

Pattern Recognition: AMOEBA Extension

Honors Program

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ABSTRACTS

Descriptive: The general field of pattern recognition is discussed with emphasis on the development of AMOEBA, a two dimensional digital clustering program, into a three dimensional program. Moreover, a program analyzing phenyl rings from X-Ray Crystallographic analysis of organic molecules is discussed. Finally, the report analyzes the steps involved in writing a pattern recognition program.

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Informative: Pattern recognition is the general scientific field dealing with computer aided analysis of information. Aspects of a computer, such as pipeline, data storage, processor, and mainframe, are described in this report. In addition, the general relationship between the researcher and the computer is explored using interactive techniques.

AMOEBA, a two dimensional digital digital clustering program written by Dr. Jack Bryant in 1972, is explained based on its unique five-point gradient technique. Moreover, the use of the Kth nearest neighbor method is discussed.

Phenyl ring identification is mentioned as an additional project used to train myself in writing a pattern recognition program.

Although the complete conversion of AMOEBA to a three dimensional digital clustering program was not accomplished, I managed to learn the necessary steps involved in developing such a program. These steps include, the choice of data units, the choice of variables, what to cluster, clustering criterion, homogenization of variables, similarity measures, algorithm and computer implementation, number of clusters, and interpretation of results.

The development of AMOEBA, as well as the development of the phenyl ring identification program, is delineated as per each step in the designing process. Starr is the current version of AMOEBA in three dimensions and is briefly discussed. Moreover, the phenyl ring program, Findp, is also discussed. Thus, two pattern recognition programs are studied within this report.

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FOREWORD

The purpose of this report is to outline my progress in understanding the development of the three dimensional pattern recognition computer program AMOEBA. The scope of the report includes my understanding of the general scientific research field of pattern recognition, of the two dimensional digital clustering program AMOEBA, of Starr, the first attempt at extending AMOEBA, of Findp, the three dimensional program analyzing phenyl rings, and of the nine step process involved in writing a pattern recognition program.

I began working on this project last summer at Cornell University. The National Science Foundation provided me with a research grant in the form of the Supercomputing Program for Undergraduate Research (SPUR). SPUR was a one month program involving nineteen students chosen nationally. SPUR provided me with the basic supercomputing skills I need to do research in the field of pattern recognition. Cornell also gave me free access to their IBM 3090 Supercomputer. This has been a valuable resource with which to do research.

Moreover, Dr. Jack Bryant of the Texas A&M University Mathematics Department approached me last year with an opportunity to work for him. Under his guidance, I became involved in the Texas A&M University Undergraduate Fellows Research Program. In addition, I acquired an additional advisor in the Department of Chemistry, Dr. John Fackler, Dean of the College of Science.

Thus, my project will be sent to the National Science Foundation, Cornell University, the Texas A&M Honors Department, Dr. John Fackler, and Dr. Jack Bryant.

SUMMARY

This report deals with the progression of my understanding of the general scientific field of pattern recognition. In the report, I explain the basic concepts necessary for understanding a pattern recognition program. In addition, the nine major steps

involved in writing a pattern recognition program are discussed and applied to two programs. First, AMOEBA, a two dimensional digital program, is discussed as being converted to three dimensions in the form of Starr. Second, Findp, a program finding phenyl rings in an organic molecule is discussed.

My main problem in this research endeavor has been a shortage of time. AMOEBA is a very complex and long program. The conversion and development of AMOEBA could take years. However, I only have one year in which to complete the Senior Honors Thesis, which is the report requested by the Honors Department and the final report requested by Cornell. Thus, I must live with the realization that I was unable to accomplish that which I set out to do.

However, I did help Dr. Bryant develop a program which uses pattern recognition techniques to develop a program which finds phenyl rings. The data used for this program was collected from X-Ray Crystallographic analysis of organic molecules.

The planned procedure of conducting my research was simply to help Dr. Bryant add another dimension to his program. However, the accessibility of Cornell's 3090 was hindered by A&M's computer failures. Thus, unexpected technical failures delayed the completion of the AMOEBA conversion.

Thus, a knowledge of pattern recognition, of supercomputing, of programming, of carbon structures, and of research in general has been gained. In addition to writing Findp, Dr. Bryant and I developed several display techniques which will be used upon AMOEBA's complete conversion.

The costs of my research were largely paid by the National Science Foundation in the sum of \$2,000. Moreover, the Honors department gave me a \$300 budget. Thus, little or no expense has come out of my own pocket.

I recommend that research be continued on both Starr and Findp. I hope that once these programs are complete the general scientific community will have been improved.

DISCUSSION

Pattern Recognition: Although the complete conversion of the computer program AMOEBA to three dimensions was the original task, only an intermediate step was accomplished. I will elaborate on the larger scope of the project and then specify exactly what has been accomplished.

Pattern recognition is a general scientific field which involves computer aided data analysis. Data used for pattern recognition programs can range from the stellar to the molecular. Moreover, data can be either digital, composed of any real number, or binary, composed of ones and zeros. Each group of data used is termed a data set. Thus, different pattern recognition programs must be developed for the wide range of existing data sets.

The development of pattern recognition programs requires the knowledge of a few basics. For example, the way in which a computer uses data must be thoroughly understood if this process is to be manipulated. In essence, computers read commands and data in a linear string of arguments called the pipeline. Thus, a three dimensional data set will be read as a line first down one row, then another, and finally the logic will skip to another plane and repeat the process.

Another basic idea used in pattern recognition is the Kth nearest neighbor method. Imagine a point in space. Now imagine the points surrounding it. If calculations are performed to compare this point with its neighbor it is necessary to know two things: the value of the points, and the distance between them. Thus, if the analyst wishes to compare the point with its six closest neighbors, then the process would be termed the sixth nearest neighbor method.

In addition to understanding the logic sequence of a computer and the Kth nearest neighbor concept, my project requires an understanding of the way in which supercomputers operate. Supercomputers are computers that are capable of processing data at a rate many times faster than that of a normal or personal computer.

A supercomputer operates by dealing through a central processing unit or a mainframe. This central processing unit is like the human brain is to the body. Moreover, a supercomputer is connected to many other units which are able to perform tasks independent of one another. Thus, these individual units or processors are like human hands are to the brain. However, a supercomputer can have many more than just two processors.

Since my research problem could possibly deal with a staggering amount of data, the use of a supercomputer becomes necessary. Using a normal computer would take too long and require too much money. However, the use of a supercomputer entails dealing with special problems. For example, since many calculations will be occurring at the same time on different processors. How will the calculations be organized? How will the processors output be organized? How will the data be accessed.? These problems and more face the supercomputer user.

Actually, the identified supercomputer problems are easily solved with a little basic training. I received this training at Cornell University last summer under the National Science Foundation's Supercomputing Program for Undergraduate Research(SPUR). The SPUR program provided me with the essential skills necessary to access and use the Cornell IBM 3090 supercomputer. Moreover, they provided me with a cash stipend of over \$1500 and with forty hours credit on the 3090.

Thus, with an understanding of a few simple concepts and techniques, pattern recognition can become an exiting field for practically any researcher.

AMOEBEA: AMOEBA is a two dimensional digital computer program. The purpose of AMOEBA is to analyze any raw data set. AMOEBA should be able to produce a list of clusters found in the data. These clusters can then be analyzed by the programmer or user to understand more about the intended research. Thus, AMOEBA is a versatile research tool because it can be used by any researcher dealing with any type of two

dimensional data set. AMOEBA's history is summarized in Appendix 1.

What makes AMOEBA different from other two dimensional digital programs?

AMOEBA uses a special five-point comparison technique. Once AMOEBA has gone through a data set and produced a cluster map, it takes five points from each cluster to represent the diversity within that cluster. Thus, AMOEBA reduces the problem of analyzing clusters to comparing sets of five points.

AMOEBA then takes five points and labels them so as to identify them with the cluster from which they were taken. Then the points are aligned based on increasing numerical value. AMOEBA then subtracts the fifth points value from the first and arrives at a difference or gradient measure for the cluster.

AMOEBA now has two values with which to categorize the identified clusters; the gradient, and the five point set. The program first separates the clusters into separate categories. Then, within each category, the clusters are classified further using the gradient. thus, each cluster is placed in a map. This map is called a cluster map.

Now that the data has been analyzed and categorized, the researcher can use his previous understanding of the data to help the computer label the clusters in the cluster map. For example, if AMOEBA had identified different geometric shapes, the researcher would then tell the computer what to call each shape. Thus, when the program runs again it will produce a labeled cluster map.

The labeled cluster map can only be developed when the programmer has some understanding of the data and is able to produce a cluster library within the program. Thus, in order for the computer to evaluate data the way a researcher would, it must be trained in recognizing clusters.

The value of AMOEBA comes from the new arrangements of data clusters it provides. This allows the researcher to identify new relationships and principles previously unnoticed. Thus, the substantive results are not the output of the computer, but the new

ideas prompted in the analyst's mind. The test version Starr will be discussed in Section V. In addition, Starr and its output is located in Appendix 2.

Carbon Rings: Organic chemistry is the study of groups of atoms containing the element carbon. Many techniques exist for the analysis of these carbon groups or organic molecules. One of which is X-Ray Crystallography.

X-Ray Crystallography is the technique involving the bombardment of organic molecules with X-Rays which are high energy electromagnetic radiation. The X-Ray Crystallographic machine collects deflected X-rays. Then, a computer evaluates the data and produces a digital map describing the electron density structure of the organic molecule. Electron density is simply a term used to define that space in which an electron is observed over a period of time.

Since the conversion of AMOEBA requires several trial runs Dr. Bryant and I decided to use X-Ray Crystallographic data as one trial run. What we did was design a program that would identify phenyl rings within an organic molecule. A phenol ring is simply a group of six carbon atoms connected to each other in a circle. Thus, a three dimensional cluster map may be produced to view the phenyl rings of an organic molecule.

Findp and its output is located in Appendix 3. Findp will be discussed more in Section VI.

Program Generation Process: According to Anderberg, the general rule in pattern recognition is that the development of a program involves nine basic steps. These are the choice of data units, the choice of variables, what to cluster, clustering criteria, homogenizing variables, similarity measures, algorithm and computer implementation, number of clusters, and interpretation of results. I will briefly explain each step and how it relates to the extension of AMOEBA and to the analysis of carbon rings.

A. Choice of Data Units

Data units are those numerical values which indicate something about the objects which the data describe. The proper choice of the data units which the analyst uses in the program is essential. For example, if an observer wished to determine the elevation of a mountain, then data pertaining to the height of the mountain relative to the sea level must be collected. Moreover, the same observer would not want or need to collect data concerning the relative locations of the mountain and of the sea. Hence, only the essential data should be used in analysis.

In AMOEBA, the program user will be allowed to specify the data units. Thus allowing AMOEBA to be used for a variety of data sets and purposes. Moreover, in the carbon ring experiment, the data units are the three dimensional coordinates of the carbon atoms.

B. Choice of Variables

Variables within the data indicate something specific about the existing interrelationships. For example, a data set describing an assortment of different colored geometric shapes would present the problem of choosing a variable to classify the objects. Should the objects be classified by color or shape? It all depends on what the analyst is intending to study about the data set.

Thus, AMOEBA should also be flexible in the analyst's choice of variables to allow a variety of things to be studied about a particular data set. Moreover, for the carbon experiment, the distance between carbon atoms is the choice of variable.

C. What to Cluster

Now that the data is collected and the aspect of the data that is intended to be studied is identified, the data can be analyzed. However, a question arises, what should be clustered that will enable the researcher to help understand what the data can tell him regarding his chosen variable?

For AMOEBA, this division will again be up to the analyst, but will be limited by both the choice of data units and data variables. Moreover, for the carbon experiment, a group of closely spaced carbon atoms is clustered. This is done because a phenol ring is composed of six closely spaced carbon atoms. If a group of atoms is found, then it is classified as a group. However, simply because a group of atoms is close to each other does not mean that they form a phenol ring. This leads to the next point.

D. Clustering Criteria

Clustering criteria is that information which tells the computer to discard or to store for later use a certain cluster. For example, a data set containing a number of different sizes of spheres was clustered for spheres. This cluster of spheres was then limited to a certain size of sphere, then those clusters not mentioning the size criteria would be discarded or stored elsewhere.

AMOEBA will allow the user to establish clustering criteria only after it has performed its unique operations. Then, the program becomes interactive with the user to develop the computer observations into a usable form. Moreover, the carbon atoms experiment clusters atoms based on their proximity to one another. However, only those groups

involving six atoms are stored. Thus the clustering criteria for the carbon atom experiment is the number of carbon atoms in a group.

E. Homogenizing Variables

Since a program can analyze data based on several variables, a relationship between the variables used must be described. For example, if the size and shape of geometric figures within a data set is studied, then what relationship do these variables have? Is there any correlation between a small cube and a small sphere or is the correlation between a small cube and a large cube? Thus, a comparative intuition must be developed in the program concerning the relationship between variables.

AMOEBAs will be interactive in this area as well since it depends on the interest of the researcher as to what relative information is important. Moreover, in the carbon experiment, only groups of six carbons were found, so only one variable, distance, is studied.

F. Similarity Measures

As the number of variables increases, the number of possible comparisons also increases. Thus, not only do these variables need to be computable or homogeneous, but they need to be comparable. For example, assume a data set composed of three dimensional colored geometric shapes of different sizes. Now study the data and decide if the shapes are related to the size or the color, or is the color related to the shape and size? Thus, many possible relationships between a multi-variable study exist.

AMOEBAs will certainly have to be user interactive in this respect since the number of possible relationships could be infinite, even with a small number of variables. Moreover, for the carbon experiment, this problem does not exist because one variable

not a set of variables is studied.

G. Algorithms and Computer Implementation

Algorithms are simply those concepts used to solve a specified problem. Computer Implementation of these algorithms means that the algorithm is written in a form that the computer can use. For example, if the relative size of geometric shapes is to be considered, then an algorithm comparing the area or volume of the different objects should be implemented into the computer logic.

The major algorithms which AMOEBA uses have previously been explained. The implementation of these algorithms has yet to take place. Moreover, the algorithms behind the carbon experiment have been completely implemented.

H. Number of Clusters

The number of clusters indicates the number of aspects found by the program based upon the decision made by the programmer. For example, the number of clusters found in a data set containing information on a deck of playing cards can vary greatly. If color is used to classify, then two clusters will be found. If suit is used, then four clusters will be found. This process could be continued on certain data sets indefinitely. Thus, the number of clusters found is a very important question which the programmer or user must answer.

AMOEBA will allow the user to decide on the number of clusters found. Moreover, the number of clusters found in the carbon experiment is not an aspect written into the program. This is because the original question posed by the researcher, myself, was how many phenol rings are there?

J. Interpretation of Results

The interpretation of results phase determines what the researcher is able to learn from the data. For example, if the program is designed to label a cluster by specific name then most of the interpretation has been done by the computer. However, if only the raw clusters are received as output, then most of the interpretation work must be done by the researcher. Thus, the ability to interpret the results depends on both the quality of the program and the skill of the user.

AMOEBA will not be trained to interpret the results as a stand alone program. However, additional supplemental programs or subprograms will hopefully be developed that will focus AMOEBA in a certain area. Moreover, the interpretation of the results of the carbon atom experiment is quite easier. I can simply read the output and determine the number of phenol rings present.

Starr: The history of AMOEBA is contained in the comment lines of the code. These comment lines have been edited out and placed in Appendix 1. AMOEBA itself was not included because it has approximately 13,000 lines of code.

In short, the ideas of AMOEBA, specifically the five point method, have been developed into a new program called Starr. Starr attempts to do in three dimensions what AMOEBA does in two. Starr is the first attempt at AMOEBA's conversion.

Starr begins by making artificial data. Starr then calculates the gradient of each point. The gradient can then be used to determine the amount of change occurring in the data. Thus, where the gradient change, or change in value, is large then that area is considered to be a boundary region. The points that comprise a connected group in which the gradient does not change a great deal are considered to be non-boundary points.

Once the gradients have been calculated Starr uses the constant data to form seed groups. These seed groups of constant data are collected until they are surrounded by

boundary points. Thus, groups are found by Starr. Starr then uses AMOEBA's five point comparison technique.

