

**STATISTICAL METHODS FOR
DIVIDING SITES INTO RECOMMENDATION
DOMAINS ON THE BASIS OF
EXPERIMENTAL RESULTS**

Training Working Document No. 4



CIMMYT

TRAINING WORKING DOCUMENT

**STATISTICAL METHODS FOR
DIVIDING SITES INTO RECOMMENDATION
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PREFACE

This is one of a new series of publications from CIMMYT entitled *Training Working Documents*. The purpose of these publications is to distribute, in a timely fashion, training-related materials developed by CIMMYT staff and colleagues. Some Training Working Documents will present new ideas that have not yet had the benefit of extensive testing in the field while others will present information in a form that the authors have tested and found useful for teaching. Training Working Documents are intended for distribution to participants in courses sponsored by CIMMYT and to other interested scientists, trainers, and students. Users of these documents are encouraged to provide feedback as to their usefulness and suggestions on how they might be improved. These documents may then be revised based on suggestions from readers and users and published in a more formal fashion.

CIMMYT is pleased to begin this new series of publications with a set of six documents developed by Professor Roger Mead of the Applied Statistics Department, University of Reading, United Kingdom, in cooperation with CIMMYT staff. The first five documents address various aspects of the use of statistics for on-farm research design and analysis, and the sixth addresses statistical analysis of intercropping experiments. The documents provide on-farm research practitioners with innovative information not yet available elsewhere. Thanks goes out to the following CIMMYT staff for providing valuable input into the development of this series: Mark Bell, Derek Byerlee, Jose Crossa, Gregory Edmeades, Carlos Gonzalez, Renee Lafitte, Robert Tripp, Jonathan Woolley.

Any comments on the content of the documents or suggestions as to how they might be improved should be sent to the following address:

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RECOMMENDATION DOMAIN CONSTRUCTION AND TESTING

The purpose of identifying recommendation domains must be for making recommendations from current data and for planning and interpreting future experiments. In a general sense every applied scientist must have a concept of a recommendation domain for his/her research. Some concept of the population to which results are relevant is integral to any research (even statistics!)

The data on which the division of sites into groups for potential domains may be some combination of

- (1) economic/sociological: based usually on surveys;
- (2) physical/meteorological/soils/vegetation: based on observation or on records from nearby available sources;
- (3) experimental results.

There is also always potential for general qualitative judgement about site similarities.

There are two stages to the identification of domains, which is a dynamic process rather than a permanent decision. We should separate the process of constructing groups from that of testing, or validating the group structure. The group construction may be attempted using any of the three forms of data. The validation process appears (to me) to be peculiar to experimental data because that data carries with it information about the precision of estimates calculated from the data. It would, of course, be possible to use the precision information inherent in experimental data to test groups (i.e. tentative domains) derived from other forms of data.

1. Group Construction

Many techniques for identifying groups have been tried. These have been based on various forms of cluster analysis, dimension-reducing methods such as principal components analysis, and breaking down the site x treatment interaction variation. The latter, of course, can be used only with experimental data. Cluster analysis or principal components analysis can be applied to any form of multiple measurement data.

The underlying information for all data-based techniques for forming groups must be that contained in the distance matrix for between-site variation. The measurements from which the distances are calculated may be chosen in many ways. For example, for experimental data we could use treatment mean yields for all, or a subset of, treatments, or we could use a defined set of treatment contrasts. Whatever the particular measurements chosen, the between-site distance for each pair of sites is calculated from the squares of difference between the two sites for each of the measurements used. For some forms of measurement, scaling of different measurements may be necessary to make information from different measurements compatible, but this is unlikely to be necessary for measurements based on experimental yield data.

There is no doubt in my mind that the appropriate technique for searching for clusters is some form of cluster analysis, rather than a more indirect method. There are, though, many different forms of cluster analysis and it is important to choose one that tends to form compact clusters. Such is, perhaps surprisingly, not true of all methods. Some, such as single link clustering, tend to produce strings of individuals in a cluster each linked to only one or two other members of the cluster.

The obvious candidate for the choice of clustering method for manual calculation is the average link method. We shall look later at some results using both average-link and complete link clustering with computer packages. Whichever clustering algorithm is used it produces a single clustering structure, regardless of whether there are alternatives which are nearly as good. This is a very clear justification for using more than one clustering method to gain some idea whether there are viable alternatives.

2. Cluster Validity Assessment

Invariably clustering methods produce clusters, or more precisely systems of clusters at various levels of clustering. Because they are thus defined to be successful we cannot assume that the resulting clusters are meaningful. The peculiar advantage of using data derived from experimental data for clustering is that we usually have an estimate of the precision of the experimental results. Hence it is possible to consider testing the validity of the clusters obtained from the clustering process by testing the prediction for the measurement values of a site from the average of other sites in the proposed cluster.

Using the precision of the treatment mean yields, or contrasts, we can test the prediction of the cluster for the individual sites within the cluster. For each site in the proposed cluster we compare, using the precision derived from the experimental error mean squares, the value for that site of each measurement with the value of the measurement predicted by the average of all other sites in the cluster. The significance of the comparison can be assessed by the extent to which the difference between site value and prediction value is large relative to the standard error of that difference.

Such a series of comparisons produces a set of t-values, one for each measurement at each site. Although the values are interdependent we can obtain a rough idea whether the t-values are compatible with the appropriate t-distribution. Significance of individual t-values is not so important as the overall pattern of the set of t-values.

3. Results

Two data sets have been clustered manually using average link clustering. The results are discussed in Documents 4B and 4C. Three further data sets have been clustered using SAS and SPSS average link and complete link clustering algorithms. The results are discussed briefly in Document 4D, which consists mainly of computer output.

CLUSTERING AND VALIDATION EXAMPLE: DATA FROM IPIALES BEANS/MAIZE VERIFICATION TRIAL 1985

The initial data is the mean yield of (3xBeans + Maize) for each of the 8 treatments in each of 7 sites (site 5 had incomplete data)

1. Finding Groups of Sites

	Site						
	1	2	3	4	6	7	8
Treatment							
1	428	165	231	244	536	171	272
2	487	290	342	303	517	310	254
3	352	328	358	315	422	355	202
4	564	328	324	441	479	382	266
5	412	461	531	504	478	248	230
6	556	274	346	350	405	360	290
7	476	436	366	320	484	471	287
8	479	382	420	370	698	256	286

To represent the similarity of the sites in terms of the eight treatment values, we define a distance measure between two sites. This is calculated from the set of differences between the treatment values at the two sites. Thus, for sites 1 and 2 the yield differences for the eight treatments are:

263 (=428-165),
 197
 24
 236
 -49
 282
 40
 97

The total distance measure between sites 1 and 2 is the sum of squares of these distances:

$$69169 + 38809 + 576 + 55696 + 2401 + 79524 + 1600 + 9409 = 257184$$

(strictly the distance is the square root of this quantity, but it is convenient to work with squared distances).

We now calculate the complete set of between site differences:

	Site						
Site	1	2	3	4	6	7	8
1		257184	191312	171327	99871	245577	366779
2			24404	40573	340417	73947	115679
3				22589	249269	126203	155059
4					282134	111892	133400
6						440430	515916
7							90182

(Since the distance between site 2 and site 1 is the same as that between site 1 and site 2 we only need to display half of the matrix.)

We can observe some patterns of similarity and dissimilarity by direct inspection of the matrix. The most similar pair of sites are sites 3 and 4; the pairs (2,3) and (2,4) are also similar, suggesting the beginning of a group (the "inner circle"). At the other extreme the most dissimilar pair are sites 6 and 8 and we can see that site 6 is dissimilar to each other site except site 1. Since site 1 is also fairly dissimilar to all other sites except site 6 this suggests the beginning of another group (the "outcasts").

