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I am submitting herewith a thesis written by James F. Barhorst entitled "Properties of the Reduced Semi-invariants of the Interclass Mahalanobis Distance and Their Application to Pattern Recognition." I have examined the final copy of this thesis for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Master of Science, with a major in Computer Science.

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PROPERTIES OF THE REDUCED SEMI-INVARIANTS
OF THE INTERCLASS MAHALANOBIS DISTANCE AND
THEIR APPLICATION TO PATTERN RECOGNITION

A Thesis
Presented for the
Master of Science
Degree
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James F. Barhorst
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DEDICATION

This work is dedicated to Karen and Thomas whose love provided the motivation to sustain me in this endeavor.

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ABSTRACT

Properties of the reduced semi-invariants of the interclass Mahalanobis distance (RSIM) are developed and used for pattern recognition in this work. These properties are understood in terms of the parameters of the Gaussian N dimensional statistical populations used to compute the RSIM. Some graphical representations of the RSIM are presented which serve as a basic framework for the use of the RSIM in pattern recognition. The implementation of computer programs to calculate the RSIM is discussed in addition to a procedure to compute the central moments of the Mahalanobis distance from the RSIM which involves solving a linear Diophantine equation iteratively. The results of a recognition program utilizing the RSIM is then presented. This program represents a typical use of the RSIM in a pattern recognition system designed to characterize changes occurring to sets of statistical data with time. A summary of the usefulness of the RSIM is then given.

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CHAPTER I

INTRODUCTION

Pattern recognition (and image processing) techniques based on the Mahalanobis distance have found wide applicability, ranging from nuclear reactor surveillance to automated analysis of image texture data to discrimination problems in biomedical monitoring (4,7,9). A pattern is a description of the observable features of an object. Recognition is the process of admitting an object to being of a particular class. The properties of the reduced semi-invariants of the interclass Mahalanobis distance (RSIM) presented in this paper use the mean vector and covariance matrix of a Gaussian population to be classified and the same features of a normal or reference population in order to compute the RSIM. The values of the RSIM are then fed into a decision function to classify the relationship between the two populations based on the features of the RSIM.

Throughout this paper, examples are given of the application of this pattern recognition system to nuclear reactor noise analysis. Nuclear reactor noise surveillance has been shown (7) to be a problem of great importance. There are other techniques for noise analysis; however due to the vital importance of reactor safety, independent monitors are always necessary. The RSIM pattern recognition system presented here will complement other safety monitoring systems. In a nuclear reactor noise analysis problem, the populations often consist of a series of power spectral densities (PSDs). A set of PSDs are collected during the normal operating condition of the reactor to

comprise the "normal" or reference population. PSDs gathered at a later time are used in the test population to be input to the classification algorithm. The basic assumptions are that if there is no change in the test population or if only certain changes have taken place, the test population is recognized as indicating no problem and no action would need to be taken by the operator. It is then possible to update the normal population to include this latest set of PSD's if desired (10). In addition to noise analysis, many other applications are possible for the use of the RSIM in pattern recognition.

As stated above, this is a statistical pattern recognition system using the RSIM, and, like other statistical problems, depends on enough data to be reliable. The semi-invariants of the interclass Mahalanobis distance have been shown to be computable directly from the means and covariance matrices of the two populations, and therefore the estimation of the probability density function of the interclass Mahalanobis distance is not required as an intermediate step in the computation (2). Since the RSIM are closely related to the semi-invariants, they are likewise only a function of the same parameters. The properties of the RSIM are developed by analyzing their values in terms of the parameters of the two populations. Interactive programs, written in Fortran on a PDP 11/34, compute the RSIM with the means and covariance matrices as the only input parameters. These parameters can be varied in an orderly way and the resulting RSIM examined to verify the properties they possess for recognition. During this step the corresponding "reduced" central moments of the Mahalanobis distance between the two populations are

also computed from the RSIM. This involves generating all of the solutions to an integer equation (linear Diophantine type). These properties present in the RSIM give a natural classification scheme for pattern recognition. This scheme has some interesting graphical representations upon which the pattern recognition system can be rigorously developed. This representation relates the values of the RSIM to a decision function for the particular pattern recognition system to be developed.

A computer program utilizing some of the properties of the pattern recognition system was also written for the PDP 11/34. This program provides both a check on the underlying assumptions and effectiveness of the system, and an example of how to implement the properties of the RSIM in a pattern recognition context. In this example the performance of this classifier is excellent on the data presented. The computation of the RSIM is found to transform the population parameters to a very useful form for the purposes of recognition.

CHAPTER II

BACKGROUND

Throughout the following development, it is assumed that the set of data (pattern vectors $\underline{x}$) constitutes a population characterized by a multivariate, Gaussian probability density function. This function is completely described by the mean vector $\underline{M}$ and covariance matrix $\underline{C}$ of the population defined as:

$$\underline{M} = E [\underline{x}] \quad (1)$$

and

$$\underline{C} = E [(\underline{x}-\underline{M})(\underline{x}-\underline{M})^T] \quad (2)$$

The covariance matrix is a symmetric positive semidefinite matrix with diagonal elements C_{ii} being the variance of the i -th component and off diagonal elements C_{ij} being the correlation of the i -th and j -th components. The contours of constant density in this distribution are hyperellipsoids with principal axes proportional in length to the eigenvalues of and in the direction of the eigenvectors of the covariance matrix. The computation of the RSIM uses the mean vector and covariance matrix of two Gaussian populations, one population A representative of a "normal" condition of the data and a second population B to be "tested" in terms of A.

Semi-Invariants

The n -th semi-invariant of a random variable which has a moment generating function is given by the n -th partial derivative with respect to t of the natural logarithm of the moment generating function evaluated at $t=0$ (3). The n -th semi-invariant χ of the interclass Mahalanobis distance from population B to population A is given by:

$$\chi_n = 2^{n-1}(n-1)! [\text{tr} (\underline{C}_A^{-1} \underline{C}_B)^n + n(\underline{M}_B - \underline{M}_A)^T \underline{C}_A^{-1} (\underline{C}_B \underline{C}_A^{-1})^{n-1} (\underline{M}_B - \underline{M}_A)] \quad (3)$$

The n -th semi-invariant calculated from A to B is given by a simple interchange of A and B:

$$\chi_n = 2^{n-1}(n-1)! [\text{tr} (\underline{C}_B^{-1} \underline{C}_A)^n + n(\underline{M}_A - \underline{M}_B)^T \underline{C}_B^{-1} (\underline{C}_A \underline{C}_B^{-1})^{n-1} (\underline{M}_A - \underline{M}_B)] \quad (4)$$

Note that these are only a function of the parameters of the two populations and n , the number of the semi-invariant. Gonzalez and Wagner (5) derived these expressions. There is a relationship of the semi-invariants to the moments and they can be defined in terms of each other (8). However, the semi-invariants do not have the strong physical interpretation that the moments possess since the semi-invariants are a logarithmic function.

Reduced Semi-Invariants

In practice the semi-invariants have the same problem as the moments in becoming quite large. This is due to the multiplicative prefactor of:

$$2^{n-1} (n-1)! \quad (5)$$

which very quickly gets quite large - more than 600,000 for n equal eight! This prefactor is independent of any of the parameters of the populations and thus adds nothing to the semi-invariants for the purpose of classification. Therefore, this prefactor is dropped in this work, yielding a new quantity the "reduced" semi-invariants of the Mahalanobis distance (RSIM). These are given by the following expressions:

$$RSIM_n(B-A) = \text{tr}[(\underline{C}_A^{-1}\underline{C}_B)^n] + n(\underline{M}_B - \underline{M}_A)^T \underline{C}_A^{-1} (\underline{C}_B \underline{C}_A^{-1})^{n-1} (\underline{M}_B - \underline{M}_A) \quad (6)$$

$$RSIM_n(A-B) = \text{tr}[(\underline{C}_B^{-1}\underline{C}_A)^n] + n(\underline{M}_A - \underline{M}_B)^T \underline{C}_B^{-1} (\underline{C}_A \underline{C}_B^{-1})^{n-1} (\underline{M}_A - \underline{M}_B) \quad (7)$$

As is true with the semi-invariants, the RSIM are functions only of the population parameters and their number n . The pattern recognition system presented in this work is based on the RSIM. If necessary, the value of the RSIM simply need to be multiplied by the prefactor in equation 5 to obtain the semi-invariants.

Equation 6 shows that the RSIM are of the form $X = A + B$. The first term of the sum:

$$A = \text{tr} (\underline{C}_A^{-1}\underline{C}_B)^n \quad (8)$$

is simply called the trace term and is not a function of the mean vector of either population. The second term:

$$B = n(\underline{M}_B - \underline{M}_A)^T \underline{C}_A^{-1} (\underline{C}_B \underline{C}_A^{-1})^{n-1} (\underline{M}_B - \underline{M}_A) \quad (9)$$

however is a function of the means. The means only appear in it as two vectors, the difference of the means and the difference of the

means transposed. Since only their difference appears, the absolute origin of the data space does not affect the value of the RSIM.

Therefore, a simplifying assumption used in this work is to consider the origin to be at the mean vector of one of the populations.

