

Clearly such a start means a considerable saving of both computer storage and calculation time as compared with clustering methods building up a hierarchy from a singlerelevé (dis) similarity matrix. As will be discussed below the possible drawbacks of automatical initial clustering can be coped with in some subroutines incorporated by the program. Another initiation would be the application of some numerical classification procedure prior to TABORD to arrive at the initial clusters. This would only fit into the TABORD strategy if the numerical procedure would be a very rapid one. In Lund (Persson 1977), the monothetic binary divisive program DIVINF, based on maximum decrease in the value of the information measure I (Lance & Williams 1968) is used.

Relocation

The initial clusters are subjected to a relocation procedure, which we adopted from the RELOC subroutine in the CLUSTAN package of clustering programs (cf. Wishart 1969, 1975). The position of each relevé is compared to the centroid of each initial cluster and placed in the cluster with which it shows the closest link. After the position of all relevés is checked, a second iteration starts in which again all relevés are compared with the centroids of the clusters formed during the first iteration. Usually after 4 to 6 iterations the clusters are stable. To avoid endless iterations in the exceptional case of relevés having equal (dis) similarity to two or more clusters, a maximum number of iterations is specified.

Measurement of (dis)similarity

To measure (dis)similarity we adopted 26 criteria from the total set of 38 in CLUSTAN, i.e. 13 coefficients for either numerical or binary data, including the information measure, product moment correlation, Canberra metric, Euclidean distance and similarity ratio. We have mostly used the *similarity ratio*, name and formula introduced by Wishart (1969), and found it an attractive measure of similarity. It is related to the well-known Jaccard formula, but it handles quantitative scores of species more efficiently:

$$S_{x,y} = \frac{\sum x_i y_i}{\sum x_i^2 + \sum y_i^2 - \sum x_i y_i} \qquad (i = 1, ..., n) \qquad (1)$$

where x_i and y_i are the scores of species *i* in relevés *x* and *y* and n is the number of species.

Comparisons of values obtained with this formula to those of the Jaccard and Sørensen formulae (cf. Goodall 1973) show that they are intermediate between the somewhat lower Jaccard and the somewhat higher Sørensen values.

The similarity ratio can also be used for the comparison

of one single relevé with a cluster in the following manner (cf. Janssen 1975):

$$S_{x,z} = \frac{N \sum x_i z_i}{N^2 \sum x_i^2 + \sum z_i^2 - N \sum x_i z_i} \qquad (i = 1, ..., n)$$
(2)

where x_i is the score of species *i* in relevé *x*, z_i is the sum of scores of species *i* in the relevés of cluster *z*, *N* is the number of relevés in cluster *z* and *n* the number of species occurring in either relevé or cluster.

The derivation of (2) follows from:

$$S_{\mathbf{x},\bar{z}} = \frac{\sum x_i \bar{z}_i}{\sum x_i^2 + \sum \bar{z}_i^2 - \sum x_i \bar{z}_i}$$
(3)

where \bar{z}_i is the centroid of cluster z and \bar{z}_i the average score of species i in cluster z.

Since $\bar{z}_i = (1/N) z_i$ we can write (3) as:

$$S_{x_i z} = \frac{\frac{1}{N} \sum x_i z_i}{\sum x_i + \frac{1}{N^2} \sum z_i^2 - \frac{1}{N} \sum x_i z_i} \qquad i = 1, \dots, n.$$
(4)

After multiplying by N^2 we obtain (2) from (4).

The results of the relocation procedure are printed iteration by iteration. For each cluster formed an average within-cluster similarity is defined as the average similarity of the individual relevés to the centroid of the cluster. The similarity between all pairs of clusters is also printed. The similarity between clusters a and b is calculated for the centroids of a and b as follows:

$$S_{a,b} = \frac{N_a N_b \sum a_i b_i}{N b^2 \sum a_i^2 + N a^2 \sum b_i^2 - N_a N_b \sum a_i b_i}$$

 $i = 1, ..., n$ (5)

where N_a and N_b are numbers of relevés in clusters a and b, a_i and b_i are the sums of scores of species i in clusters a and b, and n is the number of species occurring in either cluster.

In the computation procedure prior to eventual relocation, self comparisons may be included when the similarity between a relevé and its own cluster is calculated. If this is not desirable it is possible to have the relevé removed from its own cluster when calculating the similarity.

Naturally, species scores are expected as numerical values. In the Nijmegen versions we use a 1–9 code, which covers the Braun-Blanquet scale of combined estimates

(cf. Westhoff & van der Maarel 1973, van der Maarel 1979). In the printed table the original Braun-Blanquet, or any other symbols may be used. The species scores are expected in a matrix, either with the relevés in columns, as is usual with phytosociological tables, or with the relevés in rows.

Homogenization of clusters

If the investigator wishes to avoid the inclusion of deviating relevés with a low similarity to all clusters, including its own cluster, it is possible to homogenize the clusters by applying a threshold value. During relocation, relevés are removed to a residual group whenever the similarity values with the cluster centroids are less than the threshold value. One can also run the program first without a threshold value, obtain an idea on the average similarity of the clusters obtained and then run a second round with a threshold value adapted to the cluster similarity level.

Fusion of clusters

The program allows clusters to be fused. Logically, the first fusion to be performed is between the two clusters with the closest link. The cluster fusion is treated as a single cluster and the relocation procedure is repeated for the cluster fusion and all other clusters. This procedure goes on until either a minimal number of clusters or a fusion limit i.e. a minimal similarity level, is reached. Both limits are arbitrarily established. A minimal number of final clusters may be desirable for survey or mapping. A minimal similarity (i.e. homogeneity) level may result from considerations concerning the homogeneity of types or syntaxonomical levels (see Westhoff & van der Maarel 1973, 1978 for a review of numerical-syntaxonomical studies, and Kortekaas, van der Maarel & Beeftink 1976 for an example based on the similarity ratio).