A simple group selection strategy is to choose the grouping which makes the distances between sites within a group as small as possible and conversely makes the distances between sites in different groups as large as possible. Let us try some possible groupings.

Possible grouping 1) Two groups: (1,2,3,4) and (6,7,8)

<u>Within-group Distances</u>			<u>Between-group Distances</u>		
Group(1,2,3,4)		Group(6,7,8)			
257184	191312	440430	99871	245577	366779
171327	24404	515916	340417	73947	115679
40573	22589	90182	249269	126203	155059
			282134	111892	133400
Means					
117898		348843			191686
194880					

A poor attempt since the mean between-group distance is almost exactly the same as the mean within-group distance.

Possible grouping 2) Two groups: (1,6) and (2,3,4,7,8)

<u>Within-Group Distances</u>			<u>Between-group Distances</u>		
Group(1,6)	Group(2,3,4,7,8)				
99871	24404	40573	257184	191312	171327
	73947	115679	245577	366779	340417
	22589	126203	249269	282134	440430
	155059	111892	515916		
	133400	90182			
Means					
99871	80375			306054	
	82147				

Much better, the ratio between/within is nearly 4:

$$(306054/80375 = 3.8).$$

In fact we can not find a better pair of groups. However we can find a set of three groups which at least deserves comparison with the (1,6),(2,3,4,7,8) grouping.

Possible grouping 3) Three groups: (1,6), (2,3,4) and (7,8)

<u>Within-group Distances</u>			<u>Between-group Distances</u>		
Group(1,6)	Group(2,3,4)	Group(7,8)			
99871	24404	90182	257184	191312	171327
	40573		245577	366779	340417
	22589		73947	115679	249269
			126203	155059	282134
			111892	133400	440430
			515916		
Means					
99871	29189	90182		230409	
	55524				

The ratio between/within is slightly higher. However, we should expect this ratio to increase when groups are split to form more groups, since we will inevitably take the larger between-site distances out of the set of within-group distances to add them to the between-group distances.

There are no general theoretical results about the extent to which we should expect the ratio to increase. The decision about how many groups to select from a clustering system is always rather arbitrary, based largely on experience with other similar data. I think that, with little formal justification I would select (1,6),(2,3,4,7,8) as the best guess of the clustering for this example. However, because we are using experimental data we have the possibility of comparing the agreement between sites in a cluster with the experimental error.

2. Testing the Clusters

Any clustering method will produce clusters and these will be such that the sites within a cluster will be more similar than sites in different clusters. The actual size of the between/within ratio may give an indication of whether the clustering is "genuine", particularly for experienced users of the clustering algorithm. However, the intention of clustering sites is to attempt to define recommendation domains which should be such that the groups of sites we have identified represent a single population and that the sites in a group could have some predictive power for each other.

A reasonable way to test this potential for prediction would be to compare the treatment yields for a site with the means of the yields for that treatment at the other sites in the group. For example we consider site 2 (comparing the treatment means with the average from sites 3,4,7,8).

Site 2 yields	Prediction (3,4,7,8)	Difference
165	230	-65
290	302	-12
328	308	+20
328	353	-25
461	378	+83
274	336	-62
436	361	+75
382	333	+49

These seem to indicate quite good agreement but we should try to test this. To do this we use the standard errors of the mean yields which we can obtain from the analysis of variance for each site experiment.

The Error Mean Square values from the analyses of variance of the plot values of (3xBeans + Maize) are shown.

Site	EMS(on 7 df)
1	9929
2	9167
3	6228
4	1976
6	27828
7	1384
8	2036

Note that the error mean squares are clearly heterogeneous so that combined analyses across sites would be extremely dubious and, in particular, significance tests would not be valid.

The standard error of a treatment mean (based on two plot values) at site 2 is

$$\sqrt{(9167/2)} = 68.$$

The standard error of the average of the corresponding treatment means from sites 3,4,7,8 is

$$\sqrt{(((6228+1976+1384+2036)/16)/2)} = 19.$$

Thus the standard error of the difference between a site 2 treatment mean and the average treatment mean from sites 3,4,7,8 is

$$\sqrt{(9167 + (6228+1976+1384+2036)/16)/2)} = 70.$$

Now we can express each difference between the site 2 value and that predicted from the other sites in the group as a t-statistic.

Site 2 yields	Prediction(3,4,7,8)	Difference t-statistic
165	230	-0.92 (= -65/70)
290	302	-0.17
328	308	+0.29
328	353	-0.36
461	378	+1.19
274	336	-0.89
436	361	+1.07
382	333	+0.70

An overall measure of the agreement is provided by the sum of squares of the t-statistics. Since we would expect each t-statistic to be about 1.0 if the prediction agreement is good the sum of squares should be about 8 (the number of comparisons). In this case the sum of squares is 4.9 confirming that the predictions are reasonable.

The comparisons for other sites are listed below:

Site 3	Prediction (2,4,7,8)	t	Site 4	Prediction (2,3,7,8)	t
231	213	+0.30	244	210	+0.87
342	289	+0.89	303	299	+0.10
358	300	+0.96	315	311	+0.10
324	354	-0.50	441	325	+2.97
531	361	+2.83	504	368	+3.49
346	318	+0.47	350	318	+0.82
366	378	-0.20	320	390	-1.79
420	324	+1.60	370	336	+0.87
SE(diff) = 60			SE(diff) = 39		
sum of t-squares = 12.9			sum of t-squares = 26.4		

Site 7	Prediction (2,3,4,8)	t	Site 8	Prediction (2,3,4,7)	t
171	228	-1.58	272	203	+1.72
310	297	+0.36	254	311	-1.42
355	301	+1.50	202	339	-3.42
382	340	+1.06	266	369	-2.58
248	432	-5.11	230	436	-5.15
360	315	+1.25	290	332	-1.05
471	352	+3.31	287	398	-2.78
256	364	-3.00	286	357	-1.78
SE(diff) = 36		SE(diff) = 40			
sum of t-squares = 53.6		sum of t-squares = 60.6			

Site 1	Prediction (6)	t
428	536	-0.78
487	517	-0.22
352	422	-0.51
564	479	+0.62
412	478	-0.48
556	405	+1.10
476	484	-0.06
479	698	-1.60
SE(diff) = 137		
sum of t-squares = 5.3		

The immediate conclusions are that predictions are acceptable in the (1,6) group but sites 4,7 and 8 are not well predicted in the (2,3,4,7,8) group. We have already noted, however, that the experimental precision is very different in different site experiments and this affects the potential sensitivity if the different prediction tests.

The comparison between sites 1 and 6 (which operates in both directions) is less precise both because of the large standard errors in each site and because the prediction is based on only one site. Nevertheless the agreement is an indication that the group is predictive to the precision that should be expected.

The group (2,3,4,7,8) does not provide adequate prediction and we could look for possible subdivisions of the group. The subdivision considered earlier into (2,3,4) and (7,8) gives the following results for testing prediction:

Site	Prediction	Sum of t-squares
2	(3,4)	4.8
3	(2,4)	3.4
4	(2,3)	8.0
7	8	51.2

It is clear that the grouping (2,3,4) is acceptable (if anything, too good) but that sites 7 and 8, both of which have small error mean squares, are not adequate predictors for each other.

Overall, this data set demonstrates heterogeneity of sites more strongly than anything else, though the (2,3,4) grouping is consistently homogeneous.