Equations 6 and 7 indicate that two sets of RSIM exist. The set of RSIM computed by equation 6 are from the population B to the mean of A and denoted as $(B-A)$. The RSIM from equation 7 are computed in the other direction from the population A to the mean of B, $(A-B)$. In general these two sets of RSIM are not equal although they can be equal in specific cases. For each n in equations 6 and 7, a different individual RSIM value can be calculated using the same parameters of the two populations. The values used in this work for n range from one to ten, thus the computation of the RSIM results in twenty numbers, ten RSIM $(B-A)$ and ten RSIM $(A-B)$. The next chapter shows some special properties of the RSIM which are useful in a pattern recognition context.

CHAPTER III

PROPERTIES OF THE REDUCED SEMI-INVARIANTS OF THE INTERCLASS MAHALANOBIS DISTANCE

The computation of the RSIM from the population parameters is a transformation of these parameters to a form which is useful. In order for this transformation to be valuable, there has to be some properties or structural features in the RSIM which express or quantify the relationship of the two populations. For there to be properties for recognition, the transformation cannot be random in any manner, and the values of the RSIM must be able to be related to the state of the original parameters. Both of these conditions are met in the computation of the RSIM.

In this chapter, some properties of the RSIM are developed and understood in terms of certain relationships of the populations. These relationships include all of the basic differences in the parameters of the populations: changes in mean vectors (both radial and "tangential" movement), changes in the covariance matrices (both to the entire matrix and to parts of it), and some combinations of these changes. The properties are derived from the basic definition of the RSIM. A series of figures are presented to aid in visualizing the relationships of the populations and the values of the RSIM. Two-dimensional uncorrelated populations are used in the first set of figures. Uncorrelated data means that all of the off-diagonal elements of the covariance matrices are zero. With this type of data, the eigenvectors of the covariance matrices (which determine the

direction of the major axes of the ellipsoids of constant density of the data) lie along the axes of the data's coordinate system. A rotational transformation matrix can be applied to correlated data to make it uncorrelated (6). Thus it is possible to transform correlated data to take full advantage of the properties of the RSIM of uncorrelated data. The properties of the RSIM of correlated data are reviewed in the last section of this chapter. The implications of some of the properties for pattern recognition and reactor noise analysis is presented throughout the chapter.

Identical Populations

The first and simplest relationship is that of two identical populations. When the two populations have the same means and same covariance matrices, all RSIM computed from B to A and from A to B are equal to the dimension of the population. This result is easily derived from equation 6. The second term (equation 9) contains multiplicative terms of vectors composed of the difference of the means of the two populations. If the means are identical, as they are in this instance,

$$B = n(\underline{0})^T \underline{C}_A^{-1} (\underline{C}_B \underline{C}_A^{-1})^{n-1} (\underline{0}) = 0 ,$$

this term is zero and does not contribute to the value of the RSIM. Equation 8 contains the inverse of the covariance matrix of one population multiplied by the covariance matrix of the other population. If both matrices are identical $\underline{C}_B = \underline{C}_A$, and if $\underline{I}$ = identity matrix, equation 8 gives

$$A = \text{tr} (\underline{C}_A^{-1} \underline{C}_A)^n = \text{tr} (\underline{I})^n = \text{tr} (\underline{I}) = N .$$

The trace (summation of the diagonal elements) gives a number equal to the number of elements on the diagonal which is N the dimension of the population, since each element is equal to one. An instance of this case is shown in figure 1. In this figure, as well as in all succeeding figures in this section, the "normal" population A is represented by the cross-hatched ellipse centered at the origin. The test population B is represented by the dashed ellipse. The mean vectors and covariance matrices of both populations are given above the graphs and the resulting RSIM from B to A and from A to B are given below. With every RSIM both from B to A and from A to B being equal to the dimension of the data, this condition is trivial to detect in a pattern recognition system. In monitoring a nuclear reactor's noise, this case indicates a perfectly operating system with absolutely no change in the data. Most likely no action would need to be taken by the operator when this is observed.

Symmetry About Normal Population

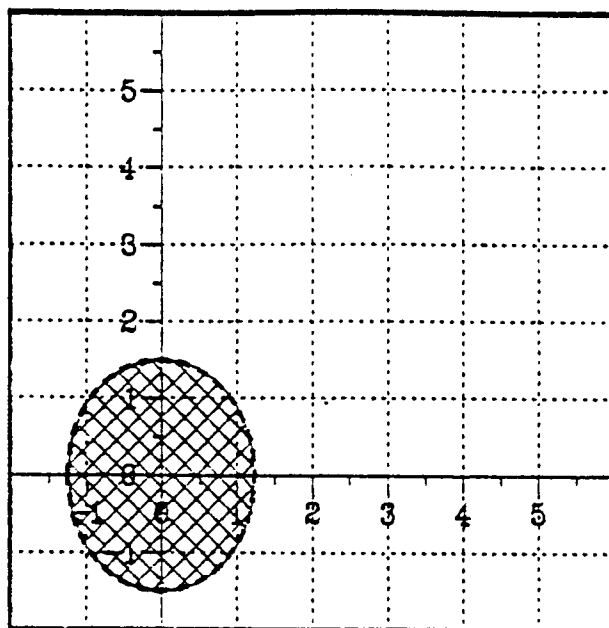
Figures 2 and 3 demonstrate the symmetry of the RSIM with respect to the orientation of the ellipsoids of constant density which in the uncorrelated case is also the quadrant or sign of the means. For each position or set of means in one position (figure 2) there are three other equivalent positions (figure 3 is one example) related only by a change in the sign of the means. The validity of this can easily be demonstrated from the definition of the RSIM. Equation 8 is only a

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 1.50 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 0.00 \\ 0.00 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 1.50 \end{pmatrix}$$



RSIM FROM B TO A

```

RSIM ( 1 ) = 2.0000
RSIM ( 2 ) = 2.0000
RSIM ( 3 ) = 2.0000
RSIM ( 4 ) = 2.0000
RSIM ( 5 ) = 2.0000
RSIM ( 6 ) = 2.0000
RSIM ( 7 ) = 2.0000
RSIM ( 8 ) = 2.0000
RSIM ( 9 ) = 2.0000
RSIM (10) = 2.0000

```

RSIM FROM A TO B

```

RSIM ( 1 ) = 2.0000
RSIM ( 2 ) = 2.0000
RSIM ( 3 ) = 2.0000
RSIM ( 4 ) = 2.0000
RSIM ( 5 ) = 2.0000
RSIM ( 6 ) = 2.0000
RSIM ( 7 ) = 2.0000
RSIM ( 8 ) = 2.0000
RSIM ( 9 ) = 2.0000
RSIM (10) = 2.0000

```

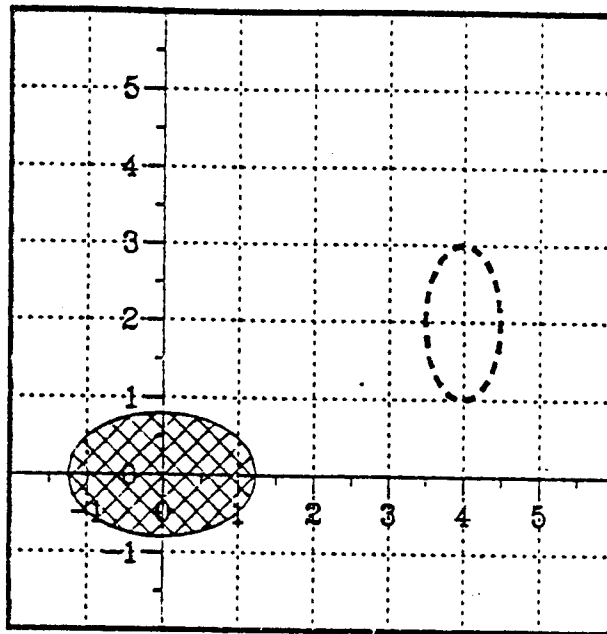
Figure 1. The case of two dimensional, uncorrelated identical populations.

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 4.00 \\ 2.00 \end{pmatrix} \begin{pmatrix} 0.50 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$



RSIM FROM B TO A

```

RSIM ( 1) = 19.450
RSIM ( 2) = 24.463
RSIM ( 3) = 31.599
RSIM ( 4) = 44.806
RSIM ( 5) = 65.736
RSIM ( 6) = 96.158
RSIM ( 7) = 138.65
RSIM ( 8) = 196.86
RSIM ( 9) = 275.75
RSIM (10) = 381.88

```

RSIM FROM A TO B

```

RSIM ( 1) = 39.300
RSIM ( 2) = 173.29
RSIM ( 3) = 623.82
RSIM ( 4) = 2047.7
RSIM ( 5) = 6356.2
RSIM ( 6) = 19002.
RSIM ( 7) = 55305.
RSIM ( 8) = 0.15778E+06
RSIM ( 9) = 0.44327E+06
RSIM (10) = 0.12302E+07

```

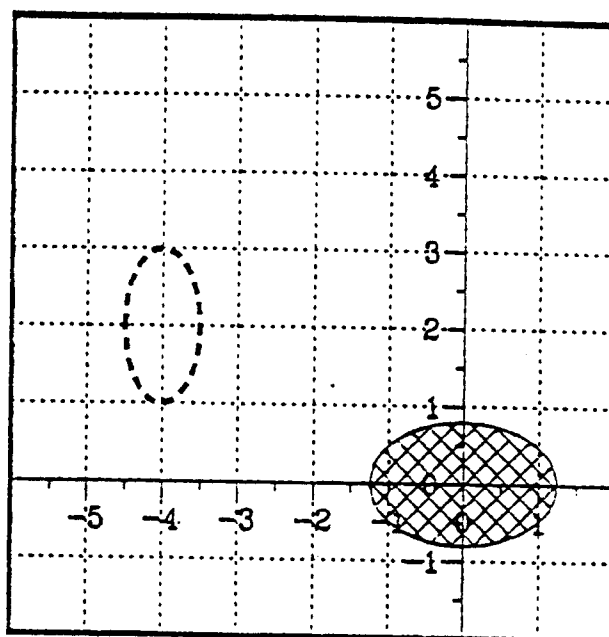
Figure 2. A two dimensional, uncorrelated population in a position in the first quadrant.