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However, Starr currently can not generate enough test sets because its data set is too small. Starr would need a minimum of about 100 test sets whereas the current data generate only seventeen.

Findp: Findp is a pattern recognition program that clusters the phenyl rings in a compound. The program has been successful on seven out of the nine data sets acquired from Dr. Fackler's research group. Thus, Findp needs a little work.

The program begins by calculating each points three closest neighbors. This data is then printed out. The point being considered is now called i and its closest neighbor j . These two points are used in a similarity measure. The program then produces a diagram of points that show a directional relationship to its most similar neighbor. If two points both point to each other, then these two points are called an attractor set.

The attractor sets are then used to cluster the program. For each set of six points in a group a centroid is calculated. Then a point not of the six is calculated for its distance away from the centroid. These calculations are completed and then the point with the largest distance associated with it is thrown out of the group. This is continued until a group of only six carbons remain.

Thus, phenyl groups are recognized. The points not clustered are thrown into a general pool which could be recalculated for phenyls if the researcher thought that the program missed some the first time around.

For this report, we print out only the first wave of calculations because we know it to be accurate. In addition, Findp prints out each group and the other points distance from the centroid of the group. Then the groups are identified as well as those points not in a group of six.

Conclusion: Thus, the general field of pattern recognition can be seen to have many applications. Although I was unable to complete the AMOEBA conversion, I was able to complete the phenyl ring clustering program which works 78% of the time, and the program Starr. In addition, I gained valuable insight into the requirements for a good pattern recognition program.

In essence, this research could produce valuable fruits for many disciplines. I hope that I will continue working with this research topic in the future. I would like to thank Dr. Bryant for everything he has taught me. I would like to thank Dr. Fackler for allowing me to work in his group. In addition, I would like to thank Cornell University and the National Science Foundation for their technical support. Finally, I would like to thank the Honors Department at Texas A&M for the fantastic experience.

Works Cited:

Anderberg, Michael R. Cluster Analysis For Applications. New York: Academic Press, 1973. pp. 1-16.

Bryant, Jack. AMOEBA. Pattern Recognition. January, 1972. pp. 1041.

APPENDIX A
AMOEBIA History

Section 1. General comments.

The program AMOEBA is copyright (C) 1983 by Jack Bryant; all rights are reserved. Copying the source is authorized only if are Jack Bryant or if you make absolutely no changes in the copy except in the I/O sections or in the main program (which contains VMS specific system calls). More precisely, the main program (module AMOBMAIN) and subroutines AMCPARM, OPEN_DATA, MAKEOUT, OPENTEMP, REWIND_DATA, READ_DATA, PRINT33, READ_LABL, OPENKEEP, and HEADER may be modified. In addition, D_LINES may be added and commented out as you please. The point of this condition is to allow experimentation (through the D_LINES code) but keep everyone's production Version 13.2 the same. The same restrictions apply to the test version.

Although considerable effort has been expended to make AMOEBA correct and reliable, no warranty is implied. I disclaim any obligation or liability for damages, including but not limited to special, indirect, or consequential damages arising out of or in connection with the use or performance of this software. This work has been a 'labor of love;' I hope that users enjoy it. The reward for the first finder of a bug is \$10.24; this will double in 1991. (THIS REFERS TO PRODUCTION VERSION 13.2, NOT TO THE TEST VERSION; THE REWARD FOR A NEW BUG IN THE TEST VERSION IS PRESENTLY \$2.56.)

LANGUAGE VAX-11 FORTRAN-77 (ANSI X3.9-1978)

PURPOSE Driver program for the AMOEBA clustering-classification-dimensionality reduction program.

----- CALLED MODULES -----

AMCPARM	Gets parameters.
AMOEBA	AMOEBA
MAKEOUT	Writes output file.
LIB\$GET_VM	Get virtual memory in program region. A VMS Run-time Library function.
LIB\$FREE_VM	Free virtual memory from program region. A VMS Run-time Library function.
PROJECT	AMOEBA CLUSTERING/CLASSIFICATION/DISPLAY PROGRAM

----- REVISION HISTORY -----

VERSION	DATE	AUTHOR	AFFILIATION	REMARKS
10	12/1/83	Jack Bryant	Texas A&M	Initial VAX Version AMOBMAIN
10.1	12/20/83	Jack Bryant		Allow testing any input size & mask.
10.2	1/17/84	Jack Bryant		Add subroutine GETPAR for RSC.
10.3	3/5/84	Jack Bryant		Replace GETPAR with AMCPARM to allow many different data types and arrangements of headers. Also, replace READBYTE with READ_DATA and add module to rewind and skip header records on input data file(s). Include file added to pass parameters.

- 10.4 12/25/85 Jack Bryant Corrected bug to allow self-generation of data. Changes in START, COUNTERR, and NUMCLU.
 - 10.5 1/1/86 Jack Bryant Sharpened estimates on memory required (trying to reduce same).
 - 11 1/20/87 Jack Bryant Extensive changes in classifier...over twice as fast now!
 - 12 4/14/88 Jack Bryant More classifier and NUMCLU changes. Also enough changes in START to mention.
 - 13 3/1/89 Jack Bryant Added Robert's-like gradient for boundaries. Added allowing old cluster map to be a mask for new run.
 - 13.1 5/10/90 Jack Bryant Removed Robert's stuff pending more study. Changes sprinkled throughout, mostly for minor increase in speed.
 - 13.2 6/20/90 Jack Bryant Big changes in NUMCLU and PERPIXEL make the program 30% faster! Minor changes in AMCPARM. Longstanding Bug fixed in THINMEAN.
 - 14 8/31/90 Jack Bryant Classification is faster yet. (Yet another simple idea.) Started putting in changes to do spatial filtering and logic on reclassification of apparent mixtures.
 - 14.1 9/10/90 Jack Bryant Implemented the pair mixture distance test in the AMOEBA classification option. Also put in logic to exit-when-classified in NUMCLU.
 - 14.2 10/21/90 Jack Bryant Put in 250 lines of help in the parameter read module. The statistic file now has file name <outfile>.TXT. Factored out mask tests everywhere. Made two read_data modules depending on whether the classification_mask is set.
 - 14.3 10/23/90 Jack Bryant Added option to allow previous cluster map (not necessarily by AMOEBA) to be used to start. Included help statements for this.
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Section 2. An outline of the model.

1. Axiom: Real classes exist.
2. Def: A pixel is "pure" if it and all four nearest neighbors are in the same real class.
3. Def: A "path" is a sequence P_1, \dots, P_n of pixels such that P_i is one of the four nearest neighbors of P_{i+1} , $i = 1, \dots, n-1$.
4. Theorem: If P and Q are pure pixels and are neighbors then they are in the same real class.
5. Def: A set is "connected" if each pair of points in the set can be joined by a path lying in the set.
6. Def: If S is a set, then C is a "component" of S if C is a maximal connected subset of S.
7. Theorem: If S is a set and P is an element of S then P is contained in a unique component C of S. Moreover, C is exactly the set $C = \{ Q : P \text{ can be joined to } Q \text{ by a path lying in } S \}$.

8. Def: A "patch" is a component of the set of pure pixels.

The set of patches is thus a partition of the set of pure pixels.

9. Def: The "classifier" is the mapping from the set of all pixels to an unknown set of labels.

Let us note that the classifier exists but is unknown. It exists by virtue of Axiom 1.

10. Theorem: If F is a patch, then each point in F has the same label; that is, the partition induced by the classifier in the set of pure pixels is refined by the component partition.

11. Def: A "NNC" is a nearest neighbor classifier determined by a distance function and a set of cluster attractors.

12. Def: A measurement vector R is a "convex combination" of vectors P and Q if $R = a P + (1-a) Q$ for some a between 0 and 1.

13. Axiom: (But with supporting arguments...) If P and Q are measurement vectors in the same real class and R is a convex combination of P and Q, then a NNC should classify R in the same class as P and Q.

14. Def: A distance function is "natural" if it is induced by a norm on the vector space in which the measurement vectors are imbedded.

Note that the maximum likelihood classifier is a NNC induced by a natural distance function. Also natural are the Minkowski distances

$$d(P,Q) = (\sum_i | p_i - q_i |^{** p})^{** 1/p}.$$

Two popular choices for p are 1 ("city block" distance) and 2 (Euclidean distance). Note also that the different p may be weighted with unequal (positive) weights w_i . A "parallelepiped" classifier can be viewed as a weighted

p=infinity classifier.

15. Theorem: If a natural distance function induces a NNC consistent with Axiom 13, then it is weighted Euclidean distance.

Let C be a classifier. Let P and Q be two pure pixels. There are four possibilities:

- (1) P and Q are in the same real class and $C(P) = C(Q)$;
- (2) P and Q are in different real classes and $C(P) \neq C(Q)$;
- (3) P and Q are in the same real class and $C(P) \neq C(Q)$; or,
- (4) P and Q are in different real classes and $C(P) = C(Q)$.

16. Def: The "pair probability of misclassification" is the probability PPMC of case (3) or (4) above.

Note a NNC is completely determined by the class attractors and the distance function. In clustering unknown data (to search for

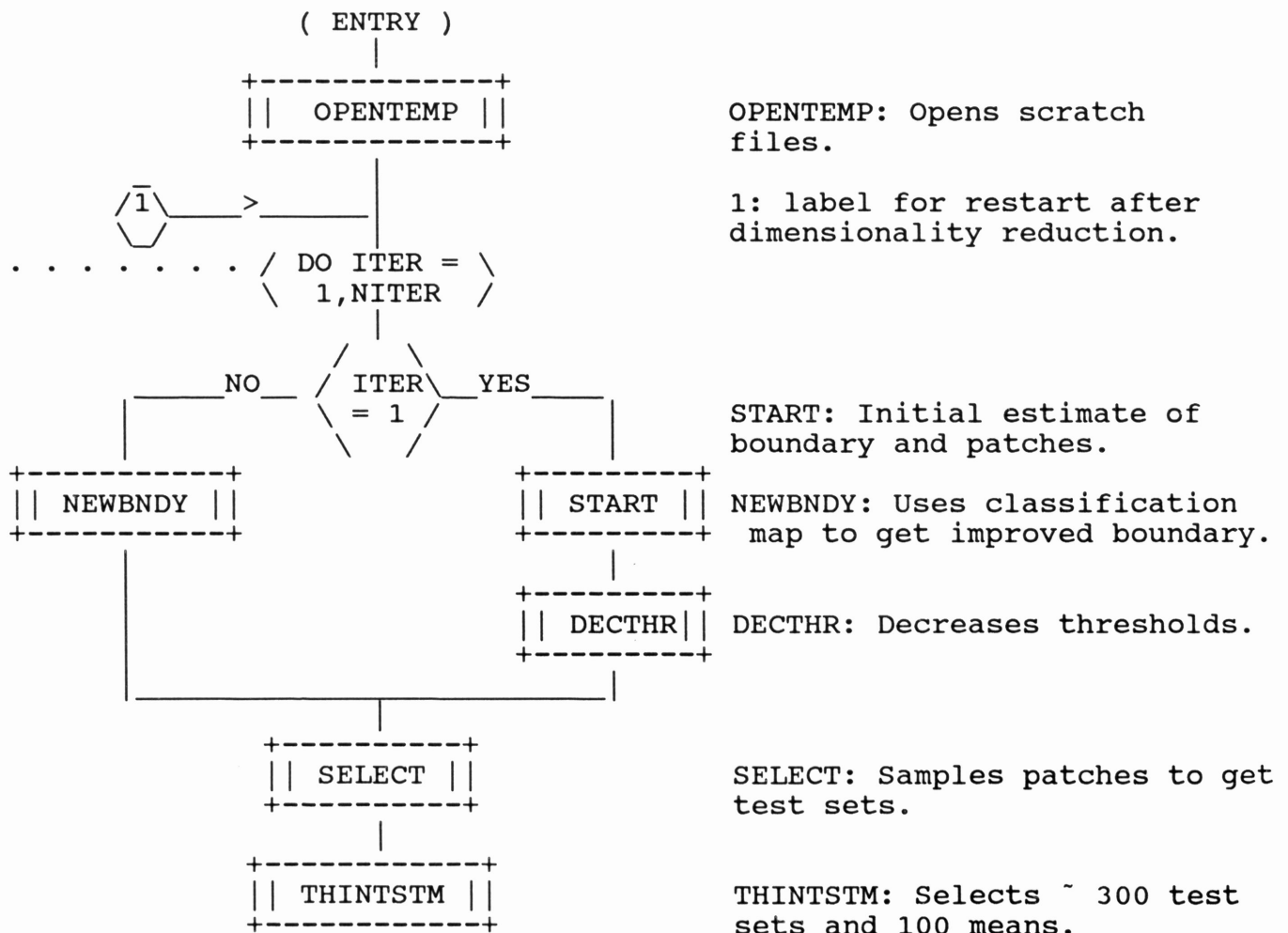
structure with little a priori knowledge), we will not know the "best" weights to apply to the only acceptable distance function (Euclidean distance). We therefore let all weights be equal. This fixes the distance function, and it remains to find the attractors.

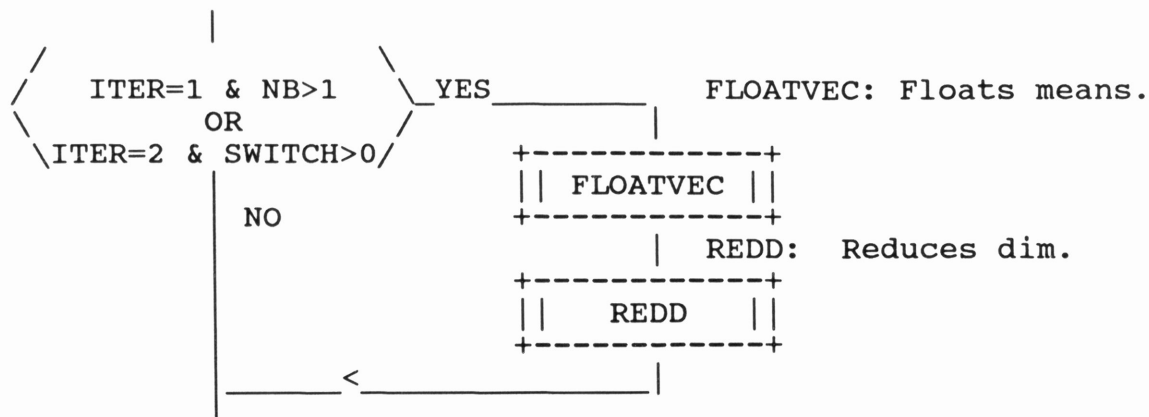
17. Objective: It is desired to minimize the PPMC.

With this objective, we need a means of estimating the PPMC. Examine again Theorem 10. If we can estimate the set of mixed (i.e. not pure) pixels, then we can get an estimate of the patches. Using Theorem 10, we can extract samples from the case "same real class". It has been observed that the average brightness of the measurements is the single most significant attribute in most multi-image analysis problems. Therefore, sort the samples on this feature, and select pairs close, but not too close, in the order. This gives a way to estimate the "different real class" case. By counting errors (disagreements between NNC and the case pairs), we obtain both an estimate of the PPMC and an indication of which attractors are the cause of the (relatively) most errors.

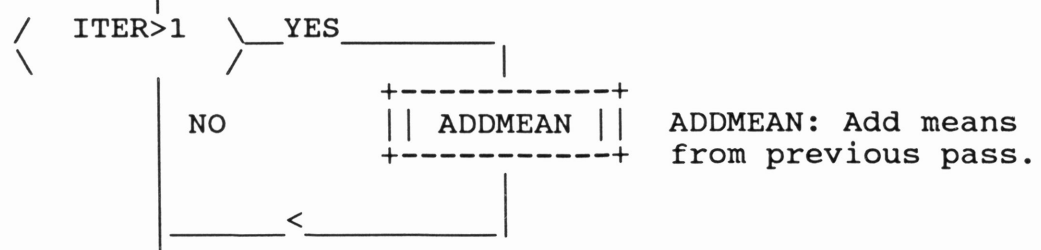
This is the general outline of the idea; refinements, such as using a prior classification to refine the boundary estimate, and on selecting starting cluster attractors from the very large number of candidates, are described in the subroutines which do the work.