3. Alternative Data for Clustering.

Clustering has also been attempted for the Ipiales data for

- (i) bean yields,
- (ii) maize yields,
- (iii) treatment contrasts instead of treatment yields

Detailed results are not given since the cluster patterns are rather less clear, even, than the (3xBeans+Maize) results.

(i) Bean yields.

The distance matrix is shown

Site	Site					
	2	3	4	6	7	8
1	5575	12756	10477	34421	20165	3317
2		3523	3020	18170	8230	14746
3			1189	13835	10275	23573
4				11058	7416	22752
6					10890	51842
7						31024

The best grouping is (1,8) and (2,3,4,6,7) with a between/within ratio of 2.7.

(ii) Maize yields.

The distance matrix (values divided by 100) is shown

Site	Site					
	2	3	4	6	7	8
1	3622	3931	4040	2674	6525	2435
2		411	135	499	650	308
3			169	445	562	211
4				670	410	340
6					1629	282
7						1111

The best grouping is the very uninteresting pattern of (1) and (2,3,4,6,7,8) which gives the large between/within ratio of 7.4. The next best grouping is the (1,6) and (2,3,4,7,8) as in (3xBeans +Maize) with a much smaller ratio of 3.9.

(iii) Treatment contrasts.

In our main analysis the basic data for each site was the set of eight treatment means. Since we are concerned to define recommendation domains an alternative form of data would be to use treatment contrasts. This would eliminate the effect on the clustering process of site mean yields and would be attempting to cluster sites on the basis of similar treatment differences.

The set of treatment comparisons intended for the Ipiales experiments was

- (i) Treatment 3 - Treatment 2
- (ii) Treatment 4 - Treatment 3
- (iii) Treatment 5 - Treatment 4
- (iv) Treatment 6 - treatment4
- (v) Treatment 7 - Treatment 6
- (vi) Treatment 8 - Treatment 6

Note these contrasts are not orthogonal so that they are not independent which may reduce the efficiency of, but in no way invalidate, the clustering process. Also since each contrast is a simple difference between two treatments the treatment contrasts will be less precise than the treatment means.

Reverting to using (3xBeans +Maize) the distance matrix (values divided by 100) is shown:

	Site					
	2	3	4	6	7	8
Site						
1	2510	2459	1969	2150	1044	545
2		342	674	804	1206	866
3			645	1245	1627	787
4				1070	897	323
6					1990	1076
7						455

The best grouping is (1,4,7,8) and (2,3,6) with a between/within ratio of 1.8. It is interesting that the grouping is distinctly different from that using the treatment mean yields, even the (2,3,4) group being now split. However the between/within ratio really is rather low and it was decided not to pursue the testing of groups.

The overall pattern of results from using clustering methods on this set of experimental mean data is not very encouraging. The groupings postulated prior to the experiments were (1,2,3,8), (4,7) with 6 grouped with site 5 for the data was incomplete. The set of site results had been felt to be surprisingly inconsistent with this grouping. The cluster analysis results tend to confirm that the results do not give clear-cut and useful patterns. They are not, of course, less valid and informative because they do not produce clear patterns.

CLUSTERING AND VALIDATION EXAMPLE: DATA FROM GHANA ZERO TILLAGE TRIAL 82 TRIAL 2 (G.EDMEADES)

The data are from 14 sites of an experiment with 18 experimental treatments arranged in four blocks of nine plots per block. The main set of treatments are all combinations of four two-level factors and there are two "satellite" treatments. Details are:

- a) Slashing/no slashing of ground cover,
- b) Two rates of Gramoxone (knock-down herbicide),
- c) Bellater/no Bellater applied (residual herbicide), and
- d) Handweeding/no handweeding.

The satellite treatments are hoeing or scraping prior to handweeding.

The experimental design was a confounded factorial in two blocks of eight treatment combinations, confounding the four-factor interaction between blocks, with one satellite treatment added to each block. The same randomization was utilized at each site with the plot and block configurations also constant across sites.

The data analysis, a summary of which is presented here, is in five stages:

- 1) The initial analysis included the analysis of variance from each site to extract treatment yields and the error mean square.
- 2) A set of eleven effect contrasts were defined and calculated from the treatment mean yields at each site. The use of effects rather than treatment mean yields was to eliminate differences in mean yield between sites and to concentrate the information by ignoring the higher order interactions. The effects used were
 - (1) the difference between the mean of 16 factorial combinations and the mean of 2 satellite treatments (Fact-Sat),
 - (2) the four main effects for the factors,
 - (3) the six interaction effects.
- 3) The inter-site distance matrix, based on sums of squared differences for the eleven effects, was calculated.
- 4) The clustering of sites was investigated both formally through minimizing mean within cluster distance and by considering alternative similar cluster patterns when there were several near alternatives for the optimum clustering.
- 5) The proposed clusterings were tested by assessing, for each site in a cluster, the significance of the deviation for that site from the average of the other sites in the cluster, for each of the eleven effects, using the site error mean squares.

1. The Analysis of Variance and Treatment Means

Treatment means (yields in kg/plot *100, uncorrected for moisture)

Treatment	Site													
	3	4	5	6	7	8	12	13	14	15	16	17	18	21
1111	0	455	150	145	190	195	450	5	170	205	232	160	5	25
1112	95	435	395	325	305	360	600	425	385	455	342	468	200	110
1121	5	462	460	480	280	465	565	60	405	525	240	435	42	302
1122	290	502	465	375	415	470	480	685	415	525	315	470	225	352
1211	5	430	160	310	255	180	540	205	300	340	390	420	30	130
1212	195	460	570	405	430	430	550	660	375	480	355	515	125	138
1221	120	460	255	425	280	500	480	535	385	540	452	535	150	315
1222	335	500	425	285	285	490	490	775	415	545	300	568	245	312
2111	0	425	105	210	245	195	455	10	390	300	428	270	8	142
2112	120	448	355	330	320	360	440	400	300	480	270	398	255	225
2121	5	492	355	490	265	395	495	25	300	495	400	485	185	365
2122	370	390	535	340	240	415	450	630	385	525	302	580	295	410
2211	0	350	90	295	240	265	490	265	230	280	365	245	40	35
2212	270	430	340	360	260	410	575	490	430	400	315	462	115	178
2221	120	415	310	315	295	575	500	475	440	600	252	545	272	345
2222	310	465	445	465	380	440	595	730	355	550	420	490	175	375
S1	385	431	360	405	290	415	320	745	460	535	240	635	102	198
S2	425	425	285	365	420	400	535	650	410	565	318	458	285	258

Site	Error Mean Square
3	2804
4	4689
5	5257
6	11117
7	6342
8	5268
12	13324
13	8722
14	7225
15	7947
16	2859
17	4731
18	8920
21	9240

2. Treatment Contrasts

	CONTRASTS										
	Fact-Sat	Main Effects				Two-factor Interactions					
		A	B	C	D	AxB	AxC	AxD	BxC	BxD	CxD
Site											
3	-365	+18	+58	+108	+216	-8	-5	+20	-5	0	+48
4	+16	-35	-12	+30	+18	-10	-6	-4	+10	+34	-12
5	+16	-43	-28	+135	+205	-13	+53	-2	-67	+35	-83
6	-38	+7	+20	+100	+27	-4	+4	+20	-69	+16	-88
7	-62	-24	+20	+24	+73	+6	+4	-34	-11	-1	-23
8	-24	-4	+54	+170	+76	+27	-20	+26	+10	-13	-106
12	+82	-19	+36	-5	+25	+45	+25	+5	-17	+24	-32
13	-300	-41	+237	+181	+401	-13	-8	-33	+41	-108	+29
14	-80	-2	+22	+64	+58	-2	-32	-28	0	0	-44
15	-97	+2	+28	+171	+84	-20	+7	-14	+13	-29	-88
16	+57	+16	+40	-3	-18	-52	+6	-18	+2	+1	+16
17	-106	-12	+64	+147	+106	-62	+35	-11	-22	-35	-80
18	-46	+40	-8	+102	+112	-28	+26	-29	+32	-71	-40
21	+7	+48	-12	+224	+55	-40	+4	+20	-8	-10	-24

