

A process supported by the utility BBPC for analysing Braun-Blanquet data on a personal computer

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Many South African vegetation scientists use utilise the Braun-Blanquet methodology. The main aim of this paper is to describe an affordable, rapid and efficient process for analysing Braun-Blanquet phytosociological data sets on a personal computer. It describes a suite of utilities joining various phases and this makes the entire process possible.

Key words: phytosociological data sets, personal computer programme package, efficient process, CEP-format.

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Introduction

In a description of the Grassland Biome Project, Mentis & Huntley (1982) stated the necessity of identifying and determining the location and extent of the major vegetation types and subtypes within the Biome. Scheepers (1987) emphasised this need as well, and as a result, phytosociological research programmes were initiated. The necessity for an ecological classification, description and mapping of the vegetation of a conservation area was also stated by Bredenkamp & Theron (1978). A sound knowledge of the ecology will contribute considerably to the compilation of an efficient conservation policy for South Africa (Edwards 1972).

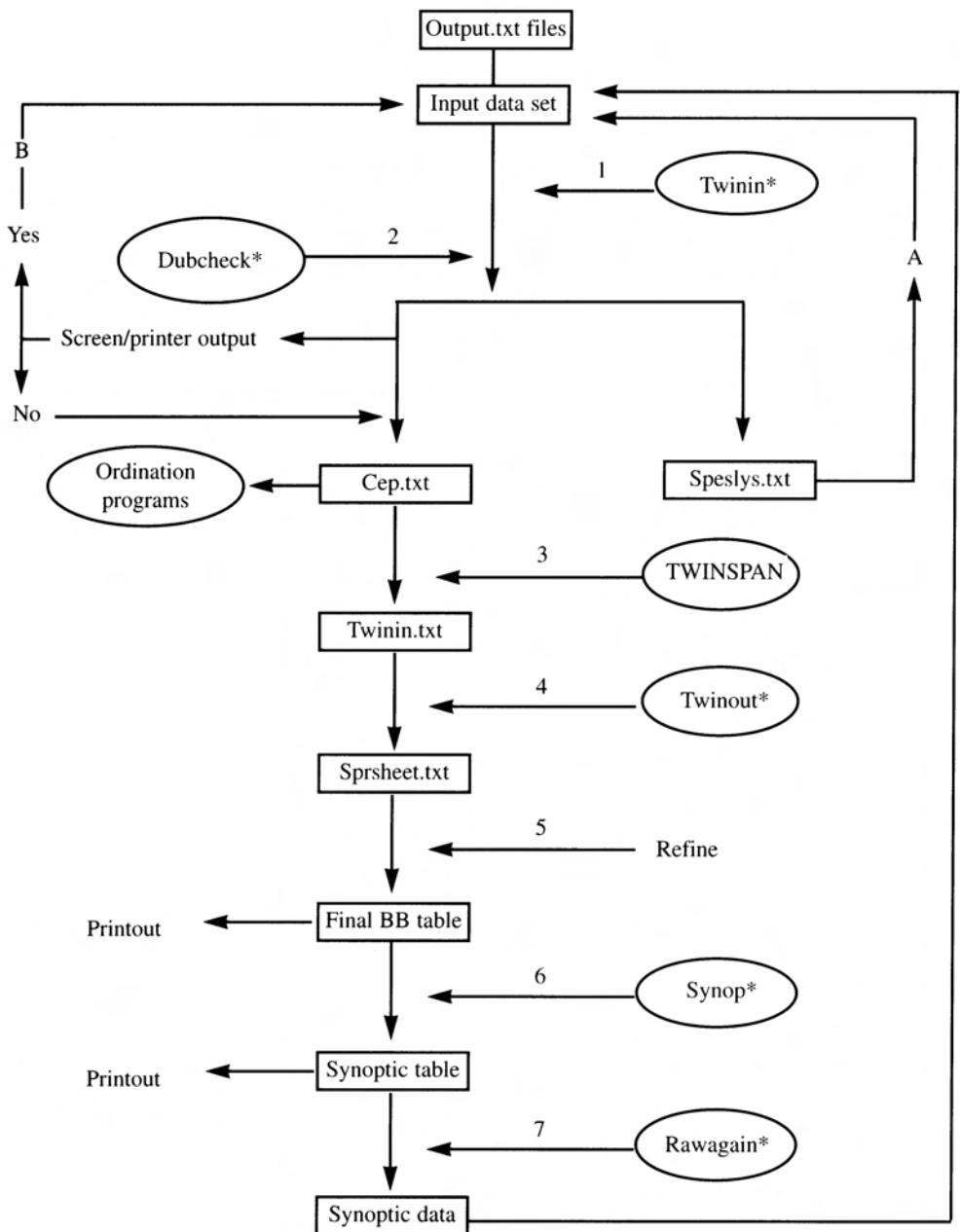
The introduction of the Braun-Blanquet method to South Africa by Werger (1973) helped to standardise the analysis and description of South African phytosociological data sets (Scheepers 1983). Many South African vegetation scientists started to utilise