Further considerations related to cluster formation and fusion include the minimum size of clusters, the homogeneity threshold value and the handling of the residual relevés. A minimum cluster size may be desired where the relevé set under consideration is to be generalized in terms of common types, or, in a table output, to avoid an irregular diagonal structure. Relevés of clusters which decrease in size below the adopted minimum during relocation are placed in the residual group. On the other hand a minimum cluster size of one may be useful in order to avoid the runoff of relevés into the residue, Although the residual relevés are processed in subsequent relocation rounds, the small but phytosociologically acceptable clusters which were formed, are lost. It is thus recommended to avoid residuals and consequently admit the single-relevé clusters in a first pass of the rearrangement.

A high threshold value should not be applied when the initial clusters are automatically formed by the program: many relevés may be placed in the residual group and may not be replaced in a cluster during the following cycles, because of the relatively low homogeneity of the initial clusters and the threshold value.

Construction of the table

The main structure of the table is determined by the sequence of the clusters determined after the fusions. The program provides several options to obtain a sequence.

The first initiates the table with the cluster which shows the lowest value of the ratio: number of constant species/ number of relevés. A species is considered constant for a cluster if its frequencey in the table exceeds a level specified by the user. One may choose here the rather high value of 80%, thus obtaining eu-constant species in the Braun-Blanquet terminology, or the more effective value of 60%, thus obtaining constants in the normal Braun-Blanquet sense. The rationale for the suggested values is that in this way a relatively high number of constant species is retained for further clusters. If two clusters have the same value for this ratio, the cluster with the highest withinsimilarity is chosen.

The second cluster is chosen according to the highest number of constant species in common with cluster 1. If no cluster shares any constant species in common with cluster 1, this cluster is placed in the table and a next starting cluster is selected following the same procedure.

The phytosociological table is then printed as follows: The relevés of the starting cluster are placed to the left, in order of their current registration numbers, followed by the relevés of cluster 2, also in order of their registration numbers. The species are then listed: in the top part of the table are the species that are constant in cluster 1 but not in cluster 2, arranged in order of their registration numbers. In the salt marsh studies this number follows from the Trieste code (Pignatti 1976). Any ad hoc or other systematical numbering will be treated likewise. An advantage of using the Trieste code here is that large series of constant species occurring in one cluster are ordered according to genus, family and order. Species are printed with their registration number, name and any other specification the user has stored (up to 24 alphanumerical characters). The species which are both constant in cluster 1 and 2 follow in the sequence, again in order of their registration numbers, then the constant species of cluster 2, those which are also constant in cluster 3, etc. The remaining species, not reaching constancy in any cluster, are printed last.

The second way of obtaining a cluster sequence is to ordinate clusters and take the end cluster on an axis as starting cluster. In the present version of TABORD one may chose between the 1st and 2nd axis of a principal components analysis of a matrix of standardized Euclidean distances, following Orlóci (1966) with extraction of components according to Householder as programmed by Roskam (1971), known as program ORDINA. In addition one may adopt a sequence according to position principal components obtained iteratively in the so-called Jacobitype solution (Harman 1967). The listing of the species is as described above.

Repetition of relocation and fusion procedure with other options. It is possible to repeat the whole relocation and fusion procedure with other options concerning homogeneity threshold and/or fusion limit. Each round takes the final classification of the former round as the initial classification. One may choose various objectives, which are then achieved through a process which is essentially a successive approximation (Poore 1962). An obvious objective is to start at a high fusion limit in order to obtain a table with many homogeneous clusters and to gradually decrease the fusion limit. Another logical procedure is to gradually increase the threshold value in order to obtain clusters with an increasing level of homogeneity but with a growing residual group.

In cases where one is in doubt about an effective number of initial clusters, one may start with a high number, allow fusions to occur and simultaneously decrease the fusion limit and increase the threshold value. Another motive for a repetition of the procedure may be uncertainty about the optimal constancy level to arrive at a comprehensible diagonal table structure.

Additional information presented in TABORD

In addition to the results of the calculations described above, the following information is produced by TABORD:

- The occurrences of species in the final clusters as absolute frequency (presence).

- The occurrences of constant species in the clusters.

- The number of constant species common to pairs of clusters.

- In addition to these, the significance of occurrence or absence of species in the clusters is calculated based on a chi-square test and the results are produced as chi-square values per species per clusters and as significance signs levels with signs for positive or negative associations at P = 0.05, P = 0.025 and P = 0.01. Since many frequency values in the cells of the two x two tables involved are very low, the results of this test are best considered in a less rigorous sense, as deterministic measures of the diagnostic value of the species. Such a measure is of particular use for species which are not constant. Species with low frequency but high positive association value resemble the average faithful species in Braun-Blanquet syntaxonomy. - the sequence of clusters is determined by the result of an ordination, distances between clusters, loadings on four dimensions and an ordination diagram with dimensions 1 and 2 are produced. Although the cluster arrangement option based on constant species may be preferred (see Discussion) it is useful to have one round with an ordination included because of the additional insight in the structure of the data.

Finishing touch by computer assisted visual sorting.

The phytosociological table produced by TABORD is usually liable to some improvement, both in the sequence of relevés and in the sequence of species. The efficiency of the cluster arrangement is often partly determined by the size of the cluster and the constancy level required. This could result in suboptimal sequences. Furthermore, the relevés within one cluster are arranged according to their current numbers, which are of course arbitrary and this might not be optimal for visual interpretation.

Changes may be preferred in species sequence in the case of species with a low presence in a cluster but a high positive association value. Species with an overall low table frequency might be deleted alltogether and placed in an addendum.