Crude flow chart and brief description of the modules.

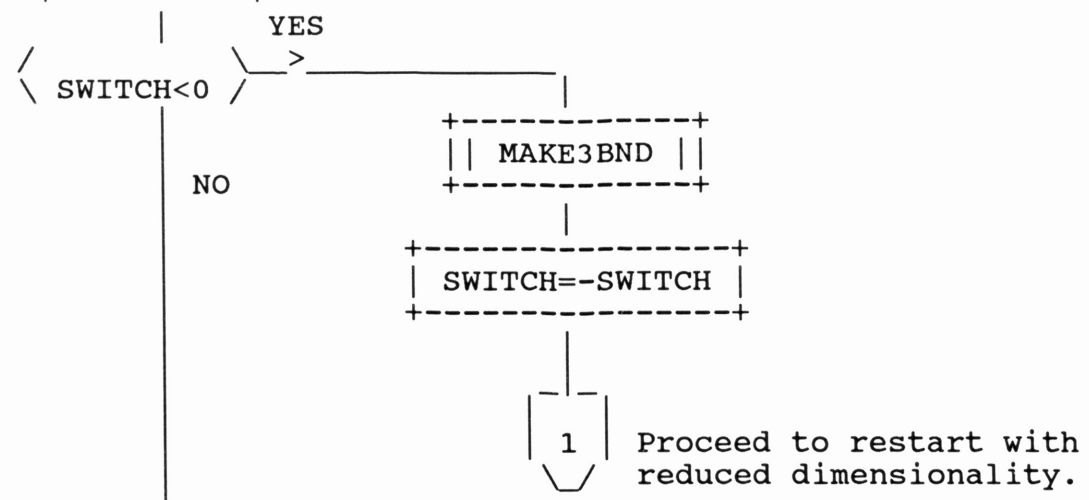




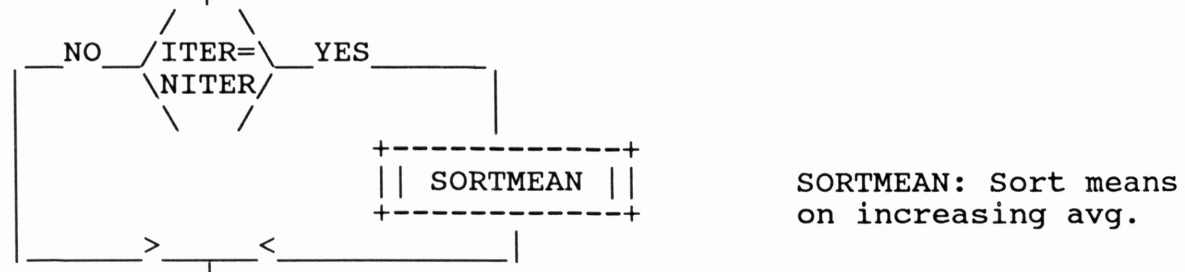
|| SORTTSTS ||
SORTTSTS: Sorts test sets on average one-d attribute.



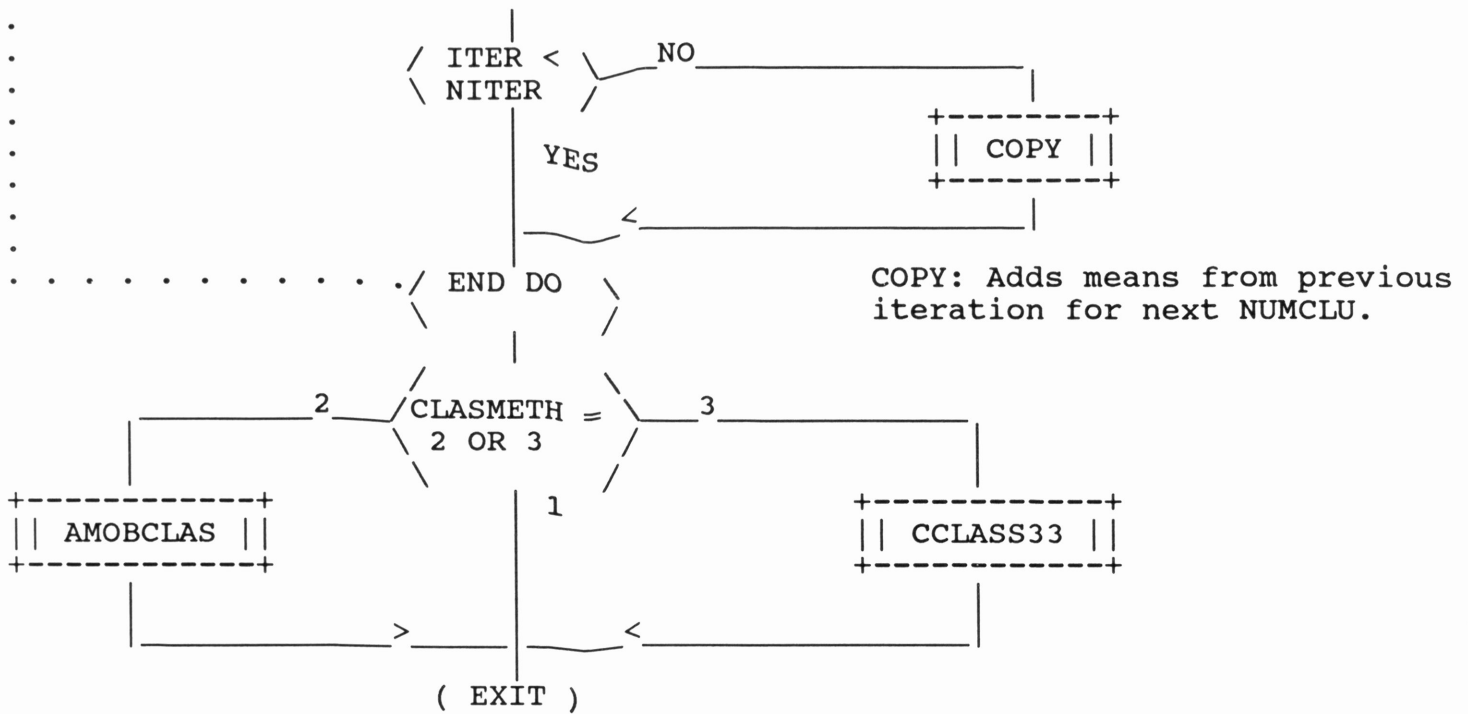
|| NUMCLU ||
NUMCLU: Clusters the data.



|| MORELESS ||
MORELESS: Detects when a class is lost and adds it.



|| PERPIXEL ||
PERPIXEL: Performs a per pixel nearest neighbor classification.



- AMOBCLAS Performs standard AMOEBA spatial classification using the boundary model.
- CCLASS33 Context classification based on the context in a 3X3 neighborhood.

Section 4. Revision history of AMOEBA.

VERSION	DATE	AUTHOR	AFFILIATION	REMARKS
1	5/1/76	Jack Bryant	Texas A&M	Initial Version AMOEBA

The first version of AMOEBA was a starting procedure for extracting samples to test other clustering procedures. These, which were among the fastest methods known, included ISODATA [1], the K-Means Algorithm [2], and a Single Linkage Tree Algorithm [3]. The purpose of the testing was to evaluate various clustering methods and their potential in the Large Area Crop Inventory Experiment (LACIE). In the LACIE, a standard image size was the "segment", a 117 by 196 multispectral scanner Landsat image, often three or more rather poorly registered temporal acquisitions. The data were generally free of clouds but not haze, and were of areas of intense large field agricultural activity. The images were thus small and not spectrally complex. Still, we lacked the computational resources to adequately test the methods. Moreover, all the methods failed to solve the clustering problem when given samples which were measurement-space mixtures--mixtures which exist owing to the resolution and precision of the sensor, atmospheric effects, registration problems, and calibration errors. To avoid testing using mixtures, as well as to sample the data, we used the Fisher Algorithm [4] down scan lines to break the data into intervals.

The Fisher method divides a sequential data set into segments so that the sum of the within-segment "diameters" is minimal for that number of intervals. It is not a true clustering method, for no information on whether two distinct segments are the same "class" is obtained. Moreover, although for a fixed number of intervals there is an objective

function, there is no way to decide how many intervals to use. We used 12 intervals for scan lines of 117 pixels, and selected the center of each interval which contained at least 5 pixels. This brought the number of points to cluster from 23,000 to 2,000, a big saving since the methods seemed to need $O(\#samples^2)$ time.

2 7/1/76 Second Version AMOEBA

One drawback was that boundaries in the direction normal to the scan line direction were missed. Another application of the Fisher method in that direction picked up those boundaries (but also the every-six-line Landsat problem). By then we were making line printer maps, and the name AMOEBA had caught on because of the appearance of the blobs. Our sampling strategy now had us picking points with no neighbors on any of the thickened boundaries, much the same as the present subroutine SELECT does. We now had between 250 and 350 samples to cluster, another big improvement. We were also pleased to be using Dynamic Programming [5]. Pleased, that is, because of our background as mathematicians. Not so pleased, however, with the time the Fisher method was taking, and not at all happy with the results of the clustering methods. At that time, the idea was to use clustering to develop training sets for a Maximum Likelihood Classifier. But they were impossible to compare; none did well, nor did the classifier seem all that likely to be maximum given the poor training.

3 8/1/76 Third Version AMOEBA

Version 3 added a module to label and sample the different components of the complement of the boundary. David Egle and I wrote the fast and elegant component labelling program; unlike relaxation methods, only one pass was required to grow all the labeled components at one time. The program was optimal in the sense that each pixel was examined once. Also, the actual computations involved in the Fisher method were studied (we were trying to speed them up). I found that simply thresholding the spectral distance of a pixel to its nearby neighbors did as well. I determined the threshold by experiment, and made it adapt to data variability. Nothing "dynamic", and no "maximum likelihood" either. But, if results get to decide, the map of boundaries was better (less sensitive to 6-line noise), and the new version could do it in less than one percent of the time we had been using. The maps and lists of blob statistics from these simple, fast methods seemed better than classical methods, for example from [6]. To some extent, I had put aside my mathematical point of view. It was to return.

4 4/1/77 Fourth Version AMOEBA

None of the clustering methods being tested was doing well. This task was yielding inconclusive results, as might be expected given the variety of methods. Yet the data were as good as could be hoped for (given the hardware). Moreover, the problem seemed to be easy, with preselected data free of clouds, with large fields, flat terrain, and multiple acquisitions. Cluster maps were confetti, not wheat fields. Everyone blamed it on the data, and wanted to correct for bad clustering (and therefore poor classifier performance) by fancy neo-statistical methods. Version 4 of AMOEBA was a clustering program which used the boundary map from Version 3. Components of the complement of the boundary (now called patches) were sampled, forming what I called test sets. The averages of the test sets were used as starting cluster centers for a nearest neighbor classifier. Unpopular clusters were eliminated, reducing the clusters to a user-supplied number. Fast and simple, and the

resulting cluster maps were, by comparison, almost great.

5 11/1/77 Fifth Version AMOEBA

Three changes marked Version 5. One was motivated by discussion with people who interpret images manually: that boundary-between-field decisions are made based on one of the multi-images, not on some multi-dimensional distance function. This led to the present vector decision thresholds. Another was the introduction of reject classifications. This was really a natural result of a simple model for the spectral appearance of a spatial boundary with registration errors possible. The third was the initial version of the heart of the clustering program NUMCLU. For the first time we had a clustering program which determined the number of classes automatically. The idea then was to count the errors made when the classifier split (i.e., classified differently) test pixels from the same patch. An estimate of the number of errors expected (depending on the number of clusters) was compared to the number of errors observed, and the number of clusters determined following this comparison to minimize the deviation.

6 2/1/78 Sixth Version AMOEBA

Version 6 was a result of a formal model for Landsat data. In particular, the objective in NUMCLU (the present version) was introduced. That objective, the pair probability of misclassification, allows one to compare the hypothetical (and desired) real clustering with the classification of samples taken from the same patch and from different patches. We also introduced spatial classification aids. Points which appeared to be misclassified were reclassified if possible within the rejection threshold model. Version 6, a finished program, can cluster and classify a four pass LACIE segment in 12 seconds (on the AMDAHL), using 'only' 320K memory in the process. Although subversions of Version 6 continued to appear until 10/31/79, the main ideas were complete [7].

Although the path that led us here has often strayed from conventional mathematics, the approach is in spirit mathematical. (The model outlined above is a mathematical model; the depth or lack of it, compared to "real" mathematics, is beside the point.)

The development of AMOEBA through Version 6 was supported in part by NASA contract NAS-9-14689, "Development and Selection of Clustering Procedures," L.F. Guseman, Jr., P.I. It is a pleasure to acknowledge this support. Significant contributions to the program came from Gary Breaux and David Egle.

7 11/1/80 Seventh Version AMOEBA

In the summer of 1980, I went to EROS Data Center, a U.S. Geological Survey center near Sioux Falls, S.D. The purpose of the visit was to transfer some of the techniques developed at Texas A&M during the LACIE to the Data Analysis Laboratory at EROS, as well as to develop new techniques as time permitted. One new technique was the use of hashing to histogram multidimensional data--e.g. Landsat data. Using this method, we were able to compress a Landsat one pass frame so it could be processed on the AMDAHL (i.e., the data were all in memory.) Version 7 uses data in this form. Unfortunately, a two pass Landsat image is too complex to be compressed in this manner. (Of course, the AMDAHL is a virtual machine: little memory limitation, in theory, is placed on a task. But the cost of memory resources at A&M was high.)

Version 8 was written at EROS the following summer. The program uses several tricks to segment essentially infinite images into strips, to find boundary and samples for NUMCLU, and to classify data, all on a tiny (by AMDAHL standards) minicomputer (the Hewlett-Packard 3000 Series III). The program runs as an IDIMS function. Comparisons with ISOCLS [8] show it performs about as well while saving time (AMOEBA is faster) [9]. Major enhancements (in addition to the ability to handle very large images) include a provision for a mask and the generation of a "statistics" file.

9 6/1/82 Ninth Version AMOEBA

Version 9 is an iterative enhancement of Version 6. I noticed that boundaries were found where the classifier (i.e. the per pixel classifier) got lost. Classification induced boundaries were used to generate patches for the next pass of the clustering procedure. Although this uses more time, it seemed to result in better clustering, at least in the LACIE data I tested the new program on. Several related techniques on finding boundaries and on classification based distance functions and gradients were presented during a special session of a meeting of the American Mathematical Society [10].

10 12/1/83 Tenth Version AMOEBA

Version 10 is a complete rewrite of Version 8 (now in FORTRAN 77). Mainly owing to the better compiler, the program is written in well structured code. The advantages of the structured approach to coding are widely recognized [11]. Additions to Version 8 include:

- @ The user may supply weights for counting error cases; these were fixed in all previous versions.
- @ A choice of classifiers is made available. They are:
 - >> a per pixel classifier (not an option of versions past number 5)
 - >> the Version 8 spatially supervised classifier
 - >> a new context classifier [12], based on 3X3 blocks (new to all versions)
- @ Each pixel is given a label; if necessary, the number of clusters is increased during the classification step. The difference between this and Version 8 lies in the more efficient classifier which only looks at the exceptional case when regular classification is rejected.
- @ The number of iterations may be specified by the user. Version 8 did not iterate at all. Other versions handle only small images.
- @ Using VAX-11 Run-time Library calls, all memory management is transparent to the user; the program runs in as little virtual memory as possible. No previous version has had this feature.

One minor change in Version 10 is the way in which the mask is labelled with 255 rather than 99 or 0 (in earlier versions). This allows 254 context classes, and reserves 0 for "unclassified".

10.1 5/1/84

The VMS version has been modified to merge clusters for the first time. The merging is carried out in subroutine MORELESS (formerly MOREQUES). The thresholds are one-fifth of the vector boundary decision thresholds determined in START.