3. The Inter-site Distance Matrix

For each pair of sites the squared distance is calculated as the sum of the squares of the differences in value for all eleven contrasts. Thus for sites 18 and 21 the squared distance is

$$\begin{aligned}
 & (-46 - 7)^2 + (40 - 48)^2 + (-8 - (-12))^2 + \dots + (-40 - (-24))^2 \\
 & = (-53)^2 + (-8)^2 + (4)^2 + (-122)^2 + (57)^2 + (12)^2 + (22)^2 + (-49)^2 \\
 & \quad + (40)^2 + (-61)^2 + (-16)^2 = 29628.
 \end{aligned}$$

The full distance matrix is shown; all values being reduced by a factor of 100 (note the matrix is split in two parts for reasons only of space).

	Site												
	4	5	6	7	8	12	13	14	15	16	17	18	21
Site													
3	1375	1170	1118	802	1071	1825	932	744	719	1756	622	816	1256
4		608	237	133	434	135	3550	178	501	134	575	378	500
5			440	544	442	704	2600	461	467	982	440	454	516
6				203	178	353	3087	128	220	420	246	327	290
7					364	284	2536	41	303	305	309	214	564
8						554	2502	237	112	699	223	286	235
12							3932	391	788	172	827	588	828
13								2469	2086	3944	1825	2321	3042
14									175	373	231	183	424
15										776	65	160	246
16											779	348	665
17												279	370
18													296

The distance matrix contains all the information about the relative similarities and dissimilarities of sites in respect of the eleven contrasts considered. Of course if we change the set of contrasts by omitting or adding contrasts we would change the set of distances, though we would hope that if the patterns of similarity have a genuine basis the patterns of distances would show consistency. We notice immediately that site 13 is very different from all other sites with the possible exception of site 3; that site 3 is not strongly similar to any other site; that site 5 is also not very similar to any other site; and that some sites (4,14,15) are similar to many other sites. In making these semi-quantitative assessments we seem to be identifying values under about 300 as indicating similarity and values over about 600 as indicating dissimilarity.

Continuing subjectively I would guess that possible groupings might be

In 3 groups (4,6,7,12,14,16) ; (5,8,15,17,18,21); (3,13);

In 6 groups (4,12,16) ; (6,7,14) ; (8,15,17,18,21) ; with 3, 5 and 13 isolated.

More formally we may use a system of developing clusters and since we desire that all pairs of sites in a particular cluster be strongly linked the method adopted is to group sites, initially, which are most similar and recalculate distance of a site from a group of sites as the average distance of the site from all sites in the group.

The two smallest distances are 41(sites 7 and 14) and 65(sites 15 and 17). If these two groups are formed then all distances of sites from these groups are recalculated and some of the other small distances become larger. For instance the 112 between sites 8 and 15 now becomes $(112+223)/2 = 168$ between site 8 and group (15,17). In the same way the 128 between sites 6 and 14 becomes $(203+128)/2 = 166$ between site 6 and group (7,14). The distance of site 4 from group (7,14) becomes 156. We could recalculate the complete matrix but shall, to keep the analysis compact make a further grouping first. After the initial two groupings the next grouping is the three-way linking of sites 4, 12 and 16.

The new distance matrix for sites and groups 3, (4,12,16), 5, 6, (7,14), 8, 13, (15,17), 18, 21 is shown:

Site	Site								
	(4,12,16)	5	6	(7,14)	8	13	(15,17)	18	21
3	1652	1170	1118	773	1071	933	670	816	1256
(4,12,16)	620	337	220	562	3809	708	438	664	
5			440	502	442	2600	454	454	516
6				166	178	3087	233	327	290
(7,14)				300	2502	254	198	494	
8						2502	168	286	235
13							1956	2321	3042
(15,17)							220	308	
18									296

The next two joins are site 6 with group (7,14) and site 8 with group (15,17) and these two groupings, being quite separate can be made together, giving the new distance matrix shown

Site	Site						
	(4,12,16)	5	(6,7,14)	(8,15,17)	13	18	21
3	1652	1170	888	804	933	816	1256
(4,12,16)	620		259	659	3809	438	664
5			481	450	2600	454	516
(6,7,14)				251	2697	241	426
(8,15,17)					2138	242	284
13						2321	3042
18							296

The distances between (6,7,14),(8,15,17) and 18 are all now very similarly small and this is the next grouping

Site	Site				
	(4,12,16)	5	(6,7,8,14,15,17,18)	3	21
3	1652	1170	842	933	1256
(4,12,16)		620	456	3809	664
5			464	2600	516
(6,7,8,14,15,17,18)			2404	306	
13					3042

The subsequent joins, for which the revised distance matrices are not shown are

21 joins (6,7,8,14,15,17,18),

5 joins (6,7,8,14,15,17,18,21)

(4,12,16) joins (6,7,8,14,15,17,18,21)

and 3 joins 13.

5. Testing the Clusters

The method of testing the membership of clusters involves comparing the observed value of each contrast at a site with the mean value predicted for the contrast by the other sites in the putative cluster. The form of the test is to calculate the ratio of the difference between site and predicted values to the standard error of that difference. The standard error is calculated from the error mean squares obtained in section 1 from the analysis of variance at each site. For example for comparing values for site 4 and the mean of sites 12 and 16 we need the error mean squares for those three sites:- 4689, 13324 and 2859. The variance of a difference between site 4 and (12,16) is

$$4689 + (13324 + 2859)/4 = 8734.$$

The standard error of a difference for a factorial main effect or interaction is

$$\sqrt{(2(8734)/16)} = 38.$$

The standard error for comparing the mean of the factorial treatments with the mean of the satellite treatments is

$$\sqrt{(8734/32 + 8734/4)} = 50.$$

Initially we shall test the clusters (4,12,16) , (6,7,14) and (8,15,17,18,21).

Contrast	Site 4	Prediction (12,16)	Difference	t-value
F-S	+16	+70	-54	-1.08
A	-35	-2	-33	-0.87
B	-12	+38	-50	-1.32
C	+30	-4	+34	+0.89
D	+18	+2	+14	+0.37
AB	-10	-4	-6	-0.16
AC	-6	+16	-22	-0.58
AD	-4	-6	+2	+0.05
BC	+10	-8	+18	+0.47
BD	+34	+12	+22	+0.58
CD	-12	-8	-4	-0.11

An overall summary of the agreement is provided by the sum of squares of the t-values which in this case is 5.5. Formal theory for testing this criterion is not, I think, available but, since the t-values should be about 1.0, if the sum of squares is less than 11.0 that must indicate an excellent agreement. If the sum of squares is greater than the 5% point of the chi-square distribution on 11 df then the agreement is becoming dubious at something like the 5% significance level (though the theoretical arguments behind this assertion are very approximate).

The unsigned t-values for sites 12 and 16 compared with (4,16) and (4,12) respectively are shown with the site 4 values repeated:

	Site 4	Site 12	Site 16	
	1.08	0.17	0.71	
	0.87	1.43	0.20	
	1.32	0.93	0.50	
	0.89	0.50	0.43	
	0.37	1.33	0.57	
	0.16	2.33	1.73	
	0.58	0.13	0.57	
	0.05	0.60	0.36	
	0.47	0.20	0.52	
	0.58	0.93	0.18	
	0.11	1.27	0.77	
SS(t)	5.5	13.3	5.6	Total 24.4

Both the individual t-value and the SS(t) give no reason to be unhappy about this cluster.