the Braun-Blanquet methodology, and main-frame programmes were developed for phytosociological table construction and manipulation, eg. Phytotab (Westfall *et al.* 1982). The comprehensive phytosociological research programme on the grassland biome, developed at the University of Pretoria, necessitated the development of a personal computer programme package for widespread use, applying generally available software packages.

The main aim of this paper is to describe an affordable, rapid and efficient process for analysing Braun-Blanquet phytosociological data sets on a personal computer. It describes a suite of utilities joining various phases and this makes the entire process possible.

Computer and accessories

A personal computer (with Intel-type chip), any standard word processing and spread-



- A - Alphabetical species list. Correct mistakes at the input data set.
- B - If there are duplicate species in the data set, these species and the plot number will be printed out. The correction must be made in the input data set. Once there are no duplicate species, continue with step 3
- * Components belonging to the BBPC suite

Fig. 1. Flow chart of the utility BBPC process.

sheet program, as well as TWINSpan (Hill 1979a) are required. The rest of the utilities needed are described in this paper, and are available from H. Bezuidenhout.

Description of input data

Any word processing program can be used provided that the input data can be saved in an ASCII file. If data sets are in different input formats, comparisons or consolidations of these data sets are difficult. Table 1 explains the most widely used (and therefore

the recommended) format of the input data ("raw data") used in South African phytosociological work (e.g. Bezuidenhout 1988; Kooij 1990; Du Preez 1991; Mustart *et al.* 1993). This format is adopted as a standard, enabling the incorporation of different researchers' input data with no problem except the renumbering of sample plots.

Description of programs

Floristic data are analysed in seven steps by using six programmes. The process is represented diagrammatically in Fig. 1.

Table 1
An example of the recommended format for the input data file

Columns									x8
* 4	8	1							
Data									
0001ARIS	ADS1SALS	CAL1TRIB	TER+HERM	QUA+GRAS	HB8+TRAG	BER+LYCI	SMA1ACAC	TOR2	
0001ZIZI	MUC+THES	LIN+TALI	CAF+ZYGO	186+CADA	APH+PROT	SUA+PENT	GLO+ENNE	DES+	
0001PROT	200+LOTO	LIS+BARL	RIG+COMM	PEN+PHAE	SPI+DIOS	LYC+CHLO	VIRRX121	+	
0002ACAC	TOR2PROT	SUA+ENNE	DES2TRAG	BER+ARIS	ADS+TRIB	TER+MONE	INC1PLIN	KAR1	
0002LYCI	SMA+TALI	CAF+EUPH	SPP+CRAS	SPP+GRAS	HB8+MEST	ARB+ZYGO	186+CADA	APH+	
0002EHRE	RIG+FING	AFR+ACAC	MEL+SALS	CAL1BARL	RIG+CENC	CIL+AMAR	PRA+X189	+	
0003ARIS	ADS2PENT	GLO+UROC	MOS+CENC	CIL+TRAG	BER1ENNE	DES1ERAG	HB8+ENNE	CEN+	
0003SALS	CAL+TALI	CAF+LOTO	PLA+HETE	CON+CYMB	PLU+PROT	187+SESA	TRI+BARL	RIG+	
0003KYPH	ANG+LYCI	SMA+EHRE	RIG+ZIZI	MUC+GREW	FLA+ACAC	TOR+NERI	LAT+CADA	APH+	
0003VYGI	HB6+SETA	VERR							
0004ZYGO	1862SALS	CAL2ENNE	DES2PLIN	SER+BARL	RIG+TRAG	BER1SPOR	SPP+PENT	INC+	
0004STAC	SPH+X190	+ERAG	HB8+LYCI	SMA+PROT	187+TARC	CAM+ACAC	TOR+VYGI	191+	
0004X192	+X193	+							
0005ENNE	DES3TRIB	TER+ZYGO	1862BARL	RIG1LYCI	SMA1PENT	GLO+PLIN	SER+TALI	CAF+	
0005LYCI	VET+TRAG	BER+SALS	CAL+PROT	187+					

- * (i) The first four columns (4) on every line represent the sample plot numbers.
- * (ii) The next eight columns (8) of which the first four from the genus name followed by a blank (1) and then the specific epithet in the next three columns.
- * (iii) Collector numbers can be used for genus and species abbreviations.
- * (iv) The next column (1) is for the Braun-Blanquet cover abundance value.
- * (v) Steps numbers (ii - iv) are repeated eight times (x8) on the same line.