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} -4.00 \\ 2.00 \end{pmatrix} \begin{pmatrix} 0.50 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$



RSIM FROM B TO A

RSIM (1) =	19.450
RSIM (2) =	24.463
RSIM (3) =	31.599
RSIM (4) =	44.806
RSIM (5) =	65.736
RSIM (6) =	96.158
RSIM (7) =	138.65
RSIM (8) =	196.86
RSIM (9) =	275.75
RSIM (10) =	381.88

RSIM FROM A TO B

RSIM (1) =	39.300
RSIM (2) =	173.29
RSIM (3) =	623.82
RSIM (4) =	2047.7
RSIM (5) =	6356.2
RSIM (6) =	19002.
RSIM (7) =	55305.
RSIM (8) =	0.15778E+06
RSIM (9) =	0.44327E+06
RSIM (10) =	0.12302E+07

Figure 3. The symmetric position of a two dimensional uncorrelated population in another quadrant (compare with figure 2).

function of the covariance matrices and is totally independent of the means; therefore it can not be affected by any sign change in their components. Equation 9 contains the difference of the means transposed (which may contain some negative components) multiplying a product of some matrices, then multiplying the difference of the means again (which of course contains the same negative terms). Since these row and column vectors are the same and all the matrices are diagonal, there is no multiplication of components having mixed signs and the resultant product always has all positive components.

$$B = n \underline{M}^T \underline{C}_A^{-1} (\underline{C}_B \underline{C}_A^{-1})^{n-1} \underline{M} = n \underline{M}^2 \underline{C}_A^{-1} (\underline{C}_B \underline{C}_A^{-1})^{n-1}$$

The implication of this for pattern recognition is that the RSIM in only one quadrant need to be examined, the others can be automatically generated if necessary. Henceforth, this study will only consider populations with all components of the mean being positive. However, results presented apply to all symmetric positions of the mean vector of the test population. For monitoring nuclear reactor noise, the independence of the sign of the mean can be a slight disadvantage. In a case where the mean vector is drifting, the RSIM give no indication of the sign or direction of the drift. The RSIM can not detect the difference between a peak and a dip (relative to the normal spectrum) in the PSDs. Knowledge of this could be a potentially useful piece of information for diagnosis.

Equal Covariance Matrices

One of the important properties of the RSIM is the value they assume when the covariance matrix of the test population is equal

to that of the normal population, but there is a difference in the means. Unlike the case of figure 1, the RSIM are not all identical; but in this case, any given RSIM (e.g. the fifth) is the same whether computed from B to A or from A to B; but has a different value than all other RSIM. (Also note that the $n+1$ RSIM is larger than the n -th RSIM.) The result in this case can be derived from equation 6. As discussed in the case of identical populations, the trace term is going to yield a constant equal to the dimension of the population space since the covariance matrices are identical. But since the means are not equal, the contribution from equation 9 is no longer zero. With $\underline{C}_B = \underline{C}_A$, the matrix product is independent of direction:

$$\underline{C}_A^{-1}(\underline{C}_B \underline{C}_A^{-1})^{n-1} = \underline{C}_B^{-1}(\underline{C}_A \underline{C}_B^{-1})^{n-1}.$$

With the difference of the means having the same absolute value, the entire rightmost term gives the same value for a given RSIM, and $\text{RSIM}(B-A) = \text{RSIM}(A-B)$ for a given n . With the different values for the n -th and $n+1$ RSIM ($n+1$ larger since value is now a function of n), this case is easily distinguishable in a pattern recognition system from the unchanging situation represented in figure 1. An example of this property is presented in figure 4. This case is analogous to a reactor with the mean values of some of its noise frequencies changing, but with no change in the spread of the data.

Constant Variance in All Components

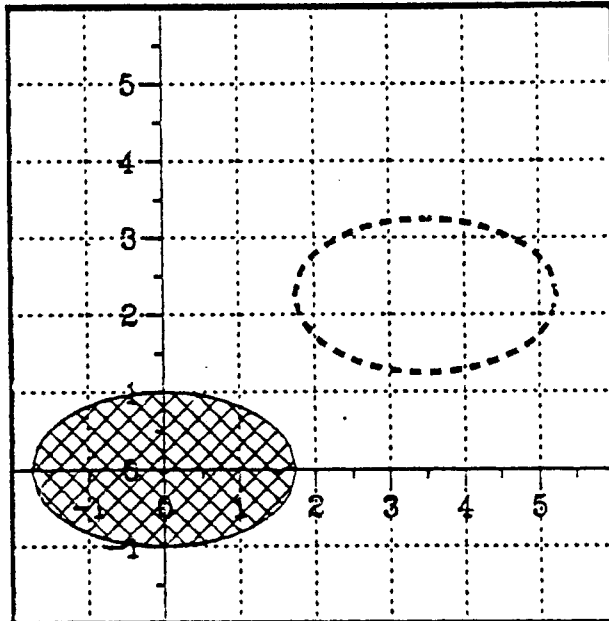
Another interesting property occurs when the spread of the data of both the normal and test populations is constant in all directions.

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.75 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 3.50 \\ 2.25 \end{pmatrix} \begin{pmatrix} 1.75 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$



RSIM FROM B TO A

```

RSIM ( 1) = 14.063
RSIM ( 2) = 26.125
RSIM ( 3) = 38.187
RSIM ( 4) = 50.250
RSIM ( 5) = 62.313
RSIM ( 6) = 74.375
RSIM ( 7) = 86.438
RSIM ( 8) = 98.500
RSIM ( 9) = 110.56
RSIM (10) = 122.63

```

RSIM FROM A TO B

```

RSIM ( 1) = 14.063
RSIM ( 2) = 26.125
RSIM ( 3) = 38.187
RSIM ( 4) = 50.250
RSIM ( 5) = 62.313
RSIM ( 6) = 74.375
RSIM ( 7) = 86.438
RSIM ( 8) = 98.500
RSIM ( 9) = 110.56
RSIM (10) = 122.63

```

Figure 4. An example of two dimensional uncorrelated populations with equal covariance matrices and different means.

In effect this means that for each covariance matrix, the plot of the contour lines of constant density are circles and every diagonal element is equal. The covariance matrices do not have to be equal in this case. When all of the components of the variance are equal, the RSIM are totally independent of the angular orientation of the means and only a function of the radial separation of the means. In equation 9, if the product of all of the matrix terms is a diagonal matrix $\underline{D}$ with equal terms on the diagonal, then this product is equal to the identity matrix $\underline{I}$ times a scalar s .

$$B = n\underline{M}^T \underline{D} \underline{M} = n\underline{M}^T s \underline{I} \underline{M} = ns\underline{M}^2 = n'\underline{M}^2$$

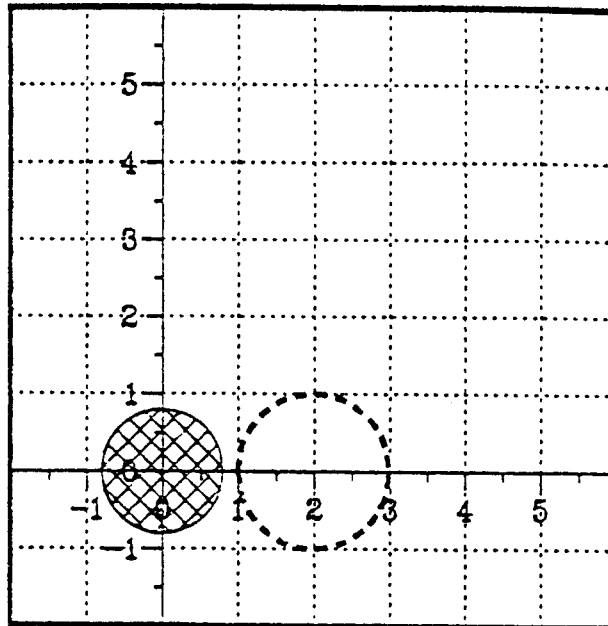
Then this term is equal to n' a scalar times the dot product of the difference of the mean vectors squared. This simply is the square of the distance between the means. Therefore this term is only proportional to the magnitude of the difference of the means and not its direction. Equation 8 does not depend on the means in any way and contributes the same value if the covariance matrices do not change. Two instances of this case are presented in figures 5 and 6. This property is another of the symmetries of the RSIM. In designing a pattern recognition system, these symmetries should be taken into account. The symmetry can reduce the amount of computation necessary or at times make it impossible to distinguish between two situations. In pattern recognition, this case of uncorrelated data with equal spread in all components can only deal with radial motion of the means. A circular motion of the means cannot be detected by a simple examination of the RSIM. This has to be accounted for in the case of