For the possible cluster (6,7,14) there are no t-values above 1.57 and the SS(t) are 8.5 for site 6, 2.8 for site 7 and 6.4 for site 14. The agreement is only worrying in the sense that it is too good!

For the possible cluster (8,15,17,18,21) there are four t-values in excess of 2.0, with no site having more than one. The SS(t) are 13.2 for site 8, 3.6 for site 15, 15.4 for site 17, 12.3 for site 18 and 12.8 for site 21. This cluster therefor gives almost exactly the degree of agreement which should be expected.

The further steps in testing involve either combining two of these three acceptable groups together or adding site 5 to one of the groups or testing the (3,13) group.

The (3,13) group test (which is identical in both directions) gives two t-values over 4.5 (for main effects B and D and a t-value of 2.7 for the BxD interaction. The SS(t) is 63.4 and the disagreement between the sites is very significant.

Adding site 5 to that group to which it seems closest, namely (8,15,17,18,21) gives SS(t) of 41.5 with a t-value of 4.4 for main effect D and three other t-values of 2.0 and over. It seems that site 5 is not sufficiently like this group nor either of the others.

Finally we try to combine groups. Clearly, from the distance matrix, group (6,7,14) could combine with either (4,12,16) or (8,15,17,18,21) but the latter two are further apart. We therefore try combining (6,7,14) with each in turn.

For the combination (4,6,7,12,14,16) the SS(t) for the six sites are shown:

Site	SS(t)	Comments
4	6.6	max t-value of 1.4 for B
6	11.1	t-values of 1.95, 1.65 for C and BxC
7	7.8	max t-value of 1.7 for D
12	7.3	max t-value of 1.6 for F-S
14	8.2	max t-value of 1.8 for F-S
16	28.6	t-values between 2.0 and 2.5 for F-S, D, AxB and CxD

The total of the 6 SS(t) is 69.6 which is about what should be expected. Also there are only 4 out of 66 t-values which could possibly be viewed as significant at 5% and the largest of these is 2.46. Therefore in spite of the discrepancy for site 16 this cluster is acceptable.

For the combination (6,7,8,14,15,17,18,21) the SS(t) for the eight sites are shown

Site	SS(t)	Comments
6	8.2	max t-value of 1.8 for BxC
7	21.1	a large t-value of 3.7 for C
8	15.4	several t-values of 1.7 or 1.8 (C,AxB,CxD)
14	11.0	one large t-value of 2.6 for D
15	5.1	max t-value of 1.5 for C
17	13.7	max t-value of 1.96 for AxB
18	10.8	max t-value of 1.7 for BxD
21	35.3	a large t-value of 4.8 for C and a smaller one of 2.2 for D

The total SS(t) is 120.5 which is about the approximate 5% significance level. On the other hand there are only four individually significant t-values out of 88 which suggests that we have two bad predictions, both for the main effect of C. I wouldn't feel bad about accepting this as a viable cluster. As in many clustering situations there are almost equally convincing alternative sets of clusters. Marginally I still feel that the (6,7,14) group goes better with (4,12,16).

My conclusion would, therefore, be that there are two main clusters

(4,6,7,12,14,16), (8,15,17,18,21).

If the other sites have to be grouped in some manner the best clustering is

(4,6,7,12,14,16), (5,8,15,17,18,21), (3,13).

Finally it is interesting to compare the observed distribution of the set of t-values in a cluster with the expected proportions for the t-distribution on 15df:

Expected Proportion	t-distribution				
	.0 to 0.69 50%	0.69 to 1.34 30%	1.34 to 1.75 10%	1.75 to 2.13 5%	over 2.13 5%
Cluster					
(4,12,16)	20(60%)	10(30%)	2(7%)	0	1(3%)
(6,7,14)	21(64%)	10(30%)	2(7%)	0	0
(8,15,17, 18,21)	23(42%)	22(40%)	6(11%)	3(5%)	1(2%)
(5,8,15, 17,18,21)	27(41%)	19(29%)	10(15%)	6(9%)	4(6%)
(4,6,7,12, 14,16)	36(55%)	17(26%)	6(9%)	4(6%)	3(4%)
(6,7,8,14, 15,17,18,21)	40(45%)	31(35%)	9(10%)	4(5%)	4(5%)

In each case the distribution of t-values is very close to that which should be expected, the agreement in the last case being startlingly good and perhaps pushing the preference back towards to accepting (6,7,8,14,15,17,18,21) and (4,12,16) as the better system of clusters.

CLUSTERING USING COMPUTER PACKAGES

Three data sets have been clustered using the SAS and SPSS packages. The primary objective was simply to demonstrate the equivalent computer procedure to the manual calculations described in documents 4B and 4C. Some comments on the procedures and results are included here, together with some brief further analysis and some suggestions on extensions to the analysis.

The experimental data on which these analyses are based are from three years of an experiment in Ghana on "Factors of Production" (data supplied by Greg Edmeades). The experimental design was two replicates of a 2⁴ factorial in four blocks of eight plots per block, with the four-factor interaction confounded in each replicate. The treatment factors were

1) Variety

V1 La Posta

V2 Local variety (was an improved variety in 1979)

2) Weed Control

W1 1 weeding (6 weeks)

W2 2 weedings (3 & 6 weeks)

3) Plant Density

D1 25,000 plants/ha

D2 50,000 plants/ha

4) Fertilizer

F1 No Fertilizer

F2 At sowing and after 4 weeks

The numbers of sites were 24 in 1979, 12 in 1980 and 7 in 1981. Sites were not repeated in different years.

The information extracted from each site was, first the set of 16 treatment mean yields, and subsequently the estimates of the four main effects and the six two-factor interactions

The three analyses are discussed in reverse chronological order, or equivalently in order of increasing size.

1. The 1981 Experiment

The values of the ten effects for the seven sites are given in Table 1. The distance matrix and the dendrograms for Average Linkage and for Complete Linkage provided by SPSS are given in Tables 2 and 3.

The distance matrix shows small distances for (1,4), (1,7), (2,7), (4,7) (3,6) and (3,7) with large distances between 5 and each of 2,3,6 and 7. The pattern of clusters appears more compact from the Complete Linkage and the two cluster structure is used for further analysis.

Distances (not squared) between sites, between sites and the cluster centroids (averages) and between the two cluster centroids are shown below

Site/Cluster	Site							Cluster	
	1	2	3	4	5	6	7	C1 (145)	C2 (2367)
1		206	196	76	196	181	118	81	147
2			182	195	309	172	180	215	123
3				174	309	139	140	217	92
4					156	166	121	51	135
5						296	264	114	278
6							119	203	81
7								158	85
C1									178

This set of distances displays the pattern one might expect. The centers of clusters are nicely closer to each site in the cluster than most of the distances between sites within a cluster. In each cluster the least close site is on the opposite side of the cluster from the alternative cluster. Site 4 is almost as close to the "wrong" cluster as one of the members of that cluster (site 2). All these are typical patterns after a clustering.

2. The 1980 Experiment.

The values of the ten effects for the 12 sites are shown in Table 4. The distance matrix and dendrograms for Average Linkage and Complete Linkage are shown in Table 5. This time the more compact clusters are obtained with the Average Linkage clustering and we shall assume clusters of (3,4,6,8,10,11,12) and (2,5,7,9) with site 1 as unclusterable. The set of distances between sites, between sites and clusters and between clusters are shown.