It is very difficult, if not impossible, to automize procedures for such additional changes. Visual sorting seems a more appropriate approach and, of course, the simple changes of columns and rows can be done with computer assistance, including display (cf Dale & Quadraccia 1973). We developed a simple 'shuffle program' for replacing relevés and species.

Capacity

The capacity of the present TABORD version run at Nijmegen on an IBM 370-158 system is adapted to a

computer storage of 512 K bytes to which we have an instant access. The requirement is determined roughly by:

$$R = 0,004(S(N+3C+7)+5N+C(C+7)+100)+150 \text{ K}$$

bytes (6)

where S = number of species, N = number of relevés, C = number of initial clusters.

Taking a ratio of 1 : 10 for initial clusters : relevé number as a reasonable average, this means that 300 relevés containing 250 species (and 30 initial clusters) could be handled, or 500 relevés containing 150 species (and 50 initial clusters). The previous version of TABORD had fixed dimensions, i.e. 200 relevés, 250 species and 20 initial clusters, requiring 384 K bytes.

Examples

Three examples will be discussed dealing with a. a simply structured table with few species; b. a relatively simple table with many species; c. a rather complicated table.

Spartinetea

Table 1 presents 50 relevés of *Spartinetea* communities selected for testing multivariate methods for the Working Group for Data-Processing (Van der Maarel, Orlóci & Pignatti 1976). The selection contains relevés of the *Spartinetum maritimae*, *Spartinetum townsendii*, *Spartinetum alterniflorae* and *Spartinetum patentis* (5 relevés each) and 30 relevés of variants and transitions, towards *Salicornietum* communities. Obviously the pure types should be reproduced in any TABORD output, while some freedom may exist with respect to the transitional relevés. Various options were tried, the results of which may be summarized as follows:

The structure of the selection allowed a visual interpretation of an initial classification array of 11 clusters, including the five *pure* types. Relocation only led to some rearrangement of three clusters within the *Spartinetum townsendii* variants. All resulting clusters showed a high internal homogeneity, with average similarity values of over 0.80, but between cluster similarities were considerably lower with one possible fusion at the level of 0.69 and one at 0.66 and further fusions at still lower levels. Inspection of the resulting table revealed that all 11 clusters could be recognized by their own characteristic species combinations, so no further fusions were performed. In this example

		00000	00000	00000	00000	00000	00000	00000	00000	00000	00000
		00000	00001	11111	11112	22222	22223	33333	33334	44444	44445
		12345	67890	12345	67890	12345	67890	12345	67890	12345	67890
TRIGLOCHIN MARITIMUM	66003		-2		L	L	-			2-	
AGROSTIS STOLONIFERA	240120			2	~	h					
SPARTINA ALTERNIFLORA	283001			98999							
SPARTINA MARITIMA	283003	79889	53333				<u> </u>	-			
SPARTINA TOWNSENDII	283004		- -			78998	55333	33333	35333	55755	25555
SPARTINA PATENS	283005				99999	 _					
PHRAGMITES COMMUNIS	333001				2-252		<u>}</u>				
PUCCINELLIA MARITIMA	384008		87253	23		h	88775	352	2-23-	35-	
SCIRPUS MARITIMUS	468016		·	5	┣		┝			5	
JUNCUS ACUTUS	936002		┼╼╌╾╸		2-						
JUNCUS MARITIMUS	936029		·	└── ─	-552-	<u> </u>		f	-		
ATRIPLEX HASTATA	2229017						⊢−			87979	
HALIMIONE PORTULACOIDES	2229101		23322			22	-22-2	22-	-2253	3	355
SALICORNIA PERENNIS	2255001		77889	 			5	∲ -	{ -		+
SALICORNIA FRUTICOSA	2255002		 -		2			- -			+
ARTHROCNEMUM GLAUCUM	2255003		╆╼╼╼-		-2	h					+
SALICORNIA EUROPAEA	2257001	2-	5-22-		└	h	35553	88777	-2523	5-	33533
SUAEDA MARITIMA	2261007	2-	552			22	22322	32222	88789	25-	55555
SPERGULARIA MARGINATA	2450006		+			·	3				
OENANTHE LACHENALII	6046009			·		\$	<u>}</u>	·}	4		
LIMONIUM VULGARE	6351017	3-		2-	-3522		₋	2-		 	
PLANTAGO CRASSIFOLIA	8116009				2			╉╌──			+
PLANTAGO MARITIMA	8116021]	┢		+	┣	·}	┣	}	2-	+
ASTER SQUAMATUS	8900023		+		2	+	+	↓			
ASTER TRIPOLIUM	8900025	3-2	2323	225	i 2	2	-3223	3232-	3523-	3323-	53353
INULA CRITHMOIDES	.9061006		+	·	-22-3	\$	+	+			+
SONCHUS ARVENSIS	9595001 [.]			┝	22	┝╌╾╾╸	+	+			+
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Table 1. 50 Spartinetea relevés (selection f, Working Group for Data-Processing in Phytosociology, see van der Maarel, Orlóci & Pignatti 1976). Species are listed according to the Trieste code number, four digits for the genus code, three digits for the species code.