10.2 1/10/86

A number of minor changes have been made. The test data generation portion was incorrect due to the removal of READBYTE. NUMCLU, COUNTERR, and COLAPS have been modified. Many fossil comments have been removed. The initial start has been given additional protection to guard against a lost boundary finder. In AMOEBA, code has been included to add the final clusters from the previous pass to the spatially determined starting clusters. The two print routines PRTSTATS and PRINT33 have been modified to make ASCII files. The AMOEBA classification method has been modified to use 8-neighborhoods instead of only 4-neighborhoods. A similar change has been made in the preliminary steps before context classification. All logic including BIGDATA has been commented out everywhere (awaiting true 12 bit data).

11 6/19/86 Eleventh Version AMOEBA

A major rewrite of the logic in the main clustering module NUMCLU is the principal change leading to Version 11. Although the objective function remains unchanged from Version 6, the minimization search has been considerably widened for the final iteration. Roughly speaking, Phase II of NUMCLU takes "subclusterings" of the results of the earlier Version (Phase I) and evaluates, in a 64 node tree search, each subclustering, looking for arrangements which make fewer errors in the way the clustering fits the model. In this way, essentially every arrangement which has any chance of improving the partition is examined. A report on this work is in preparation.

Another significant change (with a surprising improvement resulting) is the incorporation of the dimensionality reduction technique of Bryant and Guseman in the initial phase of NUMCLU; this module takes the starting means for NUMCLU and finds the best linear mapping to one dimension. Earlier versions simply used the sum of all the measurements as the one dimensional attribute. That was not bad for Landsat data, but the new method is better when far IR or UV bands are present.

Yet another change allows the user to reduce the dimensionality of the data to three to make a color display of the image, and, at the same time, save time in the program. The time saved depends on the number of bands in the input image: for six band input and two iterations, it amounts to at least 45%. The system is designed for MSS data. The reduced dimensionality image is designed for currently available systems. We hope for reproducible colors: that is, the display will be stable if the sensor and scene do not change materially.

Another change is to restart the process following the dimensionality reduction step. This is needed because the parameters which are used to detect probably identical classes are defined in START. If dimensionality reduction has been carried out, these parameters get lost.

A major change has been made in the context classifier: no one likes the many classes you get when you use it. So an option has been provided which will merge classes when they can be merged. The entire context classifier situation is incomplete, although the program does work as advertised. Probably, a 3x3 neighborhood is too small.

A number of less significant changes have also been incorporated. One is the way in which the "mask" is handled. Since experience has shown that the "unclassified" event never (well, almost never) happens on real data, and since the value 255 is hard to deal with on the IIS image display hardware, the mask label is made 0 on the final pass if the classification method is 1 or 2.

Also, the weights /default have changed to fit better with the new version of NUMCLU and the new option in the context classifier; it seems to work much better.

12 12/19/86 Twelfth Version AMOEBA

Another major change in NUMCLU uses the exhaustive search on all iterations now. Changes in the way classification is carried about, plus saving recently encountered trial arrangements, makes this possible. A seemingly minor change in the way distances are computed when performing nearest neighborhood classification has made the program at least twice as fast on 4-band data. Throughout the program, long to short integer conversions have been eliminated; this gains still more speed.

The AMOEBA classifier has been generalized to allow the user to select from one to eight neighbors (in the 8-neighborhood) which must match to accept the classification. The resulting cluster maps when (say) 4 alike is selected are very smooth and easy to interpret (if slightly less accurate). The 1-neighbor alike preserves fine detail such as urban features better and is more accurate than pure per pixel classification.

The starting boundary estimation procedure has been improved. When a very large patch is detected, a serious effort is made to detect additional boundary points without changing the thresholds. The time spent here is probably repaid later by not having to collect and analyze the extra points. In addition, a gradually changing natural feature, such as observed in rangeland or wetlands, is much less likely to be taken to be a patch.

Throughout the program, changes in the way classification is carried out have been made. This work, reported in [13], makes the program nearly three times as fast on 11 dimensional data, yet the idea is very simple and natural.

The module that makes the 3-band image has been improved. Safeguards have been incorporated to prevent the 'folding' operation to lose more than 1/2 percent of the counts (not pixels clipped, but actual counts lost). The original objectives are still met, although the resulting color displays are not as spectacular. (The spectacular appearance was probably a result of substantial 'folding.') The dimensionality reduction method is now the simple principal components method, rather than the method of Bryant and Guseman, pending the location of an efficient nonlinear optimization method. This work is presented in [14].

A number of fossil comments have been removed, shortening the source by a thousand lines.

13 1/20/90 Thirteenth Version AMOEBA

A number of changes have made this version faster. Most amount to replacing subroutines and array indexing-loops with straight line code written out. Of course, this makes the program difficult to understand. These changes are documented in the modules affected.

14 1/10/91* Fourteenth Version AMOEBA

* Projected release date.

"The future lies ahead of us" -- R.M. Nixon

The changes and additions planned for Version 14 are listed here in no particular order; a few are complete indicated by a date e.g.:

8/10/90

Classification is faster still because of the test for "when classified" (the nearest attractor has been found when the distance to attractor tested is half the distance to the other nearest attractor). This change in PERPIXEL. A similar change in NUMCLU. 8/20/90

The statistics file should have a name: make it the same as the cluster map with extension .TXT 8/21/90

Some speed-up seems likely if the mask and classmask tests are recoded. 8/21/90

Help files should be added--or built-in help. 8/20/90

An option will be added to allow one to produce a large number of clusters for the purpose of using these to make a color display in the setting of a display device with very limited palette--e.g., 256 colors. The output will be the cluster map and table of cluster attractors. The map is intended to be used to produce color display products.

An option will be added to allow dimensionality reduction from n to m dimensions (instead of just n to 3). Also the dimensionality reduction will not scale like the 3 band product does (except to make sure the full use of 8 bit unsigned integers is made).

In connection with this, the Moore-Penrose generalized inverse idea will be implemented.

Texture needs to be experimented with. Two uses: use texture measurements as additional bands to aid (?) classification, and use texture to switch how many alike in the 8-point neighborhood are required.

In connection with this, the 8-point neighborhood logic is slightly different now. The 4 nearest are weighted twice that of the corners. At the same time, the requested number is multiplied by $3/2$, keeping the intention of the user the same. 7/7/90

An option to use another cluster map as the entry to the program will be added. This would be useful if the system had a hardware clustering program built in which was much faster than one pass through AMOEBA.

AMOEBA has been known to lose a bright high variance class on the first iteration. I believe this can be corrected. The main result is that the dimensionality reduction routine receives poor training.

I propose to make a pyramid structure of high resolution data and do a multi-resolution attempt to understand the image.

A 9x9 context classifier will be implemented. I think the information in an area this big can still be kept in a 32 bit word, and I believe fewer than 2^{16} actual contexts are present even in a complex image.

The Moore-Penrose inverse can also be used to restore missing data or to recreate at apparently higher resolution low resolution data which

is registered to high resolution data. I see no reason why this could not be done automatically.

An option of making the cluster map a color map should be easy to provide, although this should clearly be a separate program which depends on the system.

Filtering: high frequency enhancement filters of the form

$$F_{a,b}(s) = (1+a||s||^2) \exp(-||s||^2/b^2)$$

are easily approximated (the Fourier transform can be computed by hand:

$$f_{a,b}(t) := \int_{\mathbb{R}^2} F_{a,b}(s) e^{-i s \cdot t} ds$$

$$= \pi b^2 / 4 [4+4ab - ab^2] e^{-b^2 ||t||^2 / 4}$$

Within reason, these filters provide modest sharpening and at the same some smoothing. They are easily implemented as small (say 7x7) real domain convolution filters.

Information about the platform which acquired the data could potentially be used to automatically produce color display products, pyramid structure, and spatial filtering. Much data is available, but it is only now being assembled in one place.

----- REFERENCES -----

- [1] Ball, G.H. and Hall, J.D., A clustering technique for summarizing multivariate data, Behav. Sci. 12(1967),153-155.
- [2] Fisher, L. and Van Ness, J.W., Admissible clustering procedures, Biometrika 58(1971),91-104.
- [3] Grower, J.C. and Ross, G.J.S., Minimum spanning trees and single linkage cluster analysis, Appl. Stat. 18(1969),54-64.
- [4] Fisher, W.D., On grouping for maximum homogeneity, J. Am. Stat. Assoc. 53(1958),789-798.
- [5] Bellman, R.E. and Dreyfus, S.E., Applied Dynamic Programming, Princeton Univ. Press, Princeton N.J., 1962.
- [6] Hartigan, J.A., Clustering Algorithms, John Wiley and Sons, New York, 1975.
- [7] Bryant, J., On the clustering of multidimensional pictorial data, Pattern Recognition 11(1979),115-126.
- [8] Kan, E.P.F. and Holly, W.A., More on clustering techniques with final recommendations on ISODATA, Tech. Rep. LEC 64-TR-112, Lockheed Electronics Co., Inc., HASD, Houston, Texas, 1972.

- [9] Jenson, S.K., Loveland, T.R., and Bryant, J., Evaluation of AMOEBA: A spectral-spatial classification method, J. Appl. Photographic Engineering 8(1982),159-162.
- [10] Bryant, J., Clustering and boundary detection in image data, Abstracts AMS 2(1981),515. Presented to the AMS at 789th Meeting, Amherst, October 17, 1981.
- [11] Tanimoto, S.L., Advances in software engineering and their relations to pattern recognition and image processing, Pattern Recognition 15(1982),113-120.
- [12] Wharton, S.W., A contextual classification method for recognizing land use patterns in remotely sensed data, Pattern Recognition 15(1982),317-324.
- [13] Bryant, J., A fast classifier for image data, Pattern Recognition 22 (1989),45-48.
- [14] Bryant, J., On displaying multispectral data, P.E. & R.S. 54 (1988), 1739-1743.
- [15] Bryant, J., AMOEBA clustering revisited, P.E. & R.S. 56 (1990), 41-47.

ONICA>

APPENDIX B

Starr: Program and Output

Starr

```

program starr
c
c One step test of first cut.
c
implicit none ! remove for old version 2.1.1 for parallel
integer nc,nr,np,nb
character*64 outfile,infile
parameter(nb=1,nc=32,nr=32,np=32)
integer i,j,k,l,m,n
integer testsets(5,356),means(256)
integer nmeans,ntstsets,nfc
real*4 max
integer nbits
parameter (nbits=32)
integer bndy(0:(nc-1)/nbits,nr,np)
real*4 a(nc,nr,np),grad(nc,nr,np),thresh
common/data/ a,grad,bndy
write(6,*) ' Percent in homogeneous blobs?'
read(6,*) thresh
write(6,*) ' Input file name?'
read(6,1) infile
write(6,*) ' Output file name?'
read(6,1) outfile
1 format(a)
write(6,*) ' Here we go'
call formdata(infile)
write(6,*) ' Oh boy, we have data'
call formgrad(max)
write(6,*) ' Gradient formed'
call findthrs(thresh,max)
write(6,*) ' Found a threshold:',thresh
call findbndy(thresh)
write(6,*) ' Boundaries marked'
call extract(testsets,means,ntstsets,nmeans)
write(6,*) ' Extracted test sets and initial means'
write(6,*) ' There are ',ntstsets,' testsets.'
call numclu(testsets,means,nb,ntstsets,nmeans,nfc)
write(6,*) ' Clusters found: there are:',nfc
call perpixel(means,nfc)
write(6,*) ' Classification step finished'
call cleanup(nfc)
write(6,*) ' Spatial fixups finished'
call storeit(outfile)
stop
end
subroutine formdata(infile)
implicit none ! remove for old version 2.1.1 for parallel
c
c The idea is to place charges at points read in and to set the stren
c equal to the charge/square of distance except not less than 2.0 on
c distance.
c
character*64 infile
integer nc,nr,np,nb
integer nbits
parameter (nbits=32)
parameter(nb=1,nc=32,nr=32,np=32)
integer bndy(0:(nc-1)/nbits,nr,np)
real*4 a(nc,nr,np),grad(nc,nr,np)
common/data/ a,grad,bndy

```



```

real*4 center1,center2,center3,charge,temp
integer k1,k2,i1,i2,j1,j2
integer nchar,i,j,k,l,is
character*1 yesno
open(99,file=infile,status='old')
nchar = 0
is = 12321
do 10 l = 1,100000
    read(99,*,end=20) center1,center2,center3,charge
    nchar = nchar+1
    charge = 1.3*sqrt(charge)
    k1 = center1-charge
    if (k1.lt.1) k1 = 1
    k2 = center1+charge
    if (k2.gt.np) k2 = np
    j1 = center2-charge
    if (j1.lt.1) j1 = 1
    j2 = center2+charge
    if (j2.gt.nr) j2 = nr
    i1 = center3-charge
    if (i1.lt.1) i1 = 1
    i2 = center3+charge
    if (i2.gt.nc) i2 = nc
    do 50 k = k1,k2
    do 50 j = j1,j2
    do 50 i = i1,i2
        a(i,j,k) = charge+(ran(is)-ran(is))*0.4
50    continue
10    continue
20    do 40 k = 1,np
    do 40 j = 1,nr
    do 40 i = 1,nc
        if (a(i,j,k).eq.0.) then
            a(i,j,k) = (ran(is)+ran(is)+ran(is)+ran(is)+ran(is)+
+ ran(is)+ran(is)-ran(is)+ran(is)+ran(is)+ran(is)-ran(is))*9.
            end if
40    continue
    write(6,*) ' Dump data?'
    read(6,1) yesno
1    format(a)
    if (yesno.eq.'y'.or.yesno.eq.'Y') then
        write(6,2) a
2    format(1x,16f7.2)
    end if

    write(6,*) ' I read',nchar
    return
end

subroutine formgrad(max)
implicit none ! remove for old version 2.1.1 for parallel
c
c Form the square of the magnitude of the gradient of a. Only inside
c
integer nc,nr,np,nb
integer nbits
parameter (nbits=32)
parameter (nb=1,nc=32,nr=32,np=32)
integer bndy(0:(nc-1)/nbits,nr,np)
real*4 a(nc,nr,np),grad(nc,nr,np),temp,max

```

```

common/data/ a,grad,bndy
integer k,j,i
max = 0.
C
C This logic defines grad inside. Easy enough.
C
do 10 k = 2,np-1
do 20 j = 2,nr-1
do 40 i = 2,nc-1
temp = (a(i+1,j,k)-a(i-1,j,k))**2+
+ (a(i,j+1,k)-a(i,j-1,k))**2+(a(i,j,k+1)-a(i,j,k-1))**2
if (temp.gt.max) then
max = temp
write(6,*) max,i,j,k,a(i,j,k)
end if
grad(i,j,k) = temp
40 continue
20 continue
10 continue
C
C Now define grad on the boundary of the parallelepiped.
C
do 110 k = 1,np,np-1
do 120 j = 2,nr-1
do 140 i = 2,nc-1
temp = ((a(i+1,j,k)-a(i-1,j,k))**2+
+ (a(i,j+1,k)-a(i,j-1,k))**2)*1.5
if (temp.gt.max) then
max = temp
write(6,*) max,i,j,k,a(i,j,k)
end if
grad(i,j,k) = temp
140 continue
120 continue
110 continue
do 210 j = 1,nr,nr-1
do 220 k = 2,np-1
do 240 i = 2,nc-1
temp = ((a(i+1,j,k)-a(i-1,j,k))**2+
+ (a(i,j,k+1)-a(i,j,k-1))**2)*1.5
if (temp.gt.max) then
max = temp
write(6,*) max,i,j,k,a(i,j,k)
end if
grad(i,j,k) = temp
240 continue
220 continue
210 continue
do 310 i = 1,nc,nc-1
do 320 k = 2,np-1
do 340 j = 2,nr-1
temp = ((a(i,j+1,k)-a(i,j-1,k))**2+
+ (a(i,j,k+1)-a(i,j,k-1))**2)*1.5
if (temp.gt.max) then
max = temp
write(6,*) max,i,j,k,a(i,j,k)
end if
grad(i,j,k) = temp
340 continue
320 continue