Sites	Sites												Clusters	
	1	2	3	4	5	6	7	8	9	10	11	12	C1	C2
1		297	291	312	382	245	355	296	335	209	200	241	244	338
2			144	140	163	105	133	141	112	137	123	166	109	88
3				153	252	108	213	99	183	160	172	94	95	184
4					209	129	186	129	117	142	140	134	95	136
5						227	88	221	158	218	217	275	217	87
6							188	92	134	116	116	79	51	150
7								176	117	190	195	237	180	56
8									147	144	160	97	56	153
9										166	171	180	133	81
10											89	129	86	163
11												146	97	163
12													64	203
C1														144

All the cluster 1 sites are clearly not in cluster 2 and only site 2 from cluster 2 is a candidate for cluster as an alternative. The neat dividing distance of 100 for being in or out of a cluster is coincidental and rather less than the corresponding distance of 125 for the 1981 data.

3. The 1979 Experiment

Tables 6, 7, and 8 give the effects data for each site, the distance matrix (two and a bit sheets) and the two dendrograms. The two clustering methods both give interesting, and interestingly different cluster patterns. Somewhat arbitrarily I have chosen to use the average linkage clusters (1,3,9,12,22), the big cluster (7,13,15,17,18,19,20,21,23,24), (4,5,6,8,11,14) and (2,10) with 16 as an outsider.

It would be interesting to look at the site and cluster distances but too long(!) and really several different clusterings should be examined. So instead I shall use the unusual circumstance of having the same set of treatment effects for all three years and compare the ten groups (two in 1981, three in 1980 and five in 1979.)

Group	Size	Effect Means									
		F1	F2	F3	F4	F1F2	F1F3	F1F4	F2F3	F2F4	F3F4
81(1)	3	-67	-28	-51	-123	-3	+7	+30	+2	+2	+22
81(2)	4	-134	-22	-25	-278	-17	-1	+24	+5	+1	+8
80(1)	7	-81	-9	-39	-74	-9	+11	+15	-11	-3	+1
80(2)	4	-112	-23	-40	-206	+15	+27	+36	+10	-28	+14
80(3)	1	-238	-38	-104	+94	-17	+22	+24	+20	-12	-6
79(1)	5	+131	-49	-91	-85	+42	+20	-8	-12	-18	+51
79(2)	10	+13	-25	-39	-48	+7	+6	+1	-8	-2	+20
79(3)	6	+29	-36	-57	-174	-20	+28	-23	+24	+8	+26
79(4)	2	+11	-5	-46	-209	-48	-6	-56	-67	+2	+82
79(5)	1	+3	-21	-71	-284	+44	+33	+39	-2	-33	+118

These means tell us quite a lot about the three sets of clusters. First, of course the clustering is dominated by the main effects of factors 1 and 4. Second, 1979 is different in the main effect of factor 1, though notice how the correlation between main effects 1 and 4 has the same pattern in 1979 as in the other two years. Third, although the 1979 clusters are different from those for the other two years the third 1980 cluster (site 1) is even more different from the rest. Notice also the much stronger interactions in 1979.

We finish with the distance matrix between clusters

	1981		1980			1979				
	C1	C2	C1	C2	C3	C1	C2	C3	C4	C5
1981(1)		178	63	104	285	219	115	126	179	211
1981(2)			213	93	396	346	276	206	211	198
1980(1)				145	243	235	183	192	208	266
1980(2)					335	286	208	166	201	179
1980(3)						420	301	383	426	472
1979(1)							146	124	229	257
1979(2)								140	200	268
1979(3)									131	179
1979(4)										180

We observe that clusters 1 in 1981 and 1980 are strikingly similar and that cluster 2 in 1980 is midway between clusters 1 and 2 in 1981. Clusters in 1980 mostly far from those in 1979, compared with distances between the 1979 clusters and cluster 2 in 1981 is similarly far from the 1979 clusters.

As the students always say "No time"!

Table 1

	F1	F2	F3	F4	F1F2	F1F3	F1F4	F2F3	F2F4	F3F4
S1	-122.0	-46.0	-87.0	-156.0	-15.5	3.0	42.0	33.5	21.0	37.0
S2	-170.5	38.0	-10.5	-257.5	-61.5	-10.0	99.5	42.5	-29.0	-55.5
S3	-86.0	-24.0	-48.0	-337.0	-28.0	13.5	33.0	-2.5	1.0	17.0
S4	-79.5	-36.0	-43.5	-167.5	3.0	10.5	32.0	16.5	-2.5	13.0
S5	-0.5	1.5	-21.5	-44.5	2.5	7.5	16.0	-11.0	-12.5	16.0
S6	-159.5	-19.0	9.5	-278.0	29.5	-22.0	68.0	-22.0	23.5	39.5
S7	-128.5	-81.0	-50.0	-239.5	-6.5	15.5	97.0	3.0	10.0	32.5

***** HIERARCHICAL CLUSTER ANALYSIS *****

AVERAGE LINKAGE

81T2FP

Data Information

7 unweighted cases accepted.
0 cases rejected because of missing value.

Squared Euclidean measure used.

1 Agglomeration method specified.

Squared Euclidean Dissimilarity Coefficient Matrix

Case	1	2	3	4
2	42291.2500			
3	38505.5000	32988.7500		
4	5846.5000	38153.2500	30297.0000	
5	38304.7500	95343.5000	95729.7500	24390.7500
6	32750.2500	29549.0000	19398.7500	27623.2500
7	13942.2500	32316.0000	19479.2500	14711.2500

Case	5	6
6	87457.0000	
7	69708.0000	14227.0000

Dendrogram using Average Linkage (Within Group)

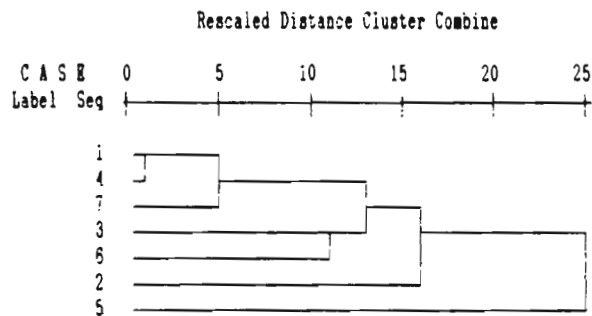


Table 3

***** HIERARCHICAL CLUSTER ANALYSIS *****

COMPLETE LINKAGE

81727P

Data Information

7 unweighted cases accepted.
0 cases rejected because of missing value.

Squared Euclidean measure used.

1 Agglomeration method specified.

Squared Euclidean Dissimilarity Coefficient Matrix

Case	1	2	3	4
2	42291.2500			
3	38505.5000	32988.7500		
4	5846.5000	38153.2500	30297.0000	
5	38304.7500	95343.5000	95729.7500	24390.7500
6	32750.2500	29549.0000	19398.7500	27623.2500
7	13942.2500	32316.0000	19479.2500	14711.2500