Steps above are repeated until all the sample plot data have been entered.

Step 1

The input data is rewritten by the suite component *Twinin* to the Cornell Ecological Programmes (CEP) condensed format (Hill 1979a). The *Twinin* program compiles an alphabetical species list (*Speslys.txt*) in a separate output file. This species list has to be checked and edited thoroughly for spelling mistakes. These corrections are then made manually in the input data file (path A) (Fig. 1).

The CEP format (*Cep.txt*) can be used in most ordination programs such as *CANOCO* (Ter Braak 1987) and *DECORANA* (Hill 1979b).

Step 2

A species name (code) should not be duplicated in the same sample plot. Duplicated species corrupt the *TWINSPAN* classification technique output. The suite component *Dubcheck* scans the input data set for duplicated species. If there are duplicated species in the data set, these species names and the plot number(s) will be printed out and shown on screen. The corrections must then be made manually in the input data set after which *Twinin* should be rerun. Once no further corrections are necessary, step 3 can be followed (path B in Fig. 1).

Step 3

An objective *TWINSPAN* classification algorithm (Hill 1979a) is used for analysing the CEP data (floristic data) as first approximation. The output file (*Twinin.txt*) is an ASCII file (Fig. 1).

Step 4

The suite component *Twinout* converts the *Twinin.txt* (*TWINSPAN* output) to a Braun-Blanquet table format with Braun-Blanquet

cover abundance values as the matrix in a spreadsheet. The output of this program (*Sprsheet.txt*) is an ASCII file which can be transferred to any spreadsheet software package (Fig. 1).

Refinement of the spreadsheet can be done on a maximum of 400 columns (sample plots) and 800 rows (species) due to the fact that the most current version of *TWINSPAN* has this restriction.

Step 5

This step is not represented by a program but is a stage enabling the user to manually refine the *TWINSPAN* classification in the spreadsheet. Whittaker (1980) describes the process of classification of plant communities as an interaction between a phytosociologist and the vegetation. Thus, after this interaction, a final Braun-Blanquet table (Final BB table) can be transferred as an ASCII file to any word processing programme the user prefers. A printout can be made of the final Braun-Blanquet table (Fig. 1).

Normally step 5 constitutes the final step required by most users. However, steps 6 and 7 can be used to consolidate data sets of related plant communities from various studies or to incorporate relevant data into one large data set.

Step 6

A suite component *Synop* can be run on the final Braun-Blanquet table to create a synoptic table output file (Mueller-Dombois & Ellenberg 1974) (Fig. 1).

Step 7

The Synoptic table created with *Synop* is converted into an input data set by the suite component *Rawagain*, enabling the whole process to be re-entered (Fig. 1).

Concluding remarks

When the data is in a CEP-format it can also be used in ISPD (Bosch & Booysen 1992) as well as CANOCO (Ter Braak 1987). According to Westfall *et al.* (1982) the use of DECORANA (Hill 1979b) in ordinating species and communities proved satisfactory. Van der Maarel (1982) recommended ordination as a tool in classification. The efficient creation of the CEP data set is sometimes the only reason why a user will need any of the utilities described here.

The objective classification technique TWINSPLAN can be used as a first approximation as proposed by Bredenkamp *et al.* (1991). Refinement of the result of this first approximation is very important. Efficient ecologically reliable classification is seldom absolutely objective and is usually accomplished with an element of personal judgement (Mueller-Dombois & Ellenberg 1974).

Bredenkamp & Bezuidenhout (1995) discussed the way to handle large data sets in more detail. Du Preez (1991), Fuls (1993) and Bezuidenhout (1993) have used this procedure (Steps 1 - 7) in their studies with success.

Bezuidenhout (1994, 1995) has used the BBPC suite for plant classification with success in national parks, while it is being used by the Potchefstroom University for Christian Higher Education for classification of urban vegetation in the North-West Province (Cilliers & Bredenkamp 1996).

One of the advantages of the BBPC suite is that the programmes can be run on a field computer. The user can then analyse the data and evaluate which vegetation classes need more sample plots. This leads to more efficient time management.

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