```

```

310 continue
C
C The corners.
C
do 410 k = 1,np,np-1
do 420 j = 1,nr,nr-1
do 440 i = 1,nc,nc-1
    grad(i,j,k) = max
440 continue
420 continue
410 continue
write(6,*) ' Down the center: data'
write(6,*) (a(i,nr/2,np/2),i=1,nc)
write(6,*) ' Down the center: gradient:'
write(6,*) (grad(i,nr/2,np/2),i=1,nc)
write(6,*) ' Maximum gradient:',max
return
end
subroutine findthrs(th,max)
implicit none ! remove for old version 2.1.1 for parallel
integer nc,nr,np,nb
parameter(nb=1,nc=32,nr=32,np=32)
real*4 max
integer nbits
parameter (nbits=32)
real*4 hist(100)
integer bndy(0:(nc-1)/nbits,nr,np)
real*4 a(nc,nr,np),grad(nc,nr,np),th
integer cs,i,j,k,count
common/data/ a,grad,bndy
th = (100.-th)*(nc-2)*(nr-2)*(np-2)/8.
do 5 i = 1,100
5 hist(i) = 0.
do 10 i = 2,nc-1,2
do 10 j = 2,nr-1,2
do 10 k = 2,np-1,2
    cs = 1+99*grad(i,j,k)/max
    hist(cs) = hist(cs)+100.
10 continue
count = 0
write(6,*) ' Histogram of counts'
write(6,*) (ifix(hist(i)/100.),i=1,100)

do 20 i = 100,0,-1
    count = count+hist(i)
    if (count.ge.th) go to 30
20 continue
30 th = (max*i-1.)/99.
return
end
subroutine findbndy(th)
implicit none ! remove for old version 2.1.1 for parallel
integer nc,nr,np,nb,ix,iy,iz,i,j,k,nbits,ipset,ibset
parameter (nbits=32)
parameter(nb=1,nc=32,nr=32,np=32)
real*4 a(nc,nr,np),grad(nc,nr,np),th
integer bndy(0:(nc-1)/nbits,nr,np)
common/data/ a,grad,bndy
ipset(ix,iy,iz) = ibset(bndy((ix-1)/nbits,iy,iz),
+ nbndy-1-mod(ix,nbits))

```

```

do 10 k = 1,np
do 10 j = 1,nr
do 10 i = 1,nc
    if (grad(i,j,k).gt.th) then
        bndy((i-1)/nbits,j,k) = ipset(i,j,k)
    end if
10 continue
return
end
subroutine extract(testsets,means,ntstsets,nmeans)
implicit none ! remove for old version 2.1.1 for parallel
integer nc,nr,np,nb,ix,iy,iz,x,y,z,nsa,map
parameter(nb=1,nc=32,nr=32,np=32,nsa=nc*nr/10,map=222)
integer knt(nsa),lab(nsa)
integer testsets(5,356),means(256)
integer nbits
parameter (nbits=32)
integer nmeans,ntstsets,c,s,llbl,nsamax,i25,i1,i2,it,l,m,nts
logical lfound
integer lold,lsave,maxslot
integer bndy(0:(nc-1)/nbits,nr,np),plane(nc,nr,2)
real*4 a(nc,nr,np),grad(nc,nr,np),dat(map,nsa)
logical point
common/data/ a,grad,bndy
point(ix,iy,iz) = btest(bndy((ix-1)/nbits,iy,iz),
+                      nbits-1-mod(ix,nbits))
c
c First, go through the array and set the gradient to -1 at points wh
c it had been thresholded. Do this for all six neighbors too.
c
do z = 1,np
do y = 1,nr
do x = 1,nc
    if (.not.point(x,y,z)) go to 10
    grad(x,y,z) = -1.
    if (x.gt.1) grad(x-1,y,z) = -1.
    if (x.lt.nc) grad(x+1,y,z) = -1.
    if (y.gt.1) grad(x,y-1,z) = -1.
    if (y.lt.nr) grad(x,y+1,z) = -1.
    if (z.gt.1) grad(x,y,z-1) = -1.
    if (z.lt.np) grad(x,y,z+1) = -1.
10 end do
end do
end do
c
c Initialization:
s = 0 ! summer of distances
c = 0 ! count of test sets encountered
llbl = 1 ! label
nsamax = 0 ! number of slots in use for labels
ntstsets = 0 ! count of number of test sets collected
i25 = 0 ! pointer used by extract
call opentemp(10,5) ! a file to store the samples
i1 = 1 ! circular buffer i1 oldest
i2 = 2 ! pointers for two planes i2 newest
c
c Build the first plane: it is special.
c
c call zap(plane(1,1,i1),nc*nr) ! not necessary in the present
do y = 1,nr ! Process this plane by rows

```

```

do x = 1,nc    ! and columns.
  if (grad(x,y,i1).ge.0.) then          ! Find a critter.
    if (x.eq.1) then ! Got one. Start of a row?
      if (y.eq.1) then ! Yep. First row?
        plane(x,y,i1) = llbl ! Yep. Assign the label.
      else if (plane(x,y-1,i1).gt.0) then ! Label above?
        plane(x,y,i1) = plane(x,y-1,i1) ! Yep. Transfe
        go to 20 ! and break out of logic.
      else
        llbl = llbl+1 ! Build a new label
        plane(x,y,i1) = llbl ! and assign.
        go to 20
      end if
    else
      if (plane(x-1,y,i1).gt.0) then ! Look to left.
        plane(x,y,i1) = plane(x-1,y,i1) ! Got one
        go to 20 ! Done...next
      end if
      if (y.eq.1) then ! First row?
        llbl = llbl+1 ! Yep. Start a new label
        plane(x,y,i1) = llbl ! and assign.
      else
        if (plane(x,y-1,i1).gt.0) then ! Nope. Look
          plane(x,y,i1) = plane(x-1,y,i1) ! above and as
        else ! else
          llbl = llbl+1 ! make a new label
          plane(x,y,i1) = llbl ! and assign.
        end if
      end if
    end if ! First column logic.
  end if ! Blob logic.
20 end do ! Column loop.
end do ! Row loop.
do z = 2,np ! Plane loop starts.

c
c now build plane i2
c
call zap(plane(1,1,i2),nc*nr)
do y = 1,nr ! Again by rows
  do x = 1,nc ! and columns.
    if (grad(x,y,z).ge.0.) then ! If a blob point is found
      if (plane(x,y,i1).gt.0) then ! then look to the pre
        plane(x,y,i2) = plane(x,y,i1) ! plane, else the logi
        go to 30 ! exactly the same as above.
      end if
      if (x.eq.1) then
        if (y.eq.1) then
          plane(x,y,i2) = llbl
        else
          if (plane(x,y-1,i2).gt.0) then
            plane(x,y,i2) = plane(x,y-1,i2)
            go to 30
          else
            llbl = llbl+1
            plane(x,y,i2) = llbl
            go to 30
          end if
        end if
      end if
    else
      if (plane(x-1,y,i2).gt.0) then

```

```

        plane(x,y,i2) = plane(x-1,y,i2)
        go to 30
    end if
    if (y.eq.1) then
        llbl = llbl+1
        plane(x,y,i2) = llbl
    else
        if (plane(x,y-1,i2).gt.0) then
            plane(x,y,i2) = plane(x-1,y,i2)
        else
            llbl = llbl+1
            plane(x,y,i2) = llbl
        end if
    end if
end if
end if
end if
30   end do
    end do
end do
c
c   doing plane z-1 in the sense of the data.
c
    do y = 1,nr      ! process one row at a time

c   throughout, l always is the pointer into the collected stuff

    do l = 1,nsamax      ! this initially falls through (no lab
        if (knt(l).gt.0) then      ! test if a label has been fou
            lfound = .false.      ! lfound is a flag that says that labe
c                                   was found. This logic starts fresh
c                                   for each scan line.
            do x = 1,nc      ! Process this line searching for
                if (plane(x,y,i1).eq.lab(l)) then      ! find it?
                    plane(x,y,i1) = 0      ! Yes.
                    lfound = .true.      ! Fly the flag.
                    if (knt(l).lt.map) then      ! Is there room?
                        m = knt(l)+1      ! Yes. Incr knt
                        knt(l) = m      !
                        dat(m,l) = a(x,y,z-1)      ! and save the data.
                    else      ! No. Close that label.
                        call gettst(l,knt,dat,nts,i25,map,nsa,c,s,nsamax)
                    end if
                end if
            end do
            if (.not.lfound)      ! If this label was not found then clo
                call gettst(l,knt,dat,nts,i25,map,nsa,c,s,nsamax)
            +
            end if
        end do      ! Label loop.
        lold = 0      ! This is to the most recently encountered lab
        do x = 1,nc
            if (plane(x,y,i1).ne.0) then      ! Test for valid label
                if (plane(x,y,i1).ne.lold) then      ! Yes. Test if old one
                    if (nsamax.eq.0) nsamax = 1      ! Now we are started.
                    do l = 1,nsamax ! Not the old one.
                        if (knt(l).eq.0) then ! Look for room for it.
                            knt(l) = 1      ! start a new critter here
                            lsave = 1      ! lsave is where lold goes
                            lold = plane(x,y,i1)
                            lab(l) = lold
                            dat(l,l) = a(x,y,z-1)

```

```

        go to 1      ! Next point.
    end if
end do ! If this falls through, then no new slots wer
nsamax = nsamax+1
if (nsamax.gt.nsa) then ! test if we are absolutely ou
    l = maxslot(knt,nsa,map)      ! Yes. Find fattest a
    call gettst(l,knt,dat,nts,i25,map,nsa,c,s,nsamax)
    knt(l) = 1      ! Start a new critter here.
    lsave = l
    lold = lab(l)
    dat(1,l) = a(x,y,z-1)
    nsamax = nsa ! Reset pointer
else ! There is room for a new one.
    knt(nsamax) = 1      ! Start a new critter here.
    lsave = nsamax
    lold = plane(x,y,i1)
    lab(nsamax) = lold
    dat(1,nsamax) = a(x,y,z-1)
end if
else ! Yes, we found the old one.
    m = knt(lsave)+1      ! Prepare to add it.
    if (m.le.map) then ! is there room?
        knt(lsave) = m      ! Yes. Add.
        dat(m,lsave) = a(x,y,z-1)
    else ! No room. Close the full label.
        call gettst(lsave,knt,dat,nts,i25,map,nsa,c,s,nsamax)
        lold = 0      ! Point to nil label.
    end if
end if ! Label search logic.
end if ! Valid label in map logic.
1 end do ! Next point loop.
c swap planes
    it = i1
    i1 = i2
    i2 = it
end do

c
c Now the last plane of labels should be gathered.
c
    do y = 1,nr ! process one row at a time
        do l = 1,nsamax ! this initially falls through (no lab
            if (knt(l).gt.0) then ! test if a label has been fou
                lfound = .false. ! lfound is a flag that says that labe
                    was found. This logic starts fresh
                    for each scan line.
                do x = 1,nc ! Process this line searching for
                    if (plane(x,y,i1).eq.lab(l)) then ! find it?
                        plane(x,y,i1) = 0 ! Yes.
                        lfound = .true. ! Fly the flag.
                        if (knt(l).lt.map) then ! Is there room?
                            m = knt(l)+1 ! Yes. Incr knt
                            knt(l) = m !
                            dat(m,l) = a(x,y,np) ! and save the data.
                        else ! No. Close that label.
                            call gettst(l,knt,dat,nts,i25,map,nsa,c,s,nsamax)
                        end if
                    end if
                end do
            end do
        if (.not.lfound) ! If this label was not found then clo
            call gettst(l,knt,dat,nts,i25,map,nsa,c,s,nsamax)
        +

```

```

        end if
    end do          ! Label loop.
    lold = 0       ! This is to the most recently encountered lab
    do x = 1,nc
        if (plane(x,y,i1).ne.0) then          ! Test for valid label
            if (plane(x,y,i1).ne.lold) then    ! Yes. Test if old one
                if (nsamax.eq.0) nsamax = 1    ! Now we are started.
                do l = 1,nsamax ! Not the old one.
                    if (knt(l).eq.0) then ! Look for room for it.
                        knt(l) = 1 ! start a new critter here
                        lsave = l ! lsave is where lold goes
                        lold = plane(x,y,i1)
                        lab(l) = lold
                        dat(1,l) = a(x,y,np)
                        go to 11 ! Next point.
                    end if
                end do ! If this falls through, then no new slots wer
                nsamax = nsamax+1
                if (nsamax.gt.nsa) then ! test if we are absolutely ou
                    l = maxslot(knt,nsa,map) ! Yes. Find fattest a
                    call gettst(l,knt,dat,nts,i25,map,nsa,c,s,nsamax)
                    knt(l) = 1 ! Start a new critter here.
                    lsave = l
                    lold = plane(x,y,i1)
                    lab(l) = lold
                    dat(1,l) = a(x,y,np)
                    nsamax = nsa ! Reset pointer
                else ! There is room for a new one.
                    knt(nsamax) = 1 ! Start a new critter here.
                    lsave = nsamax
                    lold = plane(x,y,i1)
                    lab(nsamax) = lold
                    dat(1,nsamax) = a(x,y,np)
                end if
            else ! Yes, we found the old one.
                m = knt(lsave)+1 ! Prepare to add it.
                if (m.le.map) then ! is there room?
                    knt(lsave) = m ! Yes. Add.
                    dat(m,lsave) = a(x,y,np)
                else ! No room. Close the full label.
                    call gettst(lsave,knt,dat,nts,i25,map,nsa,c,s,nsamax)
                    lold = 0 ! Point to nil label.
                end if ! If room logic.
            end if ! Label search logic.
        end if ! Valid label in map logic.
    11 end do ! Next point loop.
    end do ! Next row loop.

```

```

c
c Now all open slots should be closed.
c

```

```

    do l = 1,nsamax
        if (knt(l).ge.5)
+      call gettst(l,knt,dat,nts,i25,map,nsa,c,s,nsamax)
    end do
    ntstsets = nts
    return
end
subroutine gettst(l,knt,dat,nts,i25,map,nsa,c,s,nsamax)
implicit none
integer l ! the label about to be closed

```



```

integer nts      ! count of the number of test sets found
integer i25     ! circular buffer pointer
integer map     ! max in a blob
integer nsa     ! max open at once
integer knt(nsa) ! the count of the number with label 1
real dat(map,nsa) ! the data in each blob
integer c ! counter
real s ! summer
integer nsamax ! current number of potentially open critters
integer kn
real tdist,tsp(5),last25(25),a
integer m,is,ip
kn = knt(1)
if (kn.gt.4) then
  tsp(1) = dat(1,1)
  tsp(5) = dat(kn,1)
  tdist = abs(tsp(1)-tsp(5)) ! distance first to last
  if (tdist.eq.0.) go to 1
  s = s+tdist
  c = c+1
  if (c.gt.4096) then
    c = c/2
    s = s/2.
  end if
  a = s/c ! average so far
  if (nts.gt.25) then ! Is it initially
    if (tdist*2..lt.a) go to 1 ! interesting?
    if (tdist.gt.4.*a) go to 1 ! believable?
    do m = 1,25
      if (abs(tsp(1)-last25(m)).lt.tdist) go to 1 ! new?
    end do
  end if
  is = (kn-1)/4
  m = 1+is
  do ip = 2,4
    tsp(ip) = dat(m,1)
    m = m+is
  end do
  i25 = i25+1
  if (i25.gt.25) i25 = 25
  last25(i25) = tsp(5)
  write(10,*) (tsp(m),m=1,5)
  nts = nts+1
  type*,tsp
end if
1 knt(1) = 0
return
end
subroutine numclu(testsets,means,nb,ntstsets,nmeans,nfc)
implicit none ! remove for old version 2.1.1 for parallel
integer nb,nmeans,nfc,ntstsets
integer testsets(5,356),means(256)
return
end
subroutine perpixel(means,nfc)
implicit none ! remove for old version 2.1.1 for parallel
integer nc,nr,np,nb
parameter(nb=1,nc=32,nr=32,np=32)
integer nbits
parameter (nbits=32)

```

```

integer testsets(5,356),means(256),nfc
integer bndy(0:(nc-1)/nbits,nr,np)
real*4 a(nc,nr,np),grad(nc,nr,np)
common/data/ a,grad,bndy
return
end
subroutine cleanup(nfc)
implicit none ! remove for old version 2.1.1 for parallel
integer nc,nr,np,nb
parameter(nb=1,nc=32,nr=32,np=32)
integer nbits
parameter (nbits=32)
integer testsets(5,356),means(256),nfc
integer bndy(0:(nc-1)/nbits,nr,np)
real*4 a(nc,nr,np),grad(nc,nr,np)
common/data/ a,grad,bndy
return
end
subroutine storeit(outfile)
implicit none ! remove for old version 2.1.1 for parallel
character*64 outfile
integer nc,nr,np,nb
integer nbits
parameter (nbits=32)
parameter(nb=1,nc=32,nr=32,np=32)
integer bndy(0:(nc-1)/nbits,nr,np)
real*4 a(nc,nr,np),grad(nc,nr,np)
common/data/ a,grad,bndy
open(98,file=outfile,status='new')
return
end
subroutine opentemp(iu,nr)
implicit none
integer iu,nr
open(iu,status='new')!,disp='delete',form='unformatted'
return
end
subroutine zap(a,n)
integer a(n),n,i
do i = 1,n
  a(i) = 0
end do
return
end
function maxslot(k,n,m)
integer k(n),n,m,max
integer maxslot
maxslot = 1
max = k(1)
if (max.ge.m) return
do i = 2,n
  if (max.lt.k(i)) then
    max = k(i)
    maxslot = i
    if (max.ge.m) return
  end if
end do
return
end

```

Starr Output

*output of a
run of starr*

Trying 128.194.7.20...
Connected to 128.194.7.20.
Escape character is '^]'.