Case	5	6
6	87457.0000	
7	69708.0000	14227.0000

Dendrogram using Complete Linkage

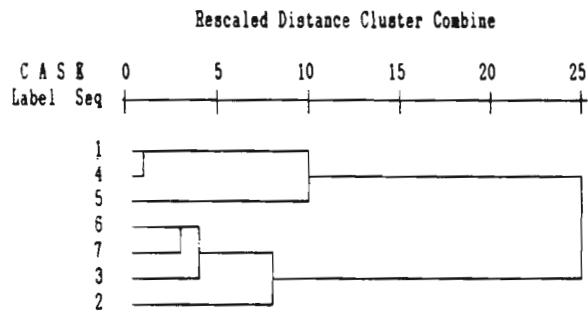


Table 4

	F1	F2	F3	F4	F1F2	F1F3	F1F4	F2F3	F2F4	F3F4
S1	-238.5	-38.5	-103.5	94.0	-17.0	21.5	23.5	20.5	-11.5	-5.5
S2	-85.0	-24.5	-46.0	-142.5	7.5	43.0	48.5	6.0	-64.0	-22.0
S3	-53.5	-12.0	27.0	-73.5	-51.5	-17.0	12.5	-14.0	-37.0	-16.0
S4	-46.0	11.5	-68.0	-124.5	17.0	12.5	-28.5	-45.5	7.5	13.0
S5	-162.5	5.5	-24.0	-264.5	28.0	48.5	20.5	16.5	-20.0	7.5
S6	-72.0	-25.5	-29.5	-63.5	-3.0	30.5	37.0	11.5	-24.5	27.0
S7	-138.0	-46.0	-30.5	-234.5	6.5	8.5	53.5	1.0	-11.5	18.0
S8	-60.0	-20.5	20.5	-94.5	8.0	-10.0	36.5	-6.0	26.5	13.5
S9	-61.5	-26.5	-77.5	-181.0	13.5	7.5	23.5	18.0	-17.0	51.0
S10	-131.5	-6.5	-80.5	-74.5	-26.0	30.0	24.0	5.5	23.5	-29.5
S11	-144.5	-17.5	-79.5	-64.0	31.5	33.5	13.0	-26.0	-27.0	-23.5
S12	-57.5	4.0	-19.5	-24.5	-24.0	-5.5	11.0	-5.0	3.0	22.5

AVERAGE LINKAGE

80T27P

Data Information

12 unweighted cases accepted.
0 cases rejected because of missing value.

Squared Euclidean measure used.

1 Agglomeration method specified.

Squared Euclidean Dissimilarity Coefficient Matrix

Case	1	2	3	4
2	87923.0000			
3	84758.0000	20780.5000		
4	97559.0000	19564.0000	23291.5000	
5	145574.7500	26425.2500	63715.2500	43592.7500
6	59939.0000	11073.5000	11681.0000	16731.5000
7	125951.5000	17573.0000	45250.0000	34875.0000
8	87388.0000	19915.0000	9729.5000	16686.0000
9	112129.0000	12634.0000	33610.0000	13784.5000

Page 3 SPSS/PC+ 4/4/90

Case	1	2	3	4
10	43780.5000	18873.0000	25515.0000	20100.5000
11	40150.0000	15195.5000	29483.5000	19612.0000
12	58244.2500	27535.7500	8889.2500	17856.7500

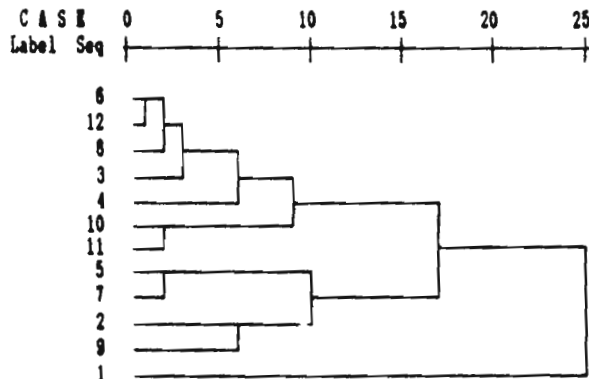
Case	5	6	7	8
6	51565.2500			
7	7768.7500	35225.0000		
8	48845.2500	8481.0000	31082.0000	
9	24863.2500	17879.5000	13662.0000	21504.5000
10	47700.2500	13348.0000	36128.0000	20827.0000
11	47243.2500	13558.5000	37907.5000	25707.5000
12	75574.0000	6163.2500	56400.2500	9435.2500

Case	9	10	11
10	27531.5000		
11	29359.5000	7939.0000	
12	32275.2500	16855.2500	21253.7500

Page 4 SPSS/PC+ 4/4/90

Dendrogram using Average Linkage (Within Group)

Rescaled Distance Cluster Combine



Dendrogram using Complete Linkage

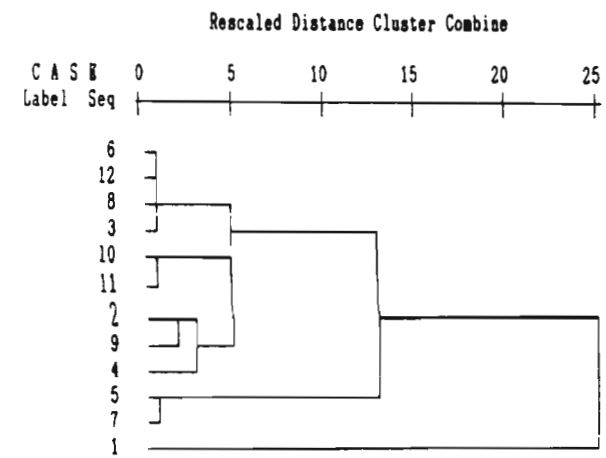


Table 6

	F1	F2	F3	F4	F1F2	F1F3	F1F4	F2F3	F2F4	F3F4
S1	133	-19	-100	-154	69	11	-27	18	-4	93
S2	15	-21	-20	-227	-68	-34	-99	-44	41	86
S3	145	-29	-161	-28	38	25	-25	-8	44	22
S4	63	-33	-5	-108	-14	57	-24	8	-5	-32
S5	52	-114	-48	-178	-12	42	24	67	7	23
S6	102	-107	-107	-234	-14	-14	-79	59	32	52
S7	8	-58	34	-51	34	76	40	-2	11	87
S8	-26	-60	-91	-155	-35	7	-30	16	37	37
S9	129	-65	-70	-133	47	12	-35	-34	-7	44
S10	7	11	-71	-192	-28	21	-14	-90	-36	79
S11	30	-37	-70	-137	-7	64	-37	11	-15	30
S12	119	-30	-81	-35	63	49	29	19	-60	44
S13	17	-11	-18	-92	41	-67	-11	-52	12	-21
S14	-46	-50	-22	-232	-40	10	7	-15	-5	52
S15	-9	-29	-41	-48	20	-32	10	-8	-64	46
S16	3	-21	-71	-284	44	33	39	-2	-33	118
S17	0	9	2	-13	-3	-6	-3	-11	11	-11
S18	-1	-36	-106	-67	-63	8	-12	-29	-23	18
S19	47	-3	16	-47	-3	16	-35	-22	-10	22
S20	44	4	-80	-10	19	14	3	8	11	12
S21	-37	-23	-55	-45	46	-17	-3	-9	-5	71
S22	130	-105	-41	-73	-5	1	19	-54	-61	50
S23	47	-43	-128	-65	-13	60	28	24	-2	-39
S24	15	-61	-12	-45	-10	12	-5	18	34	13

AVERAGE LINKAGE

79T1FF

Data Information

24 unweighted cases accepted.
0 cases rejected because of missing value.

Squared Euclidean measure used.