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	000000000000000000000000000000000000000	112
	1234 78006 7780046 78906 78906 78901 23761 23451 23451 23451 23456 78	100
	1234363001103040783007030220000220402204022040	
	000000000000000000000000000000000000000	000
	esacopococol11111pococococol1111pocococococococococococococococococo	000
	111112228800000777777777711119555556666633333444	144
SPARTINA MARITIMA	7988933353	
ASTER TRIPOLIUM	3-2323322323523-533533232-3323225	2
PUCCINELLIA MARITIMA	25387877552-233283523	
HALIMIONE PORTULACOIDES	3222322-22-22533552223	
SALICORNIA PERENNIS	│ <mark>889</mark> 77 	
SUAEDA MARITIMA	2-25523222887895555532222222	
SPARTINA TOWNSENDII	533333533325555333357899855755	
SALICORNIA EUROPAEA	2-22-5-55537-252333533887735	
SPERGULARIA MARGINATA	│╺╾╾╾╞╌╾╞ _┍ ┝╼╾╼╞╼╼╌╌╌╌┿╼╾╼ ╣┼╾╾╸ ┥╾╾╍┼╌╌╌┾┈╵	
ATRIPLEX HASTATA	│	
SPARTINA ALTERNIFLORA	│┝┝-┝-┝┝┝	
SPARTINA PATENS	│┝┝-┾┝┝┝/┾┝┼┾) 99
PHRAGMITES COMMUNIS	│╶╾╾╾ ╞ ╼╾┝╌┾╍╾╌┾╼╺╾╾╸、╌╌┽╌╌╍┾┾╼╼╾┽╌╍╸┿╼┈╾┲ <mark></mark> ═┊	252
LIMONIUM VULGARE	3- <u> </u> 2 <mark>2</mark> + + 2- -3!	522
SONCHUS ARVENSIS	│	
INULA CRITHMOIDES	╽╶─╾╌╞┝╼╞╼┾╍┯╞╶╌╌╌┑╍╼╞╼╼╼╞┟┑┈╍┾╍╍╍╪╼╍╍╪╝	2-3
ASTER SQUAMATUS	│ ┝ ┝-┝┝-┝┝	2
PLANTAGO MARITIMA	│ ╾╾╾╾┝╼╼┝╌┾╾╌╌┾╍╌╼┍╍╌╾╾┝╌╴╼┡┝╶╾╾ ┶┝╴╴ ╝╴╴╴╌┍╼╴	
PLANTAGO CRASSIFOLIA	│┝┅┝┉┝╺┝╵┈┈┝╺╌╌╸╸╸╸╸┝╸╸╸╸┝┝╺┈╺┾╸╸╴╸┍┝╸	2
OENANTHE LACHENALII		3-2
ARTHROCNEMUM GLAUCUM	╽╺╌╍╼┝╼┝╼┝╼╾╼┝╼╼╼┶╌╍╼┝╼╼╼┝┝╼╼╍┾╌╾╌┾╌╌╌┍┝╶╝	
SALICORNIA FRUTICOSA		2
JUNCUS MARITIMUS		-2-
GOLDDUG MARIMUM		- 4-
ACDOSTIC STOLONIERDA		
TOLOCUIN MADITININ		
IRIULGAIN MARITIMUM		

Table 2. Structured table of the *Spartinetea* relevés of table 1, obtained with TABORD, with options threshold value 0.55, fusion limit 0.75, and constancy limit 0.70. Relevé numbers are given in the top three rows of the tables, cluster numbers is rows 4-6.

FACTOR 1 PLOTTED AGAINST FACTOR 2



Fig. 1. PCA-ordination of 11 clusters of Spartinetea-relevés as presented in table 2.

	000000000000000000000000000000000000000
	0000000100222333334444453333222222444441111111112
	123458906777890467890678901235612345123451234567890
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	000000000000000000000000000000000000000
	000000000011111111000000000000000000000
	111112228890000111117777777777555555666663333344444
	── ╞──╞─╞─╞──╞──╞──╞──╞──
SPARTINA MARITIMA	79889333353
SALICORNIA PERENNIS	\889775
SPERGULARIA MARGINATA	╶╴╶╴╄╴╴╌┢╴╴╘┿╴╸╴╴╸╴╴╸╴╴╸╴╴╴╴╴╋╴╴╴┫╏╴┥╸╸┼╸╸╴╴
PUCCINELLIA MARITIMA	
HALIMIONE PORTULACOIDES	
ASTER TRIPOLIUM	3-232332232323-3523-53353-233232252
SUAEDA MARITIMA	2-255223222322288789555552225
SALICORNIA EUROPAEA	2-22-5-3555378877-2523335335
SPARTINA TOWNSENDII	
ATRIPLEX HASTATA	
SPARTINA ALTERNIFLORA	
SPARTINA PATENS	
PHRAGMITES COMMUNIS	
LIMONIUM VILGARE	
INILA CRITHMOTORS	
TUNCUS MADIFITMUS	
CONCOS MARITIMOS	

Table 3. Structured table of *Spartinetea* relevés as obtained in table 2 with additional changes in the sequence of relevés and species. Species lacking a high constancy in any cluster have been left out.

a threshold value (usually we use values between 0 and 0.50) did not make any difference, because of the high homogeneity level of the clusters involved.

An automatic initial array of 10 clusters with 5 relevés each led to an almost identical end classification, which would be completely identical after fusions down to the 0.60 level. However, this occurred only when no threshold value was applied. The same attempt with threshold value 0.30 led to a large residual group, obviously because of the very low homogeneity of the random clusters at the beginning.

Table 2 shows the resulting phytosociological table based on the constant-species-efficiency criterion (In our examples only data on species occurrences in the 1-9

ordinal transform scale and no data on site and vegetation structure are presented, Evidently all additional information on the stands and relevés involved can be incorporated in the structured table.). The Spartina maritima cluster with only one constant species comes first and clusters 2, 8, 9, 10, 11, 17, 5 and 6 with Spartina townsendii follow logically. All these clusters correspond to subassociations and variants described by Kortekaas et al (1976). Cluster 3, with Spartina alterniflora, is placed independently; cluster 4, with Spartina patens, joins cluster 3. Each cluster can be characterized with its own combination of constant species. (In this and other examples we used 0.70 as constancy level). The chi-square test confirms the visual observations that the Spartina patens cluster has two species with a constancy below the level chosen, but with a significant association to that cluster.