Welcome to VAX/VMS V5.3

Username: AMOEBA

Password:

Welcome to VAX/VMS version V5.3 on node MONICA
Last interactive login on Thursday, 18-APR-1991 14:40
Last non-interactive login on Tuesday, 9-APR-1991 08:16

Device Name	Device Status	Error Count	Volume Label	Free Blocks	Trans Count	Mnt Cnt
DUA0:	Mounted	0	VAXVMSRL5	2379	139	1

%TYPE-W-SEARCHFAIL, error searching for SYS\$SYSDEVICE:[AMOEBA]WELCOME.TXT;

-RMS-E-FNF, file not found

MONICA> type balls.dat

3.000000	3.000000	3.000000	17.62415
3.000000	3.000000	14.00000	19.16363
3.000000	3.000000	25.00000	10.19850
3.000000	14.00000	3.000000	19.16363
3.000000	14.00000	14.00000	10.19850
3.000000	14.00000	25.00000	4.367349
3.000000	25.00000	3.000000	10.19850
3.000000	25.00000	14.00000	4.367349
3.000000	25.00000	25.00000	4.554211
14.00000	3.000000	3.000000	19.16363
14.00000	3.000000	14.00000	10.19850
14.00000	3.000000	25.00000	4.367349
14.00000	14.00000	3.000000	10.19850
14.00000	14.00000	14.00000	4.367349
14.00000	14.00000	25.00000	4.554211
14.00000	25.00000	3.000000	4.367349
14.00000	25.00000	14.00000	4.554211
14.00000	25.00000	25.00000	10.82963
25.00000	3.000000	3.000000	10.19850
25.00000	3.000000	14.00000	4.367349
25.00000	3.000000	25.00000	4.554211
25.00000	14.00000	3.000000	4.367349
25.00000	14.00000	25.00000	10.82963
25.00000	25.00000	3.000000	4.554211
25.00000	25.00000	14.00000	10.82963
25.00000	25.00000	25.00000	19.52651

MONICA> run starr

Percent in homogeneous blobs?

45

Input file name?

balls

Output file name?

temp

Here we go

Dump data?

n

I read 27

Oh boy, we have data

4.6458825E-02	2	2	2	5.388172
0.1607398	4	2	2	5.440030
0.7804615	7	2	2	5.509752
2.574856	19	2	2	6.008701
4.938468	20	2	2	4.069189
910.2798	29	2	2	4.070025
1160.500	30	3	2	26.69777
1649.536	29	4	2	3.992256
2480.657	29	5	2	4.393729
2509.603	30	6	2	32.90219
3225.109	27	8	2	39.30929

3368.889	27	11	2	2.851958
3696.088	21	14	2	54.78817
3830.919	11	27	3	2.799880
4401.765	16	27	3	2.718645
4599.657	11	22	5	2.713610
4916.878	27	22	5	2.775974
5389.722	16	25	5	2.508463
6040.157	22	5	11	2.787701
6915.316	5	27	22	2.593717

Down the center: data

4.192015	4.101766	4.086305	4.477773	4.242034
3.987885	4.058863	26.63864	46.00188	33.09476
2.840770	2.688167	2.778892	2.902167	2.696835
2.701120	41.67275	37.79688	22.37953	27.30846
36.89902	2.596532	2.835341	2.611711	2.707472
2.887982	2.695838	48.42439	53.47391	54.88974
36.03139	51.11856			

Down the center: gradient:

0.2917202	1.4465959E-02	0.1863152	6.7582548E-02	0.2725425
4.2965472E-02	513.1008	2216.435	400.3434	1888.532
2731.161	2784.995	3468.301	2346.421	1901.320
3477.114	1545.977	693.3981	238.9257	260.4082
875.5566	3007.539	2302.260	2190.771	1688.093
3481.299	5705.418	2749.697	262.5401	462.3196
202.5814	66.00420			

Maximum gradient: 6915.316

Gradient formed

Histogram of counts

1111	120	134	137	120	108
89	88	101	67	85	87
78	75	74	73	72	62
56	62	58	43	37	45
34	34	32	34	27	21
21	20	12	18	14	15
13	14	7	12	5	5
2	6	8	2	2	3
5	4	2	1	1	1
4	2	3	1	1	0
1	2	0	0	2	0
0	1	0	1	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0

Found a threshold: 349.2483

Boundaries marked

35.39187	52.49762	34.37973	57.91971	50.60735
44.08176	28.26985	46.18728	39.66749	49.94583
27.17790	49.57285	31.75939	16.22164	36.11312
30.28798	15.71326	40.85241	48.10483	54.05400
50.10608	50.84894	38.71812	31.19532	34.46811
40.86628	30.90541	41.06978	23.77833	37.57311
47.80839	31.42234	32.52766	38.54172	35.83867
35.45852	30.60879	38.59006	48.96417	48.17749

48.81665	39.61263	31.82920	44.17275	37.47644
33.88279	31.43385	30.24509	33.16746	38.61612
44.65694	24.07245	51.83775	42.94830	33.40131
36.13909	35.52843	33.60717	46.51528	30.83201
35.39187	52.49762	34.37973	57.91971	50.60735
33.76551	33.91352	42.39333	29.63771	34.29617
44.08176	28.26985	46.18728	40.25033	24.77884
18.95086	59.50185	32.19398	38.76727	46.82760
39.72323	39.69683	26.37075	25.32755	28.58317

Extracted test sets and initial means

There are 17 testsets.

Clusters found: there are: 0

Classification step finished

Spatial fixups finished

FORTTRAN STOP

MONICA>

APPENDIX C

Findp: Program and Output

Findp

```

integer numberd,ndx(20),ktr(26)
parameter (numberd=52)
real mind,mind1,mind2,dis(numberd,numberd),
+   sim(numberd,numberd),smax,s
logical changed,found(numberd),readf
integer counter(numberd,numberd),similar(numberd,numberd)
integer seed(26,52),nf(26)
integer nbr(numberd,3)
integer weirdd(numberd,numberd)
integer rings(20,10)
integer rn      ! ring number
integer pndx(numberd)
real c(3)
character*64 filename
real carbon(3,numberd)
real pool(3,numberd)
data carbon/.46141 ,.29111 ,.32291
+ ,.16608 ,.25634 ,.43206
+ ,.16040 ,.25822 ,.10400
+ ,.30720 ,-.05160 ,.17651
+ ,.69619 ,.16068 ,.16331
+ ,.79505 ,.17274 ,.13024
+ ,.86146 ,.21187 ,.16901
+ ,.82901 ,.23895 ,.24084
+ ,.73015 ,.22689 ,.27391
+ ,.66374 ,.18776 ,.23515
+ ,.60226 ,-.02971 ,.32649
+ ,.64252 ,-.10888 ,.37558
+ ,.65167 ,-.08196 ,.44516
+ ,.62055 ,.02414 ,.46564
+ ,.58029 ,.10331 ,.41655
+ ,.57114 ,.07639 ,.34697
+ ,-.16218 ,.36745 ,.44139
+ ,-.25599 ,.34612 ,.47637
+ ,-.25765 ,.24197 ,.49470
+ ,-.16550 ,.15913 ,.47805
+ ,-.07169 ,.18046 ,.44307
+ ,-.07003 ,.28462 ,.42475
+ ,-.03087 ,.48707 ,.30682
+ ,-.05452 ,.59600 ,.29306
+ ,-.01462 ,.66104 ,.33342
+ ,.04893 ,.61715 ,.38754
+ ,.07258 ,.50823 ,.40130
+ ,.03268 ,.44318 ,.36094
+ ,.14488 ,.56935 ,.12561
+ ,.09509 ,.66912 ,.09901
+ ,.08098 ,.68239 ,.02646
+ ,.11666 ,.59590 ,-.01948
+ ,.16646 ,.49613 ,.00712
+ ,.18057 ,.48286 ,.07967
+ ,.40680 ,.20952 ,.02345
+ ,.51079 ,.17938 ,-.01289
+ ,.57960 ,.24570 ,-.01334
+ ,.54440 ,.34217 ,.02255
+ ,.44041 ,.37232 ,.05890
+ ,.37161 ,.30599 ,.05935
+ ,.27985 ,-.28881 ,.28871
+ ,.32932 ,-.39133 ,.31096
+ ,.42587 ,-.41117 ,.34145

```

```

+ ,.47295 ,-.32849 ,.34969
+ ,.42348 ,-.22597 ,.32744
+ ,.32693 ,-.20613 ,.29694
+ ,.07155 ,-.07371 ,.34792
+ ,-.03848 ,-.06758 ,.36135
+ ,-.10047 ,-.05715 ,.30442
+ ,-.05243 ,-.05285 ,.23407
+ ,.05760 ,-.05898 ,.22064
+ ,.11959 ,-.06941 ,.27757 /
type*, ' Data from external file? If so, enter file'
type*, ' name, else enter a semicolon and hit return.'
read33,filename
if (filename.ne. ';') then
  readf = .true.
  open(1,file=filename,status='old')
  read(1,*) number
  do i = 1,number
    read(1,*,end=11)(carbon(k,i),k=1,3)
  end do
else
  number = numberd
  readf = .false.
end if
11 type*,number
inpool = 0
do i = 1,number-1
  do j = i+1,number
c    type*,i,j,dist(carbon(1,i),carbon(1,j))
    dis(i,j) = dist(carbon(1,i),carbon(1,j))
    dis(j,i) = dist(carbon(1,i),carbon(1,j))
  end do
  dis(i,i) = 0
end do
if (readf) go to 44
do k = 5,number,6
  type 88,k,k+1,k+2,k+3,k+4,k+5
  smd = 10.**30
  big = 0.
  do i = k,k+5
    do j = k,k+5
      if (i.ne.j) then
        if (dis(i,j).gt.big) big = dis(i,j)
        if (dis(i,j).lt.smd) smd = dis(i,j)
      end if
    end do
    type 89,i,(dis(i,j),j=k,k+5)
  end do
  type*, ' ratio', big/smd
  type*
  call zap(c,3)
  do i = k,k+5
    c(1) = c(1)+carbon(1,i)
    c(2) = c(2)+carbon(2,i)
    c(3) = c(3)+carbon(3,i)
  end do
  c(1) = c(1)/6.
  c(2) = c(2)/6.
  c(3) = c(3)/6.
  do l = 1,number
    if (l.lt.k.or.l.gt.k+5) then

```

```

        type*,dist(carbon(1,1),c(1))
    else
        type*, ' in the group ',dist(carbon(1,1),c(1))
    end if
end do
end do
c calculate new exp. similarity measure
44   smax = 0
    type*, ' weight'
    read*,w
c   w = .65 ! found by experiment
    smin = 10.**30
    do i = 1,number-1
        do j = i+1,number
            s = w/dis(i,j)
            do k = 1,number
                if (k.ne.i.and.k.ne.j)
                    +   s = s + 1./(dis(i,k)+dis(j,k))
c                   do l = 1,number
c                       if (l.ne.k.and.l.ne.i.and.l.ne.j)
c                           +   s = s + 1./(dis(i,l)*dis(j,l)*dis(k,l))**(1/3)
c                       end do
                end do
                sim(i,j) = s
                sim(j,i) = s
                if (smax.lt.s) smax = s
                if (smin.gt.s) smin = s
            end do
        end do
    do i = 1,number-1
    c   do j = i+1,number
    c       counter(i,j) = ifix(16.99*(sim(i,j)-smin)/(smax-smin))
    c       counter(j,i) = counter(i,j)
    c   end do
    c end do
    c type8
    c do i = 1,number
    c     type7,i,(counter(i,j),j=1,number)
    c end do
    c type*
    c do i = 1,number
c find the three most similar neighbors.
        near2 = 0.
        mind2 = 0.
        do j = 1,number
            counter(i,j) = 0
            if (i.ne.j) then
                if (sim(i,j).gt.mind2) then
                    near = near1
                    near1 = near2
                    mind2 = sim(i,j)
                    near2 = j
                end if
            end if
        end do
        nbr(i,1) = near2
        if (near1.ne.0) then
            nbr(i,2) = near1
        else
            mind2 = 0.

```

```

do j = 1,number
  if (i.ne.j.and.j.ne.near2) then
    if (sim(i,j).gt.mind2) then
      near = near1
      mind2 = sim(i,j)
      near1 = j
    end if
  end if
end do
nbr(i,2) = near1
end if
if (near.ne.0) then
  nbr(i,3) = near
else
  mind2 = 0.
  do j = 1,number
    if (i.ne.j.and.j.ne.near2.and.j.ne.near1) then
      if (sim(i,j).gt.mind2) then
        mind2 = sim(i,j)
        near = j
      end if
    end if
  end do
  nbr(i,3) = near
end if
write(*,1)i,(nbr(i,k),k=1,3)
if (i.lt.nbr(i,1))then
  counter(i,nbr(i,1))=counter(i,nbr(i,1))+3
else
  counter(nbr(i,1),i)=counter(nbr(i,1),i)+3
end if
if (i.lt.nbr(i,2))then
  counter(i,nbr(i,2))=counter(i,nbr(i,2))+2
else
  counter(nbr(i,2),i)=counter(nbr(i,2),i)+2
end if
if (i.lt.nbr(i,3))then
  counter(i,nbr(i,3))=counter(i,nbr(i,3))+1
else
  counter(nbr(i,3),i)=counter(nbr(i,3),i)+1
end if
end do
nseed = 0
do i = 1,number
  found(i) = .false.
end do
do i = 1,number
  if (nbr(nbr(i,1),1).eq.i) then
    found(i) = .true.
    found(nbr(i,1)) = .true.
    nseed = nseed+1
    seed(nseed,1) = i
    seed(nseed,2) = nbr(i,1)
    nbr(i,1) = 0
    nf(nseed) = 2
  end if
end do
changed = .false.
if (nseed.gt.0) then
  do i = 1,number

```

```

        if (found(i)) go to 444
        it = nbr(i,1)          ! want to see if i points to something
here.
        do j = 1,nseed
222          do k = 1,nf(j)
              if (i.eq.seed(j,k)) go to 111    ! however, skip it if i
dy in the list.
              end do
              do k = 1,nf(j)
                if (it.eq.seed(j,k)) then
                  found(i) = .true.
                  nf(j) = nf(j)+1
                  seed(j,nf(j)) = i
                  changed = .true.
                  go to 222          ! restart the search??
                end if
              end do
111          end do          ! if this loop falls through we are through wi
444          end do
        end if
        if (changed) go to 333
        do i = 1,number
          if (.not.found(i)) then
            type*,i,'not found'! do something...but didn't have to
test.
          end if
        end do
        do j = 1,nseed
          type2,j,(seed(j,k),k=1,nf(j))
        end do
c now the problem is to get rid of the odd guy (if any)
        do j = 1,nseed
          if (nf(j).gt.14) then
            do k = 1,nf(j)
              nin = 0
              do m = 1,nf(j)
                if (m.ne.k) then
                  if (nbr(seed(j,k),2).eq.seed(j,m)) nin = nin+3
                  if (nbr(seed(j,k),3).eq.seed(j,m)) nin = nin+2
                end if
              end do
              ktr(k) = nin
            end do
            min = 1000
            do k = 1,nf(j)
              if (ktr(k).lt.min) then
                nout = k
                min = ktr(k)
              end if
            end do
            is = 0
            do k = 1,nf(j)
              if (ktr(k).eq.min) is = is+1
            end do
            if (is.eq.1) then
c              nseed = nseed+1
c              nf(nseed) = 1
c              seed(nseed,1) = seed(j,nout)
              inpool = inpool+1
              do k2 = 1,3