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 0.80 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 2.00 \\ 0.00 \end{pmatrix} \begin{pmatrix} 1.00 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$



RSIM FROM B TO A

```

RSIM ( 1 ) =    7.5000
RSIM ( 2 ) =   15.625
RSIM ( 3 ) =   27.344
RSIM ( 4 ) =   43.945
RSIM ( 5 ) =   67.139
RSIM ( 6 ) =   99.182
RSIM ( 7 ) =  143.05
RSIM ( 8 ) =  202.66
RSIM ( 9 ) =  283.12
RSIM (10) =  391.16

```

RSIM FROM A TO B

```

RSIM ( 1 ) =    5.6000
RSIM ( 2 ) =    7.6000
RSIM ( 3 ) =    8.7040
RSIM ( 4 ) =    9.0112
RSIM ( 5 ) =    8.8474
RSIM ( 6 ) =    8.3886
RSIM ( 7 ) =    7.7595
RSIM ( 8 ) =    7.0464
RSIM ( 9 ) =    6.3082
RSIM (10) =    5.5835

```

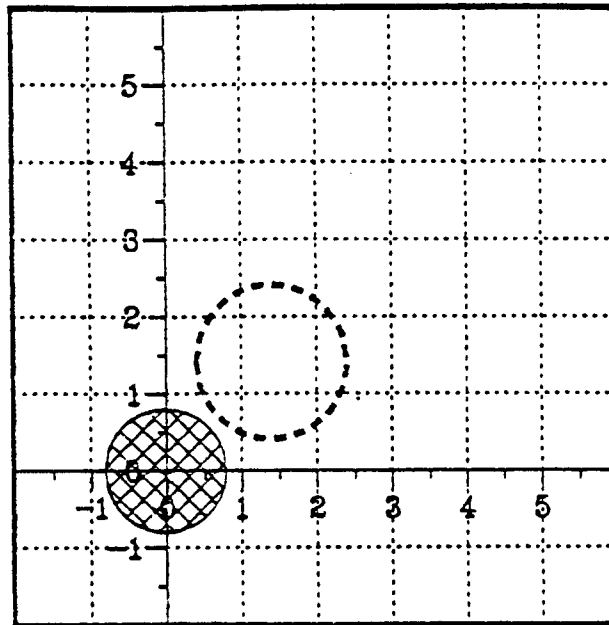
Figure 5. Two dimensional uncorrelated populations with "circular" covariance matrices and mean at (2,0)

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 0.80 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 1.41 \\ 1.41 \end{pmatrix} \begin{pmatrix} 1.00 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$



RSIM FROM B TO A

```

RSIM ( 1) =    7.5000
RSIM ( 2) =   15.625
RSIM ( 3) =   27.344
RSIM ( 4) =   43.945
RSIM ( 5) =   67.139
RSIM ( 6) =   99.182
RSIM ( 7) =  143.05
RSIM ( 8) =  202.66
RSIM ( 9) =  283.12
RSIM (10) =  391.16

```

RSIM FROM A TO B

```

RSIM ( 1) =    5.6000
RSIM ( 2) =    7.6800
RSIM ( 3) =    8.7040
RSIM ( 4) =    9.0112
RSIM ( 5) =    8.8474
RSIM ( 6) =    8.3886
RSIM ( 7) =    7.7595
RSIM ( 8) =    7.0464
RSIM ( 9) =    6.3082
RSIM (10) =    5.5835

```

Figure 6. Another case of two dimensional uncorrelated populations with "circular" covariance matrices and mean at (1.41,1.41), the same distance as figure 5.

a noise monitoring system. No change in the RSIM might not indicate a stable mean vector of the test population if the spread in each component of the data is equal. However, even if this is the case, radial motion of the means can be easily detected.

Uniform Expansion of Covariance Matrix

The next property of the RSIM is represented by situations in which the means of the two populations are identical and the two covariance matrices are related by a scalar multiple. These conditions are another simple type of deviation from case of identical populations. The RSIM in this case have the property that the product of RSIM (B-A) and RSIM (A-B) for a given n is always equal to the square of the dimension of the population vectors. This is also true in the case of identical populations, but the stronger result in that previous case of all RSIM having the exact value of the dimension of the population distinguishes it from this situation. As in the identical parameter case, there is no contribution to the RSIM from equation 9 since the means are the same. In this case, if we define the expansion factor α such that $\underline{C}_B = \alpha \underline{C}_A$, equation 8 can be expressed:

$$\begin{aligned} \text{RSIM}(B-A) &= \text{tr}((\underline{C}_A^{-1} \alpha \underline{C}_A)^n) = N \alpha^n \\ \text{RSIM}(A-B) &= \text{tr}((\frac{1}{\alpha} \underline{C}_A^{-1} \underline{C}_A)^n) = N \alpha^{-n} \end{aligned}$$

since $\underline{C}_B^{-1} = \frac{1}{\alpha} \underline{C}_A^{-1}$. Taking the product of the two RSIM yields the square of the dimension N independent of the value of α . The value of this expansion factor α (α less than one means contraction) of all components of the test population's covariance matrix can easily be

determined from the values of the RSIM. The n -th RSIM (B-A) is proportional to α^n and the $n+1$ -th to α^{n+1} . α can be found by simply dividing the $n+1$ -th by the n -th RSIM (B-A). Figure 7 is an example of a uniform expansion of 1.25 in the spread of the data. The information present in the RSIM in this case completely characterizes in a quantified way what is occurring to the test population with respect to the normal population. This can be quite important in a pattern recognition context, especially if there are two almost identical populations in which changes in the "noisiness" of the data can have important consequences to the classification scheme. This can be the case in a reactor noise surveillance system where it is important to be able to recognize what type of changes are occurring to the spread of the PSDs.

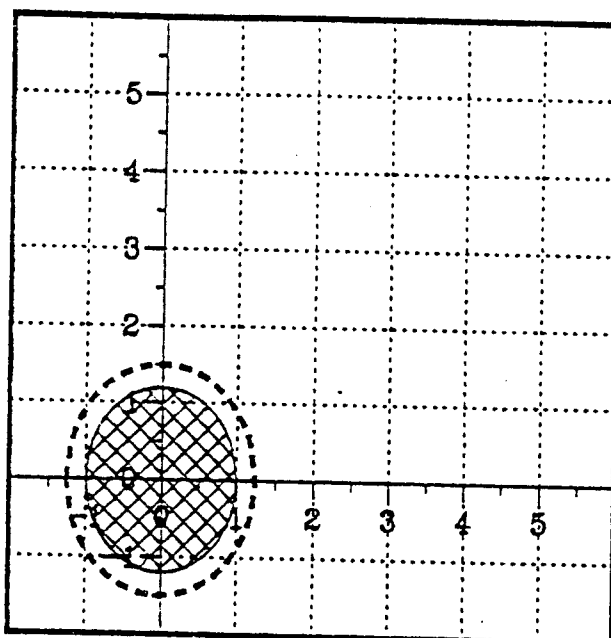
The obvious extension to the previous case is to consider a uniform expansion of the covariance matrix with different mean vectors of the two populations. This is covered in detail in the fourth chapter. A result in this instance and also in general is that if one of the populations has more spread in its data than the other, the RSIM from the mean of the population with the greater variance (i.e. with the larger hyperellipsoids of constant density) to the population with the smaller variance are larger than the RSIM computed the other direction. This is due to the fact that equations 6 and 7 for the RSIM only have terms involving the covariance matrix of the population computing from, and the inverse of the covariance matrix of the other population computing to. The inverse of a covariance matrix having large elements results in a matrix having small elements. Then the

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.00 & 0.00 \\ 0.00 & 1.20 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 0.00 \\ 0.00 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 1.50 \end{pmatrix}$$



RSIM FROM B TO A

RSIM (1) =	2.5000
RSIM (2) =	3.1250
RSIM (3) =	3.9062
RSIM (4) =	4.8828
RSIM (5) =	6.1035
RSIM (6) =	7.6294
RSIM (7) =	9.5367
RSIM (8) =	11.921
RSIM (9) =	14.901
RSIM (10) =	18.626

RSIM FROM A TO B

RSIM (1) =	1.6000
RSIM (2) =	1.2800
RSIM (3) =	1.0240
RSIM (4) =	0.81920
RSIM (5) =	0.65536
RSIM (6) =	0.52429
RSIM (7) =	0.41943
RSIM (8) =	0.33554
RSIM (9) =	0.26844
RSIM (10) =	0.21475

Figure 7. An example of two dimensional uncorrelated populations with the same means and uniform expansion in the covariance matrix of the test population.

product of a large covariance matrix with the inverse of a smaller one gives a matrix with larger terms than the product of a small matrix with the inverse of a larger one. Through this method of analysis, the relative magnitudes of the components of the covariance matrices can be determined by the values of the two sets of RSIM. This situation is demonstrated in the preceding figures, figures 5, 6, and 7 all have larger spreads in the test population and RSIM (B-A) is larger, figure 4 has equal covariance matrices and equal RSIM, and figures 2 and 3 have a larger spread in the normal population and RSIM (A-B) is greater.