On closer inspection this table can be improved. Cluster 9 (one relevé) should join cl. 10, cl. 7 and 11 could change position. Also some species may be replaced. To consider possible changes the result of the (ORDINA) ordination of the 11 clusters is used (Fig. 1). The table output of this TABORD run as such was also considered as an alternative but found less satisfactory, but the main sequence of table 1 could be altered to conform to the ordination pattern by indeed placing cl. 9 between cl. 8 and 10, and cl. 11 between cl. 10 and 7. In this way a spiral is followed in which both dimensions are involved and moreover cluster 1 instead of the more extreme cl. 4 is taken as a starting cluster. The species sequence is adapted to the new cluster sequence and through visual inspection the diagonal structure is improved. This finishing touch has been done with the shuffle program. Table 3 shows the end result.

Arrhenatheretum

Table 4 presents a version of the Arrhenatheretum table used by Ellenberg (1956) and Mueller-Dombois & Ellenberg (1974) to demonstrate the process of tabular phytosociological synthesis according to Braun-Blanquet (cf Westhoff & van der Maarel 1973). Table 4 gives the socalled differentiated table, based on table 9.7 in Mueller-Dombois & Ellenberg with the deviating relevé 19, already struck by the authors, placed to the end of the table. For this example the original % biomass estimations were converted into intervals of the ordinal transform scale. Only those species are listed which are either frequent in the table as a whole or characteristic for one of the community types involved. This list corresponds to table 9.7, left in Mueller-Dombois & Ellenberg (op. cit.), whilst the species not listed are those of table 9.7. right, called remaining species by the authors (op. cit.).

The 25 relevés in this example have been put in a random order (table 9.2. op. cit.), which we do not reproduce here. Three types of vegetation were distinguished in the differentiated table, viz. *Bromus-Arrhenatherum* (columns 1–8), *Geum-Arrhenatherum* (col. 9–14), and *Cirsium-Arrhenatherum* (col. 15–24, with deviant relevé 19 in col. 25).

Treatments were based on various initial arrays with 8–12 clusters. These numbers of initial clusters seemed effective in view of the expected number of types on one hand and the total number of relevés on the other hand. Treatments based on an initial array derived from visual inspection of table 4, and on two automatic arrays, with a fusion limit of 0.70, led to similar results. A cluster of *Bromus erectus* relevés was recognized, the same as in table 4, but without rel. 2 (col. 8), but we miss many of the differential species as indicated by Mueller-Dombois & Ellenberg (from *Bromus erectus* to *Linum catharticum*). In one case rel. 1 and 4 (table 4, col. 3 and 1), which both miss *Salvia pratensis* and *Viola hirta*, form a separate cluster. Rel. 19, the deviant one, always forms a cluster by itself.

The Geum-Arrhenatherum type (for which, incidentally, Geum urbanum is not typical) is less clearly traceable. In most outputs a cluster is formed which contains the six relevés of the type, but includes other relevés: 13, 23, also 2 in some cases. This result is confirmed by a Q-type factor analysis shown by Mueller-Dombois & Ellenberg (1974, fig. 10.12) themselves, which they have not used in the tabular sorting process.

The Cirsium-Arrhenatherum type is still weaker. In most attempts the relevés assigned to this type are distributed over several clusters, including single-relevé clusters (e.g. rel. 14 and 25). In one automatic initial array attempt, which produced only 5 final clusters, the relevés of this type were at once fused with those of the Geum-Arrhena-therum type. Again, Mueller-Dombois & Ellenberg (op. cit.) produce evidence supporting this similarity, viz. in the dendrogram of fig. 10.15.

The final TABORD table as seen in Table 5, is based on an initial classification array of 13 clusters, with 0.65 as fusion level and 0.45 as threshold value. Only three clusters are left, one of which is a single-relevé cluster with rel. 23. The two large cluster clearly show the existence of two rather than three community types in the material.

In order to enable a more detailed interpretation of the relevé set the program was run with a higher fusion limit. Fig. 2 shows the result of the ordination (ORDINA) in this TABORD run, with the same initial array but a fusion

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	0100102011120221101022131
	4019534268205233267815479
BROMUS ERECTUS	8677775
SCABIOSA CULUMBARIA	211-1
THYMUS SERPYLLUM	1321
SALVIA PRATENSIS	-4-3244
KOELERIA PYRAMIDATA	3333
FESTUCA OVINA	-233-2++
CAMPANULA ROTUNDIFOLIA	2221211-1-221-12
VIOLA HIRTA	-3-3111-1
BRIZA MEDIA	-22323
LINUM CATHARTICUM	1-11-11
GEUM RIVALE	111111-2133421-22
HOLCUS LANATUS	2-12323336321
MELANDRIUM DIURNUM	2-111314221
ALOPECURUS PRATENSIS	
LYSIMACHIA NUMMULARIA	
LYCHNIS FLOS-CUCULI	21-11111
GLECHOMA HEDERACEA	1-111-
CIRSIUM OLERACEUM	11121353633661
DESCHAMPSIA CAESPITOSA	5-734-253
ANGELICA SILVESTRIS	21-2123-
CAREX ACUTIFORMIS	4-23-53
FILIPENDULA ULMARIA	
PIMPINELLA MAGNA	
POLYGONUM BISTORTA	4-22
ARRHENATHERUM ELATIUS	3514637266564675645467546
DACTYLIS GLOMERATA	4443465466745556655566542
GALIUM MOLLUGO	2533353344443355364423643
POA PRATENSIS	4545656855644563434425432
PLANTAGO LANCEOLATA	2222221232223354121421341
FESTUCA PRATENSIS	-3-4433445536633735563335
CHRYSANTHEMUM LEUCANTH	142323412-33122224121-331
RANUNCULUS ACER	-31111111-122313132111231
VERONICA CHAMAEDRYS	1211111-2-221131121122-21
ACHILLEA MILLFOLIUM	254333314524341411162-
DAUCUS CAROTA	122212-21212113312-412-
RUMEX ACETOSA	1-1-12-221212133312322