```

```

        pool(k2,inpool) = carbon(k2,seed(j,nout))
    end do
    pndx(inpool) = seed(j,nout)
    do k = nout+1,nf(j)
        seed(j,k-1) = seed(j,k)
    end do
    nf(j) = nf(j)-1
end if
end if
end do
do j = 1,nseed
    if (nf(j).eq.14) then
c   for each set of six...
        amax = 0
        do k = 1,nf(j)-7      ! leave eight out
            do k2 = k+1,nf(j)-6
                do k3 = k2+1,nf(j)-5
                    do k4 = k3+1,nf(j)-4
                        do k5 = k4+1,nf(j)-3
                            do k6 = k5+1,nf(j)-2
                                do k7 = k6+1,nf(j)-1
                                    do k8 = k7+1,nf(j)
                                        call zap(c,3)      ! compute the centroid of the rest
                                        do l = 1,nf(j)
                                            if (l.ne.k.and.l.ne.k2.and.l.ne.k3.and.k4.ne.l
+                                             .and.k5.ne.l.and.k6.ne.l.and.k7.ne.l.and
+                                             .k8.ne.l) then
                                                do m = 1,3
                                                    c(m) = c(m)+carbon(m,seed(j,l))
                                                end do
                                            end if
                                        end do
                                        do m = 1,3
                                            c(m) = c(m)/6.
                                        end do
                                        dt = dist(carbon(1,seed(j,k)),c(1))
                                        if (dt.gt.amax) then
                                            amax = dt
                                            nout = k
                                        end if
                                        dt = dist(carbon(1,seed(j,k2)),c(1))
                                        if (dt.gt.amax) then
                                            amax = dt
                                            nout = k2
                                        end if
                                        dt = dist(carbon(1,seed(j,k3)),c(1))
                                        if (dt.gt.amax) then
                                            amax = dt
                                            nout = k3
                                        end if
                                        dt = dist(carbon(1,seed(j,k4)),c(1))
                                        if (dt.gt.amax) then
                                            amax = dt
                                            nout = k4
                                        end if
                                        dt = dist(carbon(1,seed(j,k5)),c(1))
                                        if (dt.gt.amax) then
                                            amax = dt
                                            nout = k5
                                        end if

```

```

dt = dist(carbon(1,seed(j,k6)),c(1))
if (dt.gt.amax) then
    amax = dt
    nout = k6
end if
dt = dist(carbon(1,seed(j,k7)),c(1))
if (dt.gt.amax) then
    amax = dt
    nout = k7
end if
dt = dist(carbon(1,seed(j,k8)),c(1))
if (dt.gt.amax) then
    amax = dt
    nout = k8
end if
end do
end do
end do
end do
end do
end do
end do
end do
end do
c nseed = nseed+1
c nf(nseed) = 1
c seed(nseed,1) = seed(j,nout)
    inpool = inpool+1
    pndx(inpool) = seed(j,nout)
    do k2 = 1,3
        pool(k2,inpool) = carbon(k2,seed(j,nout))
    end do
do l = nout+1,nf(j)
    seed(j,l-1) = seed(j,1)
end do
nf(j) = nf(j)-1
end if
if (nf(j).eq.13) then
c for each set of six...
    amax = 0
    do k = 1,nf(j)-6 ! leave seven out
    do k2 = k+1,nf(j)-5
    do k3 = k2+1,nf(j)-4
    do k4 = k3+1,nf(j)-3
    do k5 = k4+1,nf(j)-2
    do k6 = k5+1,nf(j)-1
    do k7 = k6+1,nf(j)
        call zap(c,3) ! compute the centroid of the rest
        do l = 1,nf(j)
            if (l.ne.k.and.l.ne.k2.and.l.ne.k3.and.k4.ne.l
                + .and.k5.ne.l.and.k6.ne.l) then
                do m = 1,3
                    c(m) = c(m)+carbon(m,seed(j,l))
                end do
            end if
        end do
        do m = 1,3
            c(m) = c(m)/6.
        end do
        dt = dist(carbon(1,seed(j,k)),c(1))
        if (dt.gt.amax) then

```



```

        amax = dt
        nout = k
    end if
    dt = dist(carbon(1,seed(j,k2)),c(1))
    if (dt.gt.amax) then
        amax = dt
        nout = k2
    end if
    dt = dist(carbon(1,seed(j,k3)),c(1))
    if (dt.gt.amax) then
        amax = dt
        nout = k3
    end if
    dt = dist(carbon(1,seed(j,k4)),c(1))
    if (dt.gt.amax) then
        amax = dt
        nout = k4
    end if
    dt = dist(carbon(1,seed(j,k5)),c(1))
    if (dt.gt.amax) then
        amax = dt
        nout = k5
    end if
    dt = dist(carbon(1,seed(j,k6)),c(1))
    if (dt.gt.amax) then
        amax = dt
        nout = k6
    end if
    dt = dist(carbon(1,seed(j,k7)),c(1))
    if (dt.gt.amax) then
        amax = dt
        nout = k7
    end if
end do
end do
end do
end do
end do
end do
end do
end do
c      nseed = nseed+1
c      nf(nseed) = 1
c      seed(nseed,1) = seed(j,nout)
        inpool = inpool+1
        pndx(inpool) = seed(j,nout)
        do k2 = 1,3
            pool(k2,inpool) = carbon(k2,seed(j,nout))
        end do
    do l = nout+1,nf(j)
        seed(j,l-1) = seed(j,1)
    end do
    nf(j) = nf(j)-1
end if
c  for each set of six...
    amax = 0
    do k = 1,nf(j)-5      ! leave six out
    do k2 = k+1,nf(j)-4
    do k3 = k2+1,nf(j)-3
    do k4 = k3+1,nf(j)-2

```

```

do k5 = k4+1,nf(j)-1
do k6 = k5+1,nf(j)
  call zap(c,3)      ! compute the centroid of the rest
  do l = 1,nf(j)
    if (l.ne.k.and.l.ne.k2.and.l.ne.k3.and.k4.ne.l
      .and.k5.ne.l.and.k6.ne.l) then
      do m = 1,3
        c(m) = c(m)+carbon(m,seed(j,l))
      end do
    end if
  end do
  do m = 1,3
    c(m) = c(m)/6.
  end do
  dt = dist(carbon(1,seed(j,k)),c(1))
  if (dt.gt.amax) then
    amax = dt
    nout = k
  end if
  dt = dist(carbon(1,seed(j,k2)),c(1))
  if (dt.gt.amax) then
    amax = dt
    nout = k2
  end if
  dt = dist(carbon(1,seed(j,k3)),c(1))
  if (dt.gt.amax) then
    amax = dt
    nout = k3
  end if
  dt = dist(carbon(1,seed(j,k4)),c(1))
  if (dt.gt.amax) then
    amax = dt
    nout = k4
  end if
  dt = dist(carbon(1,seed(j,k5)),c(1))
  if (dt.gt.amax) then
    amax = dt
    nout = k5
  end if
  dt = dist(carbon(1,seed(j,k6)),c(1))
  if (dt.gt.amax) then
    amax = dt
    nout = k6
  end if
end do
end do
end do
end do
end do
end do
end do
+
c
c
c
nseed = nseed+1
nf(nseed) = 1
seed(nseed,1) = seed(j,nseed)
  inpool = inpool+1
  pndx(inpool) = seed(j,nout)
  do k2 = 1,3
    pool(k2,inpool) = carbon(k2,seed(j,nout))
  end do
do l = nout+1,nf(j)
  seed(j,l-1) = seed(j,1)

```

```

        end do
        nf(j) = nf(j)-1
    end if
    if (nf(j).eq.11) then
c   for each set of six...
        amax = 0
        do k = 1,nf(j)-4      ! leave five out
        do k2 = k+1,nf(j)-3
        do k3 = k2+1,nf(j)-2
        do k4 = k3+1,nf(j)-1
        do k5 = k4+1,nf(j)
            call zap(c,3)      ! compute the centroid of the rest
            do l = 1,nf(j)
                if (l.ne.k.and.l.ne.k2.and.l.ne.k3.and.k4.ne.l
                    .and.k5.ne.l) then
+
                    do m = 1,3
                        c(m) = c(m)+carbon(m,seed(j,l))
                    end do
                end if
            end do
            do m = 1,3
                c(m) = c(m)/6.
            end do
            dt = dist(carbon(1,seed(j,k)),c(1))
            if (dt.gt.amax) then
                amax = dt
                nout = k
            end if
            dt = dist(carbon(1,seed(j,k2)),c(1))
            if (dt.gt.amax) then
                amax = dt
                nout = k2
            end if
            dt = dist(carbon(1,seed(j,k3)),c(1))
            if (dt.gt.amax) then
                amax = dt
                nout = k3
            end if
            dt = dist(carbon(1,seed(j,k4)),c(1))
            if (dt.gt.amax) then
                amax = dt
                nout = k4
            end if
            dt = dist(carbon(1,seed(j,k5)),c(1))
            if (dt.gt.amax) then
                amax = dt
                nout = k5
            end if
        end do
    end do
    end do
    end do
    end do
    nseed = nseed+1
c   c   nf(nseed) = 1
c   c   seed(nseed,1) = seed(j,nout)
        inpool = inpool+1
        pndx(inpool) = seed(j,nout)
        do k2 = 1,3
            pool(k2,inpool) = carbon(k2,seed(j,nout))

```

```

        end do
        do l = nout+1,nf(j)
            seed(j,l-1) = seed(j,l)
        end do
        nf(j) = nf(j)-1
    end if
    if (nf(j).eq.10) then
c   for each set of six...
        amax = 0
        do k = 1,nf(j)-3      ! leave four out
            do k2 = k+1,nf(j)-2
                do k3 = k2+1,nf(j)-1
                    do k4 = k3+1,nf(j)
                        call zap(c,3)      ! compute the centroid of the rest
                        do l = 1,nf(j)
                            if (l.ne.k.and.l.ne.k2.and.l.ne.k3.and.k4.ne.l) then
                                do m = 1,3
                                    c(m) = c(m)+carbon(m,seed(j,l))
                                end do
                            end if
                        end do
                        do m = 1,3
                            c(m) = c(m)/6.
                        end do
                        dt = dist(carbon(1,seed(j,k)),c(1))
                        if (dt.gt.amax) then
                            amax = dt
                            nout = k
                        end if
                        dt = dist(carbon(1,seed(j,k2)),c(1))
                        if (dt.gt.amax) then
                            amax = dt
                            nout = k2
                        end if
                        dt = dist(carbon(1,seed(j,k3)),c(1))
                        if (dt.gt.amax) then
                            amax = dt
                            nout = k3
                        end if
                        dt = dist(carbon(1,seed(j,k4)),c(1))
                        if (dt.gt.amax) then
                            amax = dt
                            nout = k4
                        end if
                    end do
                end do
            end do
        end do
        nseed = nseed+1
c   nf(nseed) = 1
c   seed(nseed,1) = seed(j,nout)
        inpool = inpool+1
        pndx(inpool) = seed(j,nout)
        do k2 = 1,3
            pool(k2,inpool) = carbon(k2,seed(j,nout))
        end do
        do l = nout+1,nf(j)
            seed(j,l-1) = seed(j,l)
        end do
        nf(j) = nf(j)-1
    end if
end do

```

```

        end if
        if (nf(j).eq.9) then
c   for each set of six...
            amax = 0.
            do k = 1,nf(j)-2      ! leave three out
            do k2 = k+1,nf(j)-1
            do k3 = k2+1,nf(j)
                call zap(c,3)      ! compute the centroid of the rest
                do l = 1,nf(j)
                    if (l.ne.k.and.l.ne.k2.and.l.ne.k3) then
                        do m = 1,3
                            c(m) = c(m)+carbon(m,seed(j,l))
                        end do
                    end if
                end do
                do m = 1,3
                    c(m) = c(m)/6.
                end do
                dt = dist(carbon(1,seed(j,k)),c(1))
                if (dt.gt.amax) then
                    amax = dt
                    nout = k
                end if
                dt = dist(carbon(1,seed(j,k2)),c(1))
                if (dt.gt.amax) then
                    amax = dt
                    nout = k2
                end if
                dt = dist(carbon(1,seed(j,k3)),c(1))
                if (dt.gt.amax) then
                    amax = dt
                    nout = k3
                end if
            end do
        end do
        end do
        end do
c   nseed = nseed+1
c   nf(nseed) = 1
c   seed(nseed,1) = seed(j,nout)
            inpool = inpool+1
            pndx(inpool) = seed(j,nout)
            do k2 = 1,3
                pool(k2,inpool) = carbon(k2,seed(j,nout))
            end do
            do l = nout+1,nf(j)
                seed(j,l-1) = seed(j,l)
            end do
            nf(j) = nf(j)-1
        end if
c   for each set of six...
        if (nf(j).eq.8) then
            amax = 0.
            do k = 1,nf(j)-1      ! leave two out
            do k2 = k,nf(j)
                call zap(c,3)      ! compute the centroid of the rest
                do l = 1,nf(j)
                    if (l.ne.k.and.l.ne.k2) then
                        do m = 1,3
                            c(m) = c(m)+carbon(m,seed(j,l))
                        end do
                    end if
                end do
            end do
        end if
    end do
end do

```

```

        end if
    end do
    do m = 1,3
        c(m) = c(m)/6.
    end do
    dt = dist(carbon(1,seed(j,k)),c(1))
    if (dt.gt.amax) then
        amax = dt
        nout = k
    end if
    dt = dist(carbon(1,seed(j,k2)),c(1))
    if (dt.gt.amax) then
        amax = dt
        nout = k2
    end if
end do
end do
nseed = nseed+1
nf(nseed) = 1
seed(nseed,1) = seed(j,nout)
inpool = inpool+1
pndx(inpool) = seed(j,nout)
do k2 = 1,3
    pool(k2,inpool) = carbon(k2,seed(j,nout))
end do
do l = nout+1,nf(j)
    seed(j,l-1) = seed(j,1)
end do
nf(j) = nf(j)-1
end if
if (nf(j).eq.7) then
c   for each set of six...
    amax = 0.
    do k = 1,nf(j)      ! leave one out
        call zap(c,3)   ! compute the centroid of the rest
        do l = 1,nf(j)
            if (l.ne.k) then
                do m = 1,3
                    c(m) = c(m)+carbon(m,seed(j,1))
                end do
            end if
        end do
        do m = 1,3
            c(m) = c(m)/6.
        end do
        dt = dist(carbon(1,seed(j,k)),c(1))
        if (dt.gt.amax) then
            amax = dt
            nout = k
        end if
    end do
end do
nseed = nseed+1
nf(nseed) = 1
seed(nseed,1) = seed(j,nout)
inpool = inpool+1
pndx(inpool) = seed(j,nout)
do k2 = 1,3
    pool(k2,inpool) = carbon(k2,seed(j,nout))
end do
do l = nout+1,nf(j)

```

```

        seed(j,1-1) = seed(j,1)
    end do
    nf(j) = nf(j)-1
end if
end do
if (inpool.ge.6) then
    number = inpool
    do j = 1,3
        do i = 1,inpool
            carbon(j,i) = pool(j,i)
        end do
    end do
c restart with these after printing.
    type*
    type*, ' Groups found so far ... '
    do j = 1,nseed
        type2,j,(seed(j,k),k=1,nf(j))
    end do
    go to 11
else if (inpool.gt.0) then
    type*
    type*, ' Groups found so far ... '
    do j = 1,nseed
        type2,j,(seed(j,k),k=1,nf(j))
    end do
    type*
    if (inpool.gt.0) type*, ' These are not in a group '
    do j = 1,inpool
        type2,j,pndx(j)
    end do
end if

33     format(a)
2       format(i3,2x,40i3)
88     format(2x,6i7)
89     format(1x,i3,1x,6f7.4)
8       format(5x,'
+       '2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 4 4 4 4 ',
+       '4 4 4 4 4 4 5 5 5'/
+       4x,' 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 ',
+       '3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 ',
+       '7 8 9 0 1 2')
7       format(1x,i2,1x,52z2)
1       format(1x,13I4)
end
real function dist(a,b)
real a(3),b(3)
dist = 0.
do i = 1,3
    dist = dist+(a(i)-b(i))**2
end do
dist = sqrt(dist)
return
end

subroutine zap(a,n)
real a(n)
do i = 1,n
    a(i) = 0
end do

```

return
end

Findp Output

```
bright2> telnet 128.194.7.20
Trying 128.194.7.20...
Connected to 128.194.7.20.
Escape character is '^]'.