Change in a Component of Variance

An important property of the RSIM is when a change occurs in a single component of the covariance matrix of the test population with no change in the mean vectors. The RSIM have very distinct values in this situation. As in all cases with identical mean vectors, only equation 8 contributes to the value of the RSIM. In the computation of equation 8, $\underline{C}_A^{-1} \underline{C}_B \approx \underline{I}$ the identity matrix except for the one diagonal element of the product which differs in the two populations. This diagonal element equals the ratio of the variance of the population computing from to the variance of the one computing towards. Then this resultant diagonal matrix $\underline{D}$ is raised to the n-th power and the trace is taken. The sum of all of the rest of the diagonal elements contributes N-1 to the value of the RSIM. If the odd element D_{ij} is greater than one (expansion):

$$(D_{ij})^n \gg 1 \text{ for } n > 4 \text{ or } 5$$

and it dominates the value of the RSIM. If the odd element is less than one (contraction),

$$(D_{ij})^n \ll 1 \text{ for } n > 4 \text{ or } 5$$

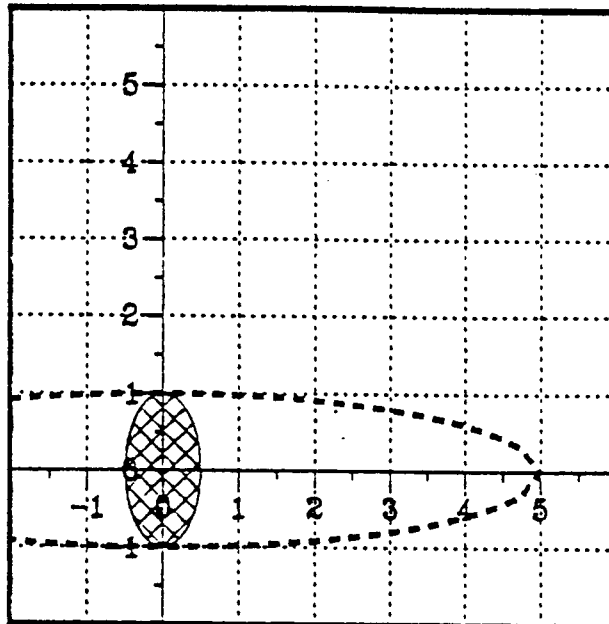
and the RSIM approaches the value of $N-1$ as $(D_{ij})^n$ goes to zero in the higher RSIM. (Of course if k elements are contracting, the RSIM approaches $N-k$. If k elements are expanding, the largest expansion ratio dominates the value.) Figure 8 is an example of a factor of ten expansion in the first component of the variance and figure 9 represents a factor of ten less spread in the same component of the test population. In figure 8 the factor of ten causes the RSIM (B-A) to be approximately equal to ten to the power of the number of the RSIM being calculated. In computing RSIM (A-B) the factor is one-tenth and the RSIM are close to one (the dimension of the population vectors minus one.) In figure 9 the situation is exactly reversed with respect to the direction of the computation. This result is easily monitorable in a pattern recognition system. An algorithm could not only give the approximate value of a change in the spread of some components of the data by dividing the $n+1$ increasing RSIM by the n -th RSIM, but can also determine exactly how many components have greater or smaller variances ("noisier" or "quieter") than the normal population. This type of monitoring has important applications for PSDs. When combined with the uniform expansion case discussed with figure 7, most of the simple changes which can occur to a second population with the same means are covered.

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 0.50 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 0.00 \\ 0.00 \end{pmatrix} \begin{pmatrix} 5.00 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$



RSIM FROM B TO A

```

RSIM ( 1) = 11.000
RSIM ( 2) = 101.00
RSIM ( 3) = 1001.0
RSIM ( 4) = 10001.
RSIM ( 5) = 0.10000E+06
RSIM ( 6) = 0.10000E+07
RSIM ( 7) = 0.10000E+08
RSIM ( 8) = 0.10000E+09
RSIM ( 9) = 0.10000E+10
RSIM (10) = 0.10000E+11

```

RSIM FROM A TO B

```

RSIM ( 1) = 1.1000
RSIM ( 2) = 1.0100
RSIM ( 3) = 1.0010
RSIM ( 4) = 1.0001
RSIM ( 5) = 1.0000
RSIM ( 6) = 1.0000
RSIM ( 7) = 1.0000
RSIM ( 8) = 1.0000
RSIM ( 9) = 1.0000
RSIM (10) = 1.0000

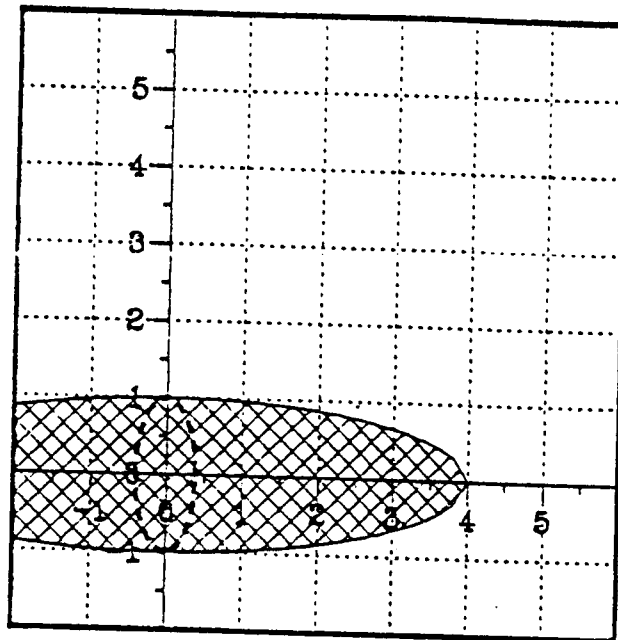
```

Figure 8. Two dimensional uncorrelated populations with the same means and expansion in one component of the variance.

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 4.00 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 0.00 \\ 0.00 \end{pmatrix} \begin{pmatrix} 0.40 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$


RSIM FROM B TO A

```

RSIM ( 1) = 1.1000
RSIM ( 2) = 1.0100
RSIM ( 3) = 1.0010
RSIM ( 4) = 1.0001
RSIM ( 5) = 1.0000
RSIM ( 6) = 1.0000
RSIM ( 7) = 1.0000
RSIM ( 8) = 1.0000
RSIM ( 9) = 1.0000
RSIM (10) = 1.0000

```

RSIM FROM A TO B

```

RSIM ( 1) = 11.000
RSIM ( 2) = 101.00
RSIM ( 3) = 1001.0
RSIM ( 4) = 10001.
RSIM ( 5) = 0.10000E+06
RSIM ( 6) = 0.10000E+07
RSIM ( 7) = 0.10000E+08
RSIM ( 8) = 0.10000E+09
RSIM ( 9) = 0.10000E+10
RSIM (10) = 0.10000E+11

```

Figure 9. Two dimensional uncorrelated populations with the same means and contraction in one component of the variance.

The next relationship of populations to be presented is similar to the last case, but with different mean vectors (assuming the difference in the same component that the variance has changed). In this case the contribution to the RSIM from equation 9 is no longer zero. However if the RSIM are being computed from a population with a smaller variance in that component to one with a larger variance, the only non-zero component of the mean vector in this equation is multiplying a very small element (resulting from the product of the covariance matrices):

$$\text{if } C_{Bjj} < C_{Ajj}$$

$$(M_j) C_{Ajj}^{-1} (C_{Bjj} C_{Ajj}^{-1})^{N-1} (M_j) \approx 0$$

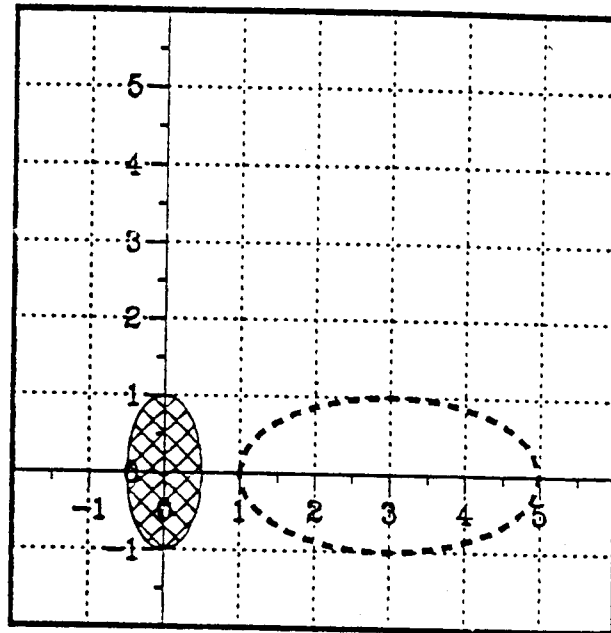
thus this term contributes very little to the value of the RSIM. (This depends on all off-diagonal elements of the covariance matrix being zero; the result is different if some of the terms of the product of the vector and matrices is no longer zero). Therefore the RSIM in this direction approach $N-1$ as seen in figure 10. As in the above case of equal means this can be monitored in a pattern recognition system by checking the RSIM computed in one direction to go to $N-1$ (or any integer value less than N). This case can be distinguished from the case presented with figures 8 and 9. If the other (not $N-1$) RSIM is increasing by an almost constant factor (ten in figures 8 and 9), then the means are identical. If each successive RSIM does not increase by an approximately constant factor, the means are not the same. In noise analysis, this case corresponds to a peak