1 Agglomeration method specified.

Squared Euclidean Dissimilarity Coefficient Matrix

Case	1	2	3	4
2	57553.0000			
3	29023.0000	102040.0000		
4	40977.0000	52400.0000	46778.0000	
5	36411.0000	54690.0000	63328.0000	22614.0000
6	30030.0000	38145.0000	65959.0000	52369.0000
7	56311.0000	79800.0000	70356.0000	29698.0000
8	43414.0000	27589.0000	57615.0000	27029.0000
9	9136.0000	49873.0000	24969.0000	23641.0000

Page 3 SPSS/PC+ 4/3/90

Case	1	2	3	4
10	41623.0000	24858.0000	78506.0000	40962.0000
11	24946.0000	37547.0000	41047.0000	10391.0000
12	24993.0000	107850.0000	23272.0000	31974.0000
13	49364.0000	51401.0000	54731.0000	25605.0000
14	60979.0000	22660.0000	108542.0000	39266.0000
15	47085.0000	66672.0000	55554.0000	30150.0000
16	41978.0000	50335.0000	113241.0000	70389.0000
17	66689.0000	73028.0000	54576.0000	20396.0000
18	51703.0000	51780.0000	41516.0000	25126.0000
19	44507.0000	53046.0000	46944.0000	11082.0000
20	39881.0000	81512.0000	20886.0000	22818.0000
21	45925.0000	63124.0000	51800.0000	36984.0000
22	35421.0000	75356.0000	40712.0000	30964.0000
23	46291.0000	89504.0000	25754.0000	20362.0000
24	49883.0000	58326.0000	44144.0000	13154.0000

Case	5	6	7	8
6	24445.0000			
7	40326.0000	94559.0000		
8	19613.0000	30688.0000	46159.0000	

Page 4 SPSS/PC+ 4/3/90

Case	5	6	7	8
9	29539.0000	30630.0000	45317.0000	36354.0000
10	50150.0000	59209.0000	55470.0000	27269.0000
11	16477.0000	33756.0000	30985.0000	11242.0000
12	46016.0000	78185.0000	35608.0000	60861.0000
13	52167.0000	73034.0000	43939.0000	33114.0000
14	27098.0000	47875.0000	51448.0000	15759.0000
15	45786.0000	80499.0000	26866.0000	32347.0000
16	41643.0000	52792.0000	71555.0000	43874.0000
17	57928.0000	99853.0000	26648.0000	39341.0000
18	39772.0000	62839.0000	43804.0000	16073.0000
19	46052.0000	76121.0000	20546.0000	36555.0000
20	49040.0000	79829.0000	30980.0000	35297.0000
21	49738.0000	80541.0000	22410.0000	26741.0000
22	38988.0000	82397.0000	40046.0000	53787.0000
23	30350.0000	63711.0000	47516.0000	28229.0000
24	28138.0000	63805.0000	16672.0000	21635.0000

Case	9	10	11	12
10	35491.0000			
11	18510.0000	21721.0000		

Table 7 (con't)

Page 5 SPSS/PC+ 4/3/90

Case	9	10	11	12
12	22389.0000	63570.0000	30261.0000	
13	31608.0000	39655.0000	33014.0000	47973.0000
14	52721.0000	18552.0000	24475.0000	86774.0000
15	37025.0000	37778.0000	25519.0000	27674.0000
16	53716.0000	26915.0000	40170.0000	83001.0000
17	49427.0000	55448.0000	32489.0000	40426.0000
18	36995.0000	28132.0000	15863.0000	39672.0000
19	28513.0000	40030.0000	20443.0000	29672.0000
20	32559.0000	53472.0000	23891.0000	17430.0000
21	40513.0000	39584.0000	26081.0000	35368.0000
22	15135.0000	48426.0000	33411.0000	21184.0000
23	35347.0000	55480.0000	18249.0000	24638.0000
24	33615.0000	51744.0000	19105.0000	34290.0000
Case	13	14	15	16
14	44907.0000			
15	17773.0000	44966.0000		
16	76324.0000	22265.0000	68627.0000	
17	14833.0000	60100.0000	14856.0000	103831.0000
18	29035.0000	39072.0000	16578.0000	74059.0000

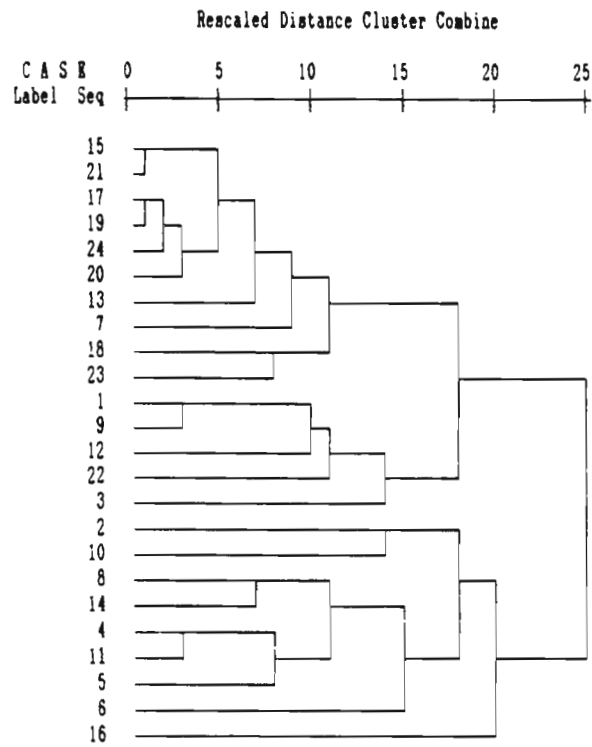
Page 6 SPSS/PC+ 4/3/90

Case	13	14	15	16
19	16779.0000	50670.0000	15608.0000	84117.0000
20	23453.0000	69562.0000	16066.0000	93017.0000
21	19829.0000	45490.0000	6202.0000	66291.0000
22	40509.0000	65754.0000	29658.0000	80543.0000
23	41615.0000	61304.0000	33160.0000	84015.0000
24	20167.0000	44090.0000	16880.0000	83553.0000
Case	17	18	19	20
18	22804.0000			
19	6864.0000	23104.0000		
20	10504.0000	17096.0000	14016.0000	
21	16172.0000	20670.0000	19610.0000	14892.0000
22	46636.0000	33650.0000	28772.0000	36240.0000
23	32112.0000	16144.0000	34566.0000	14338.0000
24	8668.0000	18558.0000	9758.0000	12454.0000
Case	21	22	23	
22	44604.0000			
23	36754.0000	39478.0000		

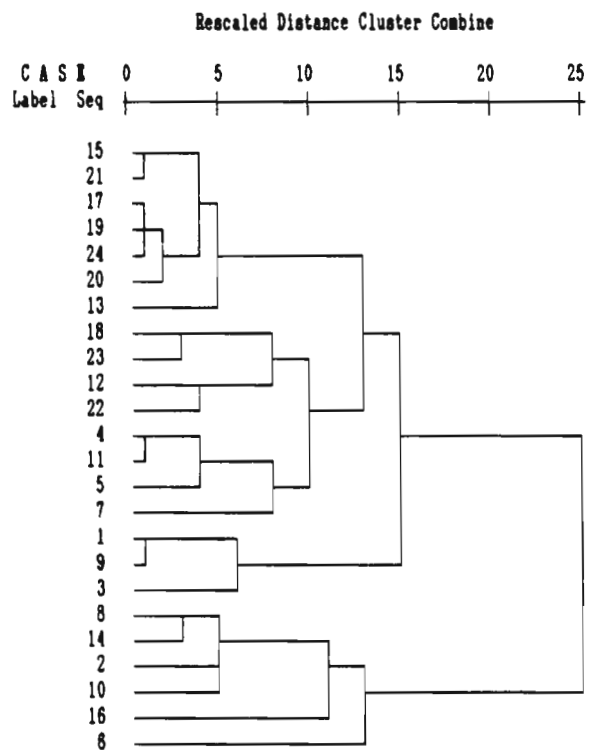
Page 7 SPSS/PC+ 4/3/90

Case	21	22	23
24	15592.0000	33086.0000	22642.0000

Dendrogram using Average Linkage (Within Group)



Dendrogram using Complete Linkage





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