```

Welcome to VAX/VMS V5.3

Username: AMOEBA

Password:

Welcome to VAX/VMS version V5.3 on node MONICA
Last interactive login on Thursday, 18-APR-1991 14:45
Last non-interactive login on Tuesday, 9-APR-1991 08:16

Device Name	Device Status	Error Count	Volume Label	Free Blocks	Trans Count	Mnt Cnt
DUA0:	Mounted	0	VAXVMSRL5	2376	139	1

%TYPE-W-SEARCHFAIL, error searching for SYS\$SYSDEVICE:[AMOEBA]WELCOME.TXT;
-RMS-E-FNF, file not found

MONICA> sd

MONICA> run findp

Data from external file? If so, enter file name, else enter a semicolon and hit return.

```
;
      52
      5   6   7   8   9  10
10  0.0000 0.1049 0.1731 0.1726 0.1333 0.0834
  6  0.1049 0.0000 0.0863 0.1333 0.1667 0.1687
  7  0.1731 0.0863 0.0000 0.0833 0.1687 0.2099
  8  0.1726 0.1333 0.0833 0.0000 0.1049 0.1731
  9  0.1333 0.1667 0.1687 0.1049 0.0000 0.0863
10  0.0834 0.1687 0.2099 0.1731 0.0863 0.0000
ratio  2.518283
```

0.3371215
0.6418127
0.6129234
0.5208189

in the group 8.6282626E-02
in the group 8.3346076E-02
in the group 0.1049382
in the group 8.6281128E-02
in the group 8.3343178E-02
in the group 0.1049403

0.3063810
0.3739187
0.3883196
0.3471391
0.2975718
0.2699718
0.9698404
1.064973
1.062222
0.9691162
0.8686152

0.8660532
0.8503419
0.9126476
0.9132637
0.8472840
0.7816249
0.7856509
0.7238655
0.8224595
0.8534200
0.7894360
0.6936812
0.6586781
0.3982403
0.3317176
0.2863543
0.3163954
0.3925098
0.4295547
0.6923202
0.7409720
0.7114174
0.6203169
0.5585796
0.6029915
0.7573878
0.8594168
0.9063084
0.8538952
0.7512286
0.7011728

	11	12	13	14	15	16
11	0.0000	0.1015	0.1388	0.1503	0.1621	0.1125
12	0.1015	0.0000	0.0752	0.1621	0.2249	0.2006
13	0.1388	0.0752	0.0000	0.1125	0.2006	0.2030
14	0.1503	0.1621	0.1125	0.0000	0.1015	0.1388
15	0.1621	0.2249	0.2006	0.1015	0.0000	0.0752
16	0.1125	0.2006	0.2030	0.1388	0.0752	0.0000
ratio	2.991955					

0.3379711
0.5164840
0.5973534
0.3783226
0.2967898
0.3676921
0.4001977
0.3603922
0.2859595
0.2548333

in the group 7.5161621E-02
in the group 0.1124452
in the group 0.1014902
in the group 7.5161584E-02
in the group 0.1124452

in the group 0.1014903

0.8588144
0.9383804
0.9082348
0.7978216
0.7088068
0.7401204
0.8126745
0.9014487
0.9146012
0.8371202
0.7426279
0.7314651
0.7862124
0.8979306
0.9420315
0.8808371
0.7734148
0.7222019
0.4751616
0.4588591
0.4799675
0.5128325
0.5325630
0.5159658
0.4508483
0.4876290
0.4518676
0.3569372
0.2997278
0.3634570
0.5466185
0.6540291
0.7198058
0.6851465
0.5836367
0.5102568

	17	18	19	20	21	22
17	0.0000	0.1024	0.1664	0.2115	0.2077	0.1250
18	0.1024	0.0000	0.1058	0.2077	0.2500	0.2026
19	0.1664	0.1058	0.0000	0.1250	0.2026	0.2047
20	0.2115	0.2077	0.1250	0.0000	0.1024	0.1664
21	0.2077	0.2500	0.2026	0.1024	0.0000	0.1058
22	0.1250	0.2026	0.2047	0.1664	0.1058	0.0000

ratio 2.442571

0.6406472
0.3311506
0.4813473
0.6334385
0.9154456
1.017953
1.066957
1.016982
0.9138212

0.8608288
0.8309692
0.8920808
0.8857016
0.8200586
0.7623565
0.7667078

in the group 0.1057722
in the group 0.1250173
in the group 0.1023641
in the group 0.1057749
in the group 0.1250200
in the group 0.1023632

0.3018885
0.3878425
0.4431957
0.4191622
0.3454016
0.2841439
0.5482795
0.6015433
0.6506119
0.6472579
0.6067619
0.5579138
0.7203155
0.8279666
0.8813624
0.8360291
0.7332553
0.6699458
0.7286441
0.8329865
0.9036840
0.8762500
0.7757707
0.6983622
0.4260026
0.3672441
0.3616867
0.4040748
0.4583173
0.4735000

	23	24	25	26	27	28
23	0.0000	0.1123	0.1767	0.1726	0.1417	0.0943
24	0.1123	0.0000	0.0863	0.1417	0.1886	0.1886
25	0.1767	0.0863	0.0000	0.0943	0.1886	0.2246
26	0.1726	0.1417	0.0943	0.0000	0.1123	0.1767
27	0.1417	0.1886	0.1886	0.1123	0.0000	0.0863
28	0.0943	0.1886	0.2246	0.1767	0.0863	0.0000
ratio	2.602268					

0.5228370
0.3454710
0.4103922

0.6946232
 0.8119211
 0.8993405
 0.9349577
 0.8841639
 0.7944505
 0.7575936
 0.8311837
 0.9159837
 0.9080932
 0.8165437
 0.7297761
 0.7363958
 0.2688649
 0.3596641
 0.4348198
 0.4494689
 0.3922188
 0.2895158
 in the group 8.6321287E-02
 in the group 9.4306767E-02
 in the group 0.1123122
 in the group 8.6318716E-02
 in the group 9.4303660E-02
 in the group 0.1123155
 0.2604720
 0.2875511
 0.3535683
 0.3846312
 0.3788918
 0.3252436
 0.6167586
 0.7213477
 0.7412240
 0.6603644
 0.5491076
 0.5242960
 0.8853878
 0.9969854
 1.049619
 0.9953328
 0.8817991
 0.8237202
 0.6289373
 0.6216717
 0.6204986
 0.6185061
 0.6259428
 0.6351050

	29	30	31	32	33	34
29	0.0000	0.1146	0.1634	0.1502	0.1409	0.1042
30	0.1146	0.0000	0.0751	0.1409	0.2085	0.2058
31	0.1634	0.0751	0.0000	0.1042	0.2058	0.2293
32	0.1502	0.1409	0.1042	0.0000	0.1146	0.1634
33	0.1409	0.2085	0.2058	0.1146	0.0000	0.0751

34 0.1042 0.2058 0.2293 0.1634 0.0751 0.0000
ratio 3.053133

0.5168346
0.5013439
0.3297131
0.6697809
0.7140642
0.7843630
0.8275298
0.8005663
0.7311445
0.6878421
0.8197653
0.9187382
0.9309915
0.8497087
0.7509524
0.7325141
0.5319006
0.6202481
0.6796764
0.6691324
0.5956778
0.5169901
0.3156753
0.3034965
0.3254029
0.3460691
0.3608167
0.3519293
in the group
in the group
in the group
in the group
in the group
in the group
0.4650539
0.5580047
0.5651314
0.4794129
0.3743489
0.3668361
0.9149598
1.026898
1.076047
1.017449
0.9026543
0.8485794
0.7219574
0.7392245
0.7252344
0.6856784
0.6671527
0.6896936

7.5086616E-02
0.1042383
0.1146309
7.5087868E-02
0.1042395
0.1146324

	35	36	37	38	39	40
35	0.0000	0.1142	0.1803	0.1911	0.1700	0.1088
36	0.1142	0.0000	0.0956	0.1700	0.2176	0.2015
37	0.1803	0.0956	0.0000	0.1088	0.2016	0.2284
38	0.1911	0.1700	0.1088	0.0000	0.1142	0.1803
39	0.1700	0.2176	0.2016	0.1142	0.0000	0.0956
40	0.1088	0.2015	0.2284	0.1803	0.0956	0.0000
ratio	2.390187					

0.3006300

0.5133337

0.3259191

0.3989295

0.2856721

0.3523889

0.4174896

0.4167873

0.3607572

0.2969200

0.4489002

0.5478930

0.5807254

0.5294275

0.4422754

0.3922562

0.7682474

0.8635427

0.8725270

0.7947966

0.6964788

0.6776365

0.6178031

0.6756165

0.6964551

0.6568285

0.5996138

0.5817055

0.4539264

0.5524763

0.5665824

0.4827816

0.3799284

0.3648415

in the group 9.5567234E-02

in the group 0.1087767

in the group 0.1142161

in the group 9.5562533E-02

in the group 0.1087848

in the group 0.1142102

0.6540306

0.7412436

0.7588633

0.6869891

0.5892524

0.5739740

0.6253147
0.7047697
0.7224546
0.6568166
0.5708718
0.5574501

	41	42	43	44	45	46
41	0.0000	0.1160	0.1977	0.2064	0.1615	0.0955
42	0.1160	0.0000	0.1032	0.1615	0.1910	0.1857
43	0.1977	0.1032	0.0000	0.0955	0.1857	0.2320
44	0.2064	0.1615	0.0955	0.0000	0.1160	0.1977
45	0.1615	0.1910	0.1857	0.1160	0.0000	0.1032
46	0.0955	0.1857	0.2320	0.1977	0.1032	0.0000
ratio	2.429042					

0.6057661
0.6133400
0.6436676
0.3020320
0.5889291
0.6653641
0.7271731
0.7147459
0.6434230
0.5796993
0.3589895
0.3375008
0.3781908
0.4379539
0.4698505
0.4323780
0.8729894
0.9237661
0.8579059
0.7332855
0.6748018
0.7499402
0.8939756
1.002381
1.045657
0.9843845
0.8754086
0.8277283
0.9284191
1.040986
1.074769
1.000189
0.8883347
0.8498302
0.5974039
0.6054062
0.6776252
0.7347047
0.7318283
0.6673279

in the group 0.1031749
in the group 9.5500655E-02
in the group 0.1159861
in the group 0.1031759
in the group 9.5500983E-02
in the group 0.1159874

0.3859472
0.4816814
0.5393289
0.5065330
0.4167521
0.3534404

	47	48	49	50	51	52
47	0.0000	0.1110	0.1782	0.1696	0.1289	0.0853
48	0.1110	0.0000	0.0848	0.1289	0.1706	0.1789
49	0.1782	0.0848	0.0000	0.0853	0.1789	0.2220
50	0.1696	0.1289	0.0853	0.0000	0.1110	0.1782
51	0.1289	0.1706	0.1789	0.1110	0.0000	0.0848
52	0.0853	0.1789	0.2220	0.1782	0.0848	0.0000
ratio	2.618008					

0.5751342
0.3828247
0.4013503
0.3191126
0.7334319
0.8357884
0.9035051
0.8748468
0.7770073
0.7029162
0.5947101
0.6402128
0.6606217
0.6414452
0.6076587
0.5813889
0.4874850
0.5220048
0.4539543
0.3392665
0.2985591
0.3811291
0.5520599
0.6623901
0.7259642
0.6883720
0.5854591
0.5117896
0.6677458
0.7619602
0.7944201
0.7364668
0.6466391
0.6100587

0.5511804
 0.6343986
 0.7162639
 0.7228460
 0.6551696
 0.5666568
 0.3520308
 0.4585432
 0.5448735
 0.5371329
 0.4462354
 0.3480879
 in the group 8.4805638E-02
 in the group 8.5300371E-02
 in the group 0.1110153
 in the group 8.4805682E-02
 in the group 8.5300423E-02
 in the group 0.1110154

weight

.65

1	16	10	5
2	28	22	3
3	40	34	28
4	52	46	16
5	10	9	6
6	10	5	1
7	10	5	1
8	10	5	1
9	10	5	1
10	5	1	9
11	16	15	12
12	11	10	5
13	11	10	5
14	16	15	11
15	16	11	10
16	15	11	10
17	22	21	20
18	22	17	2
19	22	21	17
20	21	17	2
21	22	20	17
22	21	17	2
23	28	27	24
24	23	22	2
25	23	22	2
26	28	23	22
27	28	23	22
28	23	22	2
29	34	33	30
30	29	23	3
31	29	28	23
32	34	29	3
33	34	29	3
34	33	29	3
35	40	39	36

```

36 35 10 5
37 36 35 10
38 40 39 35
39 40 35 1
40 39 35 3
41 46 45 4
42 46 45 41
43 45 44 41
44 45 41 11
45 46 41 4
46 45 41 4
47 52 51 48
48 47 21 4
49 48 47 21
50 51 47 21
51 52 47 4
52 47 4 2
1 5 10 6 7 8 9
2 15 16 1 11 12 13 14
3 21 22 17 18 19 20
4 23 28 2 24 25 26 27
5 33 34 29 30 31 32
6 39 40 3 35 36 37 38
7 45 46 41 42 43 44
8 47 52 4 48 49 51 50

```

Groups found so far ...

```

1 5 10 6 7 8 9
2 15 16 11 12 13 14
3 21 22 17 18 19 20
4 23 28 24 25 26 27
5 33 34 29 30 31 32
6 39 40 35 36 37 38
7 45 46 41 42 43 44
8 47 52 48 49 51 50

```

These are not in a group

```

1 1
2 2
3 3
4 4

```

MONICA> run findp

Data from external file? If so, enter file name, else enter a semicolon and hit return.

mh01

28

weight

.65

```

1 5 3 2
2 11 4 1
3 5 1 10
4 11 2 1
5 10 6 1
6 5 1 10
7 5 1 6

```

```

 8  5  1 10
 9 10  5  3
10  5  3  1
11 12  2  1
12 11  2  1
13 12 11  2
14 11  2  1
15 16 11  2
16 11  2  1
17 18 10  5
18 17 10  5
19 18 17 10
20 19 18 17
21 17 10  5
22 17 10  5
23 24 11  2
24 23 11  2
25 23 11  2
26 23 11  2
27 23 11  2
28 23 11  2
1   5 10  1  3  6  7  8  9
2  11 12  2  4 13 14 16 15
3  17 18 19 20 21 22
4  23 24 25 26 27 28

```

Groups found so far ...

```

1   5 10  6  7  8  9
2  11 12 13 14 16 15
3  17 18 19 20 21 22
4  23 24 25 26 27 28

```

These are not in a group

```

1   3
2   1
3   2
4   4

```

MONICA> run findp

Data from external file? If so, enter file name, else enter a semicolon and hit return.

mh06

%FOR-F-FILNOTFOU, file not found

```

unit 1 file SYS$SYSDEVICE:[SHAPES.DAT]MH06.DAT;
user PC 0000FE7E

```

-RMS-E-FNF, file not found

%TRACE-F-TRACEBACK, symbolic stack dump follows

module name	routine name	line	rel PC	abs PC
			00043D9E	00043D9E
			00043CAB	00043CAB
			0003EA38	0003EA38
			0003D49A	0003D49A
FINDP\$MAIN	FINDP\$MAIN	74	0000007E	0000FE7E

MONICA> run findp

Data from external file? If so, enter file