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 0.50 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 3.00 \\ 0.00 \end{pmatrix} \begin{pmatrix} 2.00 & 0.00 \\ 0.00 & 1.00 \end{pmatrix}$$



RSIM FROM B TO A

```

RSIM ( 1) = 23.000
RSIM ( 2) = 161.00
RSIM ( 3) = 929.00
RSIM ( 4) = 4865.0
RSIM ( 5) = 24065.
RSIM ( 6) = 0.11469E+06
RSIM ( 7) = 0.53248E+06
RSIM ( 8) = 0.24248E+07
RSIM ( 9) = 0.10879E+08
RSIM (10) = 0.48234E+08

```

RSIM FROM A TO B

```

RSIM ( 1) = 5.7500
RSIM ( 2) = 3.3125
RSIM ( 3) = 1.8594
RSIM ( 4) = 1.2852
RSIM ( 5) = 1.0889
RSIM ( 6) = 1.0266
RSIM ( 7) = 1.0078
RSIM ( 8) = 1.0022
RSIM ( 9) = 1.0006
RSIM (10) = 1.0002

```

Figure 10. Two dimensional uncorrelated populations with a difference in one component of the means and variance (expansion).

or dip occurring in one component of the PSDs (different mean) with a change in the variance (spread) of that component. This is one of the most important indications of a problem with a set of PSD's in a reactor surveillance problem. But due to the properties of the RSIM, it is easy to recognize this case in a monitoring algorithm.

Surfaces of Equal RSIM

If the covariance matrices of both populations are equal, there is another property of the RSIM in addition to its value being the same whether calculated from B to A or A to B. For any given mean vector of the test population, a mean vector in any different direction from the normal population gives the same set of RSIM. The loci of mean vectors that give the same set of RSIM are hyperellipsoids with the same ratio of major axes as the hyperellipsoids of constant data density of the populations. This is an extension of the case with constant variance in each component; however, these surfaces of equal RSIM exist only when the covariance matrices are equal. As discussed before, equation 8 is not a function of the means and contributes the same to the value in each position. If $\underline{C}_B = \underline{C}_A$ then equation 9 reduces to:

$$B = n\mathbf{M}^T \underline{C}_A^{-1} (\underline{C}_A \underline{C}_A^{-1})^{n-1} \underline{M} = n\mathbf{M}^T \underline{C}_A^{-1} \underline{M}$$

Since the diagonal elements of $\underline{C}_A$ are the lengths of the hyperellipsoids mean vectors falling on these same hyperellipsoids give the same value for this term because they are multiplying the inverse of $\underline{C}_A$.

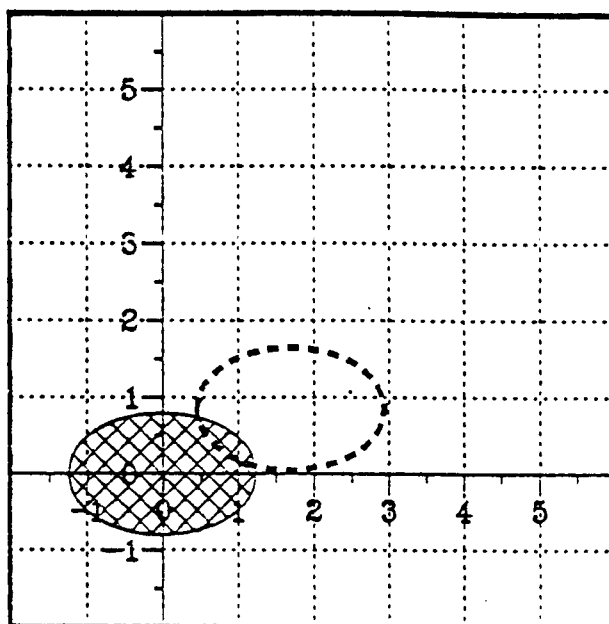
Figures 11 and 12 show two mean vectors on the ellipse $x^2/1.25 + y^2/0.8 = 3.2$ giving the same sets of RSIM. These surfaces of equal

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 1.70 \\ 0.84 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$



RSIM FROM B TO A

RSIM (1) = 5.2000
 RSIM (2) = 8.4000
 RSIM (3) = 11.600
 RSIM (4) = 14.800
 RSIM (5) = 18.000
 RSIM (6) = 21.200
 RSIM (7) = 24.400
 RSIM (8) = 27.600
 RSIM (9) = 30.800
 RSIM (10) = 34.000

RSIM FROM A TO B

RSIM (1) = 5.2000
 RSIM (2) = 8.4000
 RSIM (3) = 11.600
 RSIM (4) = 14.800
 RSIM (5) = 18.000
 RSIM (6) = 21.200
 RSIM (7) = 24.400
 RSIM (8) = 27.600
 RSIM (9) = 30.800
 RSIM (10) = 34.000

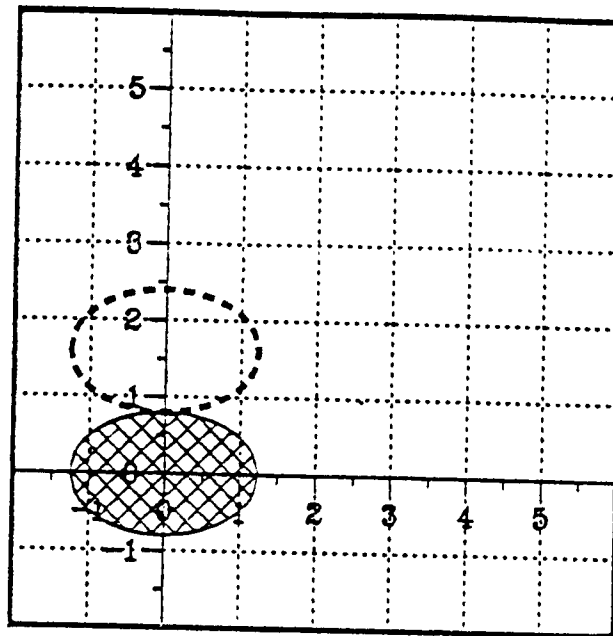
Figure 11. The case of two dimensional uncorrelated populations, a position on a contour of constant RSIM at (1.7,.84).

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 0.00 \\ 1.60 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$



RSIM FROM B TO A

RSIM (1) = 5.2000
 RSIM (2) = 8.4000
 RSIM (3) = 11.600
 RSIM (4) = 14.800
 RSIM (5) = 18.000
 RSIM (6) = 21.200
 RSIM (7) = 24.400
 RSIM (8) = 27.600
 RSIM (9) = 30.800
 RSIM (10) = 34.000

RSIM FROM A TO B

RSIM (1) = 5.2000
 RSIM (2) = 8.4000
 RSIM (3) = 11.600
 RSIM (4) = 14.800
 RSIM (5) = 18.000
 RSIM (6) = 21.200
 RSIM (7) = 24.400
 RSIM (8) = 27.600
 RSIM (9) = 30.800
 RSIM (10) = 34.000

Figure 12. Another position on the contour of constant RSIM at (0,1.6) giving the same RSIM as figure 11.

RSIM are of interest in a pattern recognition context; movement of the means of a test population along a precise elliptical orbit cannot be detected in the RSIM. The values of the RSIM do increase with increasing separation of the means. These surfaces form a boundary which could be used in a decision function.

Small Changes in Parameters

Figures 13, 14 and 15 demonstrate the effect of very small (compared to those presented in the previous figures) changes in the parameters of the test population. These small changes have a definite measurable effect on the values of the RSIM; however the magnitude of this effect can be useful in a pattern recognition system. Figure 13 represents two populations with identical covariance matrices and only a small difference in the means. As in the case of figure 4 on page 16, the value of the RSIM is independent of the direction between the populations that the RSIM is being computed, but the values remain very close to the dimension of the data. Equation 8 contributes two every time to the sum, the small contribution from equation 9 is simply:

$$B = n(.1)(1.25)(.1) = (.0125)n$$

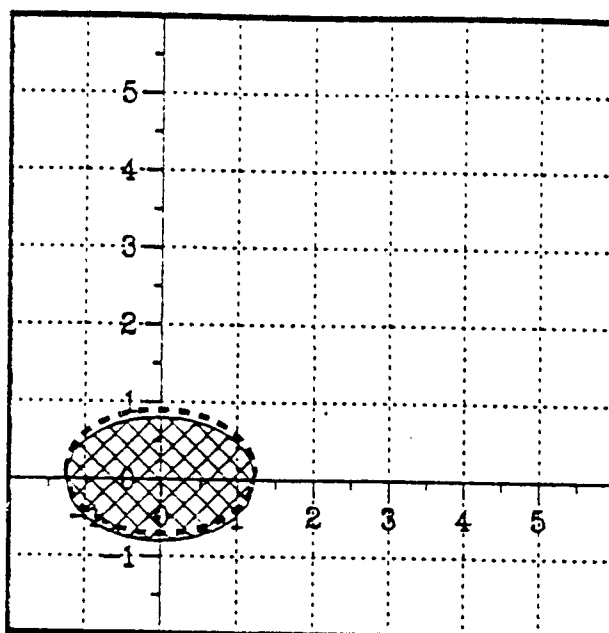
(the second diagonal component of the inverse of the covariance matrix is 1.25). Figure 14 represents the other incremental possibility, identical means with a slightly different (nonuniformly larger) covariance matrix for the test population. The RSIM are all close to two (contrast with the values in the previous figures!) and