Table 4 25 Arrhenatheretum relevés taken from table 9.7 in Mueller-Dombois & Ellenberg (1974). The remaining species as listed in this table have been left out.

limit of 0.80. Fig. 2 resembles the diagram presented by Mueller-Dombois & Ellenberg (op. cit. fig. 10.12) in showing the main environmental gradient from dry to moist underlying the variation in the table. This gradient can be followed along the horseshoe configuration from clusters 1 and 3 via cl. 2, 12 and 4, to cl. 5, 13 and 7. Finally Table 6 presents the floristic composition of these 8 clusters in the described sequence using species with a differentiating value for one or two clusters. This table can be used for the interpretation of Fig. 2 and also for the inspection of the orginal division into three community types. Note that some of these species are not used by Mueller-Dombois & Ellenberg (op. cit. table 9.7.) to differentiate their types. Helictotrichon pubescens and Heracleum sphondylium are even usable as differentiators for the Geum-Arrhenatherum type.

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h 	
GEUM RIVALE	1324312-1112121
HOLCUS LANATUS	22233-23-3-1-3-16
CIRSIUM OLERACEUM	15663-16-3-113123
RUMEX ACETOSA	1323322321-2212121-11-
ARRHENATHERUM ELATIUS	44445555666666667713345672
DACTYLIS GLOMERATA	5545576566624655646434454
GALIUM MOLLUGO	3644445643434235335235333
POA PRATENSIS	4334463454524256545455668
PLANTAGO LANCEOLATA	3244124331212235122222212
FESTUCA PRATENSIS	63355533475536633-3-43434
CHRYSANTHEMUM LEUCANTH	1432132322-13122-23134241
RANCUNCULUS ACER	2331213211-12131111-13111
VERONICA CHAMAEDRYS	1221121-21-1221321111211-
ACHILLEA MILLFOLIUM	3-2246415-4141143235331
DAUCUS CAROTA	1224-13-112-2113-221221-2
BROMUS ERECTUS	7787675-
SALVIA PRATENSIS	
CAMPANULA ROTUNDIFOLIA	1-2-21212121221-
VIOLA HIRTA	1-3311-
FESTUCA OVINA	
BRIZA MEDIA	232322
POLYGONUM BISTORTA	2124
PIMPINELLA MAGNA	112
FILIPENDULA ULMARIA	-3-311
CAREX ACUTIFORMIS	5-43-23
ANGELICA SILVESTRIS	-231221
DESCHAMPSIA CAESPITOSA	5372-5-3-4
GLECHOMA HEDERACEA	1-11111
LYCHNIS FLOS-CUCULI	1121-1-11
LYSIMACHIA NUMMULARIA	-1-2111111
ALOPECURUS PRATENSIS	35-54-4365-2
MELANDRIUM DIURNUM	-3211221-1-11-4
LINUM CATHARTICUM	11111
KOELERIA PYRAMIDATA	
THYMUS SERPYLLUM	211-3-+
SCARTOSA COLIMBARIA	2

Table 5. Structured table of the *Arrhenatheretum* relevés of table 4 obtained with TABORD, with threshold value 0.45, fusion limit 0.65 and constancy limit 0.70.

Thus, in one combined TABORD-analysis we obtain most of the numerical results produced in separate analyses by Mueller-Dombois & Ellenberg and moreover structured directly in a phytosociological table.

Glauco-Puccinellietalia

Table 7 presents the 58 relevés of another selection of the Working Group for Data-Processing. The relevés are placed in order of the collection from 17 tables of communities from the order *Glauco-Puccinellietalia*. Communities 1–8 are represented with 3 relevés (col. 1–24), comm. 9 with 4 rel. (col. 25–28), comm. 10 with 3 rel. (col. 29–31), comm. 11 and 12 with 4 rel. (col. 32–39), comm. 13 with 3 rel. (col. 40–42), comm. 14–17 with 4 rel. (rol. 43–58). The various community types involved can be

FACTOR 1 PLOTTED AGAINST FACTOR 2



Fig. 2. PCA-ordination of 8 clusters of *Arrhenatheretum* relevés as obtained with TABORD with threshold value 0.55 and fusion limit 0.80. Cluster 1: relevés 1, 4; cl. 2: rel. 2; cl. 3: rel. 3, 9, 10, 15, 24; cl. 4: rel. 5, 12, 13, 16, 18, 20, 22; cl. 5: rel. 6, 7, 8, 14; cl. 7: rel. 19; cl. 12: rel. 23; cl. 13: rel. 11, 17, 21, 25. See also table 6.

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	BBBBBBBBCGGCGGGGCCCCCCCC
LINUM CATHARTICUM CAREX FLACCA KOELERIA PYRAMIDATA PROMUS EDECTUS	1111
CAMPANULA ROTUNDIFOLIA VIOLA HIRTA SALVIA PRATENSIS	$\begin{array}{c} 7877675 \\ 2211221 \\ -2 \\ -13111 \\ -43424 \\ -2 \\ -2 \\ -4 \\ -2 \\ -2 \\ -2 \\ -2 \\$
SCABIOSA COLUMBARIA FESTUCA OVINA SILENE INFLATA	12 - 11 - 3
TRISETUM FLAVESCENS CREPIS BIENNIS HERACLEUM SPHONDYLIUM	43-43345-4545645-4 1114322222-51111 1-21-23-71121142-1-
HELICTOTRICHON PUBESCENS AJUGA REPTANS GEUM RIVALE CIPSIIM OLEPACEIM	2 - 41 - 22 - 624647353 - 41 - 41 - 41 - 121 - 11112312121 - 121 - 11112312121 - 121 - 11112312121 - 121 - 1112111324 - 31212 - 3122
FILIPENDULA ULMARIA ANGELICA SILVESTRIS HOLCUS LANATUS	
LYCHNIS FLOS CUCULI DESCHAMPSIA CAESPITOSA CAREX ACUTIFORMIS	2
PHALARIS ARUNDINACEA	

Table 6. Structured table of the *Arrhenatheretum* relevés of table 4 according to a Tabord-run with threshold value 0.55 and fusion limit 0.80. The resulting 8 clusters are arranged according to the ORDINA-configuration presented in Fig. 2.

derived from the dominant species characterizing them (see further Feoli 1977a).