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 0.00 \\ 0.10 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$



RSIM FROM B TO A

RSIM (1) =	2.0125
RSIM (2) =	2.0250
RSIM (3) =	2.0375
RSIM (4) =	2.0500
RSIM (5) =	2.0625
RSIM (6) =	2.0750
RSIM (7) =	2.0875
RSIM (8) =	2.1000
RSIM (9) =	2.1125
RSIM (10) =	2.1250

RSIM FROM A TO B

RSIM (1) =	2.0125
RSIM (2) =	2.0250
RSIM (3) =	2.0375
RSIM (4) =	2.0500
RSIM (5) =	2.0625
RSIM (6) =	2.0750
RSIM (7) =	2.0875
RSIM (8) =	2.1000
RSIM (9) =	2.1125
RSIM (10) =	2.1250

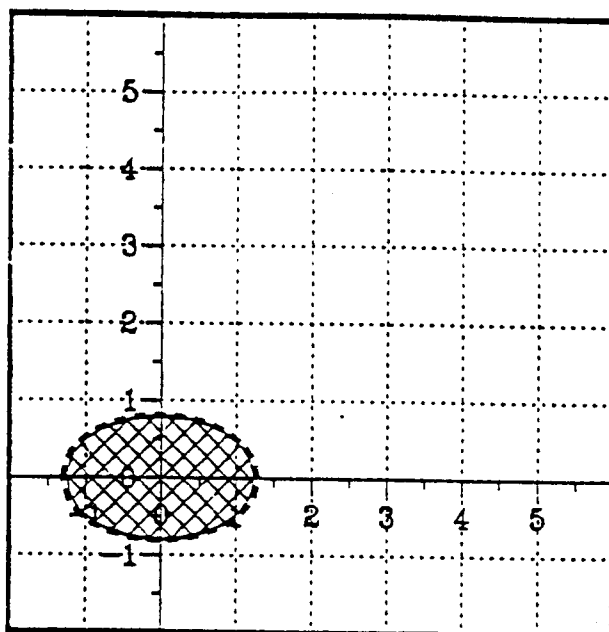
Figure 13. A case of two dimensional uncorrelated populations with only a small difference in means.

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 0.00 \\ 0.00 \end{pmatrix} \begin{pmatrix} 1.30 & 0.00 \\ 0.00 & 0.81 \end{pmatrix}$$



RSIM FROM B TO A

RSIM (1) =	2.0525
RSIM (2) =	2.1068
RSIM (3) =	2.1628
RSIM (4) =	2.2208
RSIM (5) =	2.2807
RSIM (6) =	2.3427
RSIM (7) =	2.4068
RSIM (8) =	2.4731
RSIM (9) =	2.5416
RSIM (10) =	2.6125

RSIM FROM A TO B

RSIM (1) =	1.9492
RSIM (2) =	1.9000
RSIM (3) =	1.8524
RSIM (4) =	1.8063
RSIM (5) =	1.7617
RSIM (6) =	1.7185
RSIM (7) =	1.6766
RSIM (8) =	1.6361
RSIM (9) =	1.5968
RSIM (10) =	1.5587

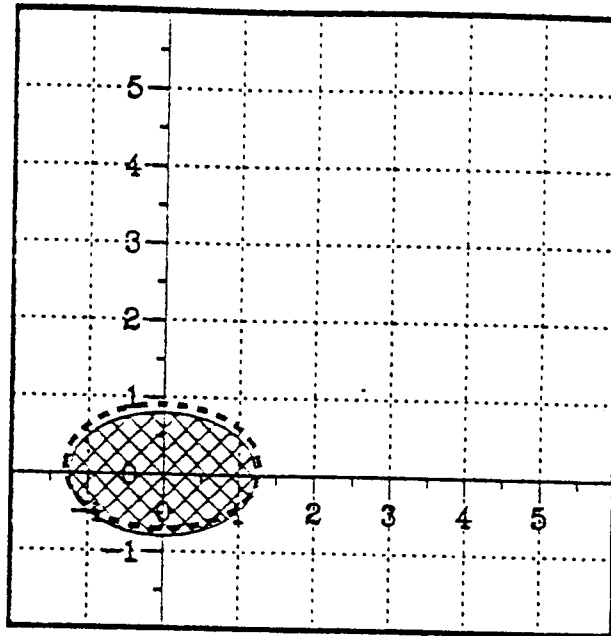
Figure 14. Two dimensional uncorrelated populations with only slightly different covariance matrices.

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.25 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 0.00 \\ 0.10 \end{pmatrix} \begin{pmatrix} 1.30 & 0.00 \\ 0.00 & 0.81 \end{pmatrix}$$



RSIM FROM B TO A

RSIM (1) = 2.0650
 RSIM (2) = 2.1321
 RSIM (3) = 2.2013
 RSIM (4) = 2.2727
 RSIM (5) = 2.3464
 RSIM (6) = 2.4225
 RSIM (7) = 2.5011
 RSIM (8) = 2.5821
 RSIM (9) = 2.6659
 RSIM (10) = 2.7523

RSIM FROM A TO B

RSIM (1) = 1.9615
 RSIM (2) = 1.9244
 RSIM (3) = 1.8885
 RSIM (4) = 1.8539
 RSIM (5) = 1.8204
 RSIM (6) = 1.7881
 RSIM (7) = 1.7568
 RSIM (8) = 1.7266
 RSIM (9) = 1.6974
 RSIM (10) = 1.6691

Figure 15. The effect of both a small difference in means and covariance matrices on the RSIM.

the fact that the RSIM from B to A are increasing while the ones from A to B are all decreasing with n indicates that the covariance matrix of B is somewhat "larger." Also note that the product of the n -th pair of RSIM is not exactly the dimension squared (four) but rather close to it indicating a degree of almost uniform expansion. This is in great contrast to the case of a change in a single component (figure 8) and could be recognized as such. Figure 15 shows the effect of both possible types of small changes. The RSIM are still close to two in value and of course both populations are still relatively similar. The situation in these figures has important implications in a pattern recognition system. If both RSIM for a given n have a value close to the dimension of the data, then it is recognized that both populations are very similar. This condition can be monitored in conjunction with the other cases, figure 13 is a prime example of the RSIM fulfilling two conditions. A classification algorithm using this method has to be carefully designed. The first and second RSIM can often have values close to N , the dimension of the space; therefore it is better to use some of the higher numbered RSIM. Also meaning of similar and close have to be defined. Two populations can be considered to be close if, for the purposes of classification, they are put in the exact same category. This is very dependent on the individual problem to determine what threshold is proper. The best approach is to compute the RSIM of two populations which are the most dissimilar but yet classified as the same, thus finding out the limits for classification. This concept of slightly different populations has another important application to statistical pattern

recognition. In a real situation it is not always possible to collect enough data to have a population with exactly the same parameters as another population collected under the same conditions. One approach is to develop some type of rounding off or discretization algorithm for the population parameters. Like any other transformation of this type, valuable information can be lost in the process. To prevent this from happening, a method can use the RSIM to apply one measure of closeness or threshold to indicate the expected statistical inaccuracies and also apply a second "looser" threshold for another classification test. This is possible due to the smoothly varying nature of the RSIM (discontinuities would render this approach useless if they existed). In the case of continually monitoring a population with means different than the normal or reference population, slight changes in the mean and covariance matrix are not going to greatly effect the RSIM although they would be recognizable. This fact can be used in a system in which it is important that any changes in the population being tested are detected, but that its exact relationship to the reference population is not important.

In summary, the cases described above cover the main relationships possible between the population parameters and present the easily recognizable information which is contained in the RSIM. The RSIM of identical populations is the dimension of the space. The sign of the means does not affect the value. With only a difference in the means of the populations, the RSIM are independent of the direction being calculated. With certain relationships of the population parameters (e.g. circular equidensity contours), certain loci of points

give the same RSIM. Uniform expansion or contraction of the covariance matrix can be quantified by examining the RSIM. If expansion or contraction occurs in only a few components of the data, this too can be recognized and sometimes quantified by the RSIM. And finally small changes in population parameters can be detected and identified. The preceding cases are presented using two dimensional uncorrelated data to be able to present a visual representation of the relationship of the population parameters. But most of the analysis is not limited to uncorrelated data and none of it is limited to two dimensions.