After various trials with varying threshold values and fusion levels, three runs were compared with a given fusion level, 0.70, and threshold, 0.20, all with 17 initial clusters, one according to the community representation as described in Table 7, one automatic array, and one similarly deviced regular array. The similarity between the three classifications was very high: 39 relevés were placed in the same multi-relevé clusters and 8 relevés became single-relevé clusters in all attempts.

A new run was applied to an array of 18 initial clusters on the basis of these results. Only 6 relocations were needed to achieve stable clusters. The resulting clusters were considered reasonably clear and homogeneous, but still some clusters incorporated deviant relevés. Thus a further run was applied with 24 initial clusters, based on fusion limit 0.65 and threshold 0.45 (Table 8). This table may be further improved manually with the help of the ORDINA cluster ordination as shown in Fig. 3. This is not demonstrated here. It appears that on fusion limit 0.65 the 24 clusters remain unfused and that, indeed, deviant relevés remain on their own.

⁽table 6 cont'd) Relevé and cluster numbers are indicated in rows 1-3 and 4-6 respectively. The community type according to Mueller-Dombois & Ellenberg (1974, table 9.7) is indicated in row 7: **B** = Bromus-Arrhenatherum type, G = Geum-Arrhenatherum type, C = Cirsium-Arrhenatherum type.

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	00000000111111111222222223333333334444444444
	123456789012345678901234567890123456789012345678901234567890123456
TRIGLOCHIN MARITIMUM	5-4-5+3442325342-433242-4-3-422224-7-22-2325-55-
PARAPHOLIS STRIGOSA	+-+-++++++
AGROSTIS STOLONIFERA	
POA PRATENSIS	│ ++35- 22 <mark>++</mark> -3- <u>+</u> <u>+</u> +++++++++
PUCCINELLIA DISTANS	│━━┿━━┿━━┿━━┿━━┿═╊═╊═╊═╊═╋═╋
PUCCINELLIA MARITIMA	79857+
FESTUCA RUBRA	2-8 233 333 -288 777 55 +++
ELYTRIGIA PUNGENS	+7-5+42++++++++++++-
SCIRPUS RUFUS	╶╇╴╍┿╍╼┝╌╍┝╌┉┝╌┉┾╴┥╌┈┝╴┼╴┥
SCIRPUS MARITIMUS	
CAREX EXTENSA	
JUNCUS GERARDII	
JUNCUS MARITIMUS	│
ATRIPLEX HASTATA	
HALIMIONE PORTULACOIDES	2-575227232
HALIMIONE PEDUNCULATA	
SALICORNIA RADICANS	
SALICORNIA EUROPAEA	-3-22-3-2
SUAEDA MARITIMA	
SPERGULARIA MEDIA	
SPERGULARIA MARINA	
COCHLEADIA ANGLICA	
DOTENTILIA ANGEDINA	
DAUCUS CABOTA	
CLAUX NADITINA	
GLAUA MARITIMA	
ARMERIA MARITIMA	
DIAWAGO WADJELKA	
PLANTAGO MARITIMA	
ASTER TRIPOLIUM	72225-2-222272333-23
ARTEMISIA MARITIMA	2#225 +++++ ++7777 +++++++++++
LEONTODON AUTUMNALIS	+++2532-2+-+2+++8++++++++++-

Table 7. 58 relevés of 17 Glauco-Puccinellietalia communities (selection e, see further table 1).

The main structure of the table reflects the variation present in the relevé selection comprising the Puccinellietum maritimae of the low salt marsh, the Plantagini-Limonietum of the upper low marsh, various forms of the Juncetum gerardii of the wet upper salt marsh, and the Artemisietum maritimae of the dry upper marsh. This picture is confirmed in Fig. 3, where the position of the major dominants is indicated. Thus the main division within the data set, marked by the alliances Puccinellion maritimae and Armerion maritimae, as shown by Feoli (1977, 1977a) for the same selection, is confirmed. Due to the relatively high fusion limit chosen, many of the clusters have a distinct species combination, e.g. clusters with Armeria maritima, Scirpus rufus, Puccinellia distans and Carex extensa. It should be realized that these clusters were built into the selection (see selection procedure mentioned above). Thus it is no surprise to find these clusters back in the final configuration. Still many of the single relevés ended up in quite different positions as compared with the original position in the author's tables.

Discussion

According to the general phytosociological approach as developed in our Department we attempted to combine the theoretical and technical advantages of selected numerical methods with the conceptual framework and the common sense of the Braun-Blanquet approach (see van der Maarel 1975). TABORD is an outcome of this combined approach.

The essentials of TABORD incorporate elements of the intuitive table rearrangement method of Braun-Blanquet and Tüxen. The first step, i.e. initiating clusters and homogenizing them, resembles the polythetic subdivisive element in the Braun-Blanquet approach as pointed out by Moore et al. 1970, Moore & O'Sullivan 1972). The structuring of the table as realized in TABORD is another link to the classical approach.

The procedure of finding a diagonal structure of relevés combines two ideas: the choice of the most efficient starting cluster as the one with relatively many relevés and few constant species and the subsequent arrangements of

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	1290153453426564218678785436783568906901790778901212342345
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	8888881111110332594477711566338000002222444733344449992222
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PUCCINELLIA MARITIMA	79999985792-85355
ASTER TRIPOLIUM	7272332252-5535-322
HALIMIONE PORTULACOIDES	2
ARTEMISIA MARITIMA	222++++++++++++++++++++++++++++++++++++
SALICORNIA EUROPAEA	-322532252
SUAEDA MARITIMA	
SPERGULARIA MEDIA	-23-22-333322332
LIMONIUM VULGARE	22735-37-+++++
PLANTAGO MARITIMA	3-532-3775-5523323335255227237255-5-22222-23-5
TRIGLOCHIN MARITIMUM	5-535-5525-7-2-2322333-22-2223-222
PARAPHOLIS STRIGOSA	│
JUNCUS GERARDII	
ARMERIA MARITIMA	23537725523-885323-22
JUNCUS MARITIMUS	
SALICORNIA RADICANS	-
COCHLEARIA ANGLICA	-2
GLAUX MARITIMA	-25-2
AGROSTIS STOLONIFERA	
CAREX EXTENSA	573573
SCIRPUS RUFUS	
FESTUCA RUBRA	
POTENTILLA ANSERINA	
POA PRATENSIS	
LEONTODON AUTUMNALIS	
ATRIPLEX HASTATA	
SPERGULARIA MARINA	55588
ELYTRIGIA PUNGENS	b
SCIRPUS MARITIMUS	
DAUCUS CAROTA	┠╼┉┉┉┢╼┈╌┾┝┼╶┿┽┽┽╌┼╌┑┽╌┼┼ ╌╋╌┝┝┉┈╌╌╎╌╴╴┾ ┱╌ <mark>╞</mark> ┢┑┥╌╍╴╴
PUCCINELLIA DISTANS	└─────└──└──└────────────────────────
HALIMIONE PEDUNCULATA	

Table 8. Structured table of *Glauco-Puccinellietalia* relevés of table 7 obtained with TABORD, with threshold value 0.55, fusion limit 0.75, and constancy limit 0.70.



Fig. 3. PCA-ordination of 24 clusters of *Glauco-Puccinellietalia* relevés as obtained with TABORD, with threshold value 0.45 and fusion limit 0.65. See also table 8. The position of the main dominant species and the borderline between *Puccinellion maritimae* and *Armerion maritimae* are indicated.

clusters as well as (joint) constant species, combined with a check on the basis of an ordination of the clusters. In this way, an optimal structure may be expected, also with multidimensional data sets.

Finally we should emphasize the great speed of the program. Simple tables are fully elaborated in seconds, large and complicated tables within tens of seconds.

Some drawbacks we have encountered may now be mentioned: First the final cluster structure is dependent on the structure of the initial array. This would suggest the adoption of an initial array cluster based on a numerical classification, but then some of the practical advantages would be lost. We would prefer a combination of runs based on different initial arrays, in which the number of initial clusters varies. Since nowadays some of the numerical techniques can be done at high speed and with a large capacity, it is becoming feasible to adapt the results of such a classification as input for TABORD.

A second drawback is the distortion brought about by deviant relevés. This drawback may be overcome by removing such relevés from the table. This can be done during the final preparation of the table, on the basis of visual inspection.

Thirdly, users sometimes remark that the tables produced in TABORD are difficult to read. However, if this happens the data-set is probably very complex. It may, for instance, incorporate different plant communities of a region. For this, however, TABORD can hardly be blamed.

This brings us to a final comment. TABORD can be a guide in creating some order in an apparently chaotic ensemble of phytosociological data. In doing so, it does not claim statistical perspective of objectivity. We are sentially dealing with a vegetational polyversum which cannot be approached with statistical methods assuming a universum. We consider an approach based on successive approximation (Poore 1962) as more productive.

Summary

TABORD, a program in FORTRAN IV for structuring phytosociological tables, is described. It is a clustering procedure based on relevé similarity combined with a procedure for obtaining a diagonal structure in the table presenting the clusters arrived at. The following steps are described:

- Establishment of initial clusters, either by the investigator or on the basis of previous knowledge on the data, or automatically by the program.

- Relocation, based on the RELOC-subroutine in the

CLUSTAN-package of clustering programs. Various measures of (dis-) similarity are available, of which the similarity ratio is emphasized and descirbed.

- Homogenization of clusters through removal of deviant relevés by adopting a threshold value.

- Fusion of clusters on the basis of the between-cluster similarity pattern by adopting a fusion limit.

- Construction of the table. The first cluster is chosen either as one showing the lowest value of the ratio number of constant species: number of relevés, or as the one placed at the end of an axis of a cluster ordination.

- Repetition of relocation and fusion procedure with other options.

- Finishing touch by computer assisted visual sorting. Various additional information on cluster structure and species occurrence in clusters is presented. The capacity of the program for an IBM 370–158 system, with 512 K bytes instantly available, is roughly 300–500 relevés with 250–150 species and 30–50 initial clusters.

Three examples are discussed. An example with relevés of *Spartinetea* showed that the resulting TABORD table reflects the various communities and subunits as described in earlier work. An example of *Arrhenatheretum* relevés was used to demonstrate various numerical options in TABORD, which confirmed in a concise way what was shown in the original treatment through many separate analyses. The third example comprises relevés of 17 *Glauco-Puccinellietalia* communities. Again the TABORD table very well reflects the structure and earlier ecological interpretations.

TABORD is considered a numerical elaboration of the intuitive table sorting procedure according to the Braun-Blanquet method.

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