Correlated Data

The difference between correlated and uncorrelated data is that the direction of the spread of the data is not as obvious in the correlated cases since the eigenvectors of a non-diagonal matrix, although orthogonal to each other, no longer lie along the axial directions. Therefore the hyperellipsoids which represent the contour lines of constant density of the data are rotated with respect to the data's coordinate system. If two populations are correlated in the same way, a rotation matrix can be applied to transform them so that their eigenvectors lie in the axial directions. This transformation is not always necessary as the RSIM of correlated populations possess much of the same structure as the RSIM of uncorrelated populations. Some four dimensional correlated cases are now presented to show these values of the RSIM. The covariance matrices are generated as described in chapter five with the adjacent to the diagonal elements a function of the diagonal elements of the covariance matrices

and the other off-diagonal elements fixed. The RSIM computed in both directions are given in the figures as well as the values of the "reduced" moments calculated from the RSIM. No analysis of the moments is given and no graphs are presented, four dimensional plotting is not highly developed.

Figure 16 shows that with identical populations, all RSIM are equal to the dimension of the data. This is exactly the same as with the uncorrelated data. The covariance matrix presented in this figure and many of the other four dimensional figures contains widely varying values along the diagonal (from .2 to 8, a factor of 40) arranged in a random order to simulate the most general conditions possible.

Figures 17 and 18 represent cases with the same covariance matrices for both populations but different means. As with the uncorrelated data discussed with figure 4, the n -th RSIM has the same value whether computed from B to A or from A to B. But the sign change in the means of figure 18 results in a different value for the RSIM than in figure 17. This is because these two positions are no longer equivalent (i.e. related by symmetry). The hyperellipsoids are not oriented along the axial directions as they are in the similar case of figures 2 and 3 on pages 12 and 13. The four-fold symmetry is related to the axes of the hyperellipsoids, therefore the points of symmetry are not easily found without knowing the orientation of the eigenvectors, although these points still exist.

The case of uniform variance in each component of correlated data is given in figures 19, 20, and 21. All three figures have the same total distance between the means of the two populations, but they lie

NORMAL POPULATION					TEST POPULATION				
0	8.00	1.00	0.01	0.01	0.00	8.00	1.00	0.01	0.01
0	1.00	2.00	0.22	0.01	0.00	1.00	2.00	0.22	0.01
0	0.01	0.22	0.20	0.12	0.00	0.01	0.22	0.20	0.12
0	0.01	0.01	0.12	1.00	0.00	0.01	0.01	0.12	1.00

RSIM FROM B TO A		RSIM FROM A TO B	
RSIM (1) =	4.0000	RSIM (1) =	4.0000
RSIM (2) =	4.0000	RSIM (2) =	4.0000
RSIM (3) =	4.0000	RSIM (3) =	4.0000
RSIM (4) =	4.0000	RSIM (4) =	4.0000
RSIM (5) =	4.0000	RSIM (5) =	4.0000
RSIM (6) =	4.0000	RSIM (6) =	4.0000
RSIM (7) =	4.0000	RSIM (7) =	4.0000
RSIM (8) =	4.0000	RSIM (8) =	4.0000
RSIM (9) =	4.0000	RSIM (9) =	4.0000
RSIM (10) =	4.0000	RSIM (10) =	4.0000

MOMENT FROM B TO A		MOMENT FROM A TO B	
MOMENT (1) =	4.0000	MOMENT (1) =	4.0000
MOMENT (2) =	32.000	MOMENT (2) =	32.000
MOMENT (3) =	19.333	MOMENT (3) =	19.333
MOMENT (4) =	31.500	MOMENT (4) =	31.500
MOMENT (5) =	45.233	MOMENT (5) =	45.233
MOMENT (6) =	58.828	MOMENT (6) =	58.828
MOMENT (7) =	70.563	MOMENT (7) =	70.563
MOMENT (8) =	79.076	MOMENT (8) =	79.076
MOMENT (9) =	83.591	MOMENT (9) =	83.591
MOMENT (10) =	83.972	MOMENT (10) =	83.972

Figure 16. The case of four dimensional, correlated identical populations.

NORMAL POPULATION

0	8.00	1.00	0.01	0.01
0	1.00	2.00	0.22	0.01
0	0.01	0.22	0.20	0.12
0	0.01	0.01	0.12	1.00

TEST POPULATION

0.40	8.00	1.00	0.01	0.01
0.80	1.00	2.00	0.22	0.01
0.62	0.01	0.22	0.20	0.12
0.05	0.01	0.01	0.12	1.00

RSIM FROM B TO A

RSIM (1) =	6.0514
RSIM (2) =	8.1029
RSIM (3) =	10.154
RSIM (4) =	12.206
RSIM (5) =	14.257
RSIM (6) =	16.309
RSIM (7) =	18.360
RSIM (8) =	20.411
RSIM (9) =	22.463
RSIM (10) =	24.514

RSIM FROM A TO B

RSIM (1) =	6.0514
RSIM (2) =	8.1029
RSIM (3) =	10.154
RSIM (4) =	12.206
RSIM (5) =	14.257
RSIM (6) =	16.309
RSIM (7) =	18.360
RSIM (8) =	20.411
RSIM (9) =	22.463
RSIM (10) =	24.514

MOMENT FROM B TO A

MOMENT (1) =	6.0514
MOMENT (2) =	148.36
MOMENT (3) =	63.143
MOMENT (4) =	149.01
MOMENT (5) =	307.96
MOMENT (6) =	573.48
MOMENT (7) =	980.70
MOMENT (8) =	1561.1
MOMENT (9) =	2336.6
MOMENT (10) =	3314.0

MOMENT FROM A TO B

MOMENT (1) =	6.0514
MOMENT (2) =	148.36
MOMENT (3) =	63.143
MOMENT (4) =	149.01
MOMENT (5) =	307.96
MOMENT (6) =	573.48
MOMENT (7) =	980.70
MOMENT (8) =	1561.1
MOMENT (9) =	2336.6
MOMENT (10) =	3314.0

Figure 17. A case of four dimensional correlated populations with equal covariance matrices and different means.

NORMAL POPULATION					TEST POPULATION				
0	8.00	1.00	0.01	0.01	-.40	8.00	1.00	0.01	0.01
0	1.00	2.00	0.22	0.01	0.80	1.00	2.00	0.22	0.01
0	0.01	0.22	0.20	0.12	-.62	0.01	0.22	0.20	0.12
0	0.01	0.01	0.12	1.00	-.05	0.01	0.01	0.12	1.00

RSIM FROM B TO A		RSIM FROM A TO B	
RSIM (1) =	7.5731	RSIM (1) =	7.5731
RSIM (2) =	11.146	RSIM (2) =	11.146
RSIM (3) =	14.719	RSIM (3) =	14.719
RSIM (4) =	18.292	RSIM (4) =	18.292
RSIM (5) =	21.866	RSIM (5) =	21.866
RSIM (6) =	25.439	RSIM (6) =	25.439
RSIM (7) =	29.012	RSIM (7) =	29.012
RSIM (8) =	32.585	RSIM (8) =	32.585
RSIM (9) =	36.158	RSIM (9) =	36.158
RSIM (10) =	39.731	RSIM (10) =	39.731

MOMENT FROM B TO A		MOMENT FROM A TO B	
MOMENT (1) =	7.5731	MOMENT (1) =	7.5731
MOMENT (2) =	319.63	MOMENT (2) =	319.63
MOMENT (3) =	117.05	MOMENT (3) =	117.05
MOMENT (4) =	331.74	MOMENT (4) =	331.74
MOMENT (5) =	818.60	MOMENT (5) =	818.60
MOMENT (6) =	1811.7	MOMENT (6) =	1811.7
MOMENT (7) =	3667.9	MOMENT (7) =	3667.9
MOMENT (8) =	6890.2	MOMENT (8) =	6890.2
MOMENT (9) =	12136.	MOMENT (9) =	12136.
MOMENT (10) =	20204.	MOMENT (10) =	20204.

Figure 18. A second case of four dimensional correlated populations with equal covariance matrices and different means.

NORMAL POPULATION					TEST POPULATION				
0	2.00	0.40	0.01	0.01	0.00	2.00	0.40	0.01	0.01
0	0.40	2.00	0.40	0.01	2.83	0.40	2.00	0.40	0.01
0	0.01	0.40	2.00	0.40	2.83	0.01	0.40	2.00	0.40
0	0.01	0.01	0.40	2.00	0.00	0.01	0.01	0.40	2.00

RSIM FROM B TO A		RSIM FROM A TO B	
RSIM (1) =	10.907	RSIM (1) =	10.907
RSIM (2) =	17.815	RSIM (2) =	17.815
RSIM (3) =	24.722	RSIM (3) =	24.722
RSIM (4) =	31.629	RSIM (4) =	31.629
RSIM (5) =	38.537	RSIM (5) =	38.537
RSIM (6) =	45.444	RSIM (6) =	45.444
RSIM (7) =	52.351	RSIM (7) =	52.351
RSIM (8) =	59.259	RSIM (8) =	59.259
RSIM (9) =	66.166	RSIM (9) =	66.166
RSIM (10) =	73.073	RSIM (10) =	73.073

MOMENT FROM B TO A		MOMENT FROM A TO B	
MOMENT (1) =	10.907	MOMENT (1) =	10.907
MOMENT (2) =	1059.7	MOMENT (2) =	1059.7
MOMENT (3) =	317.55	MOMENT (3) =	317.55
MOMENT (4) =	1205.5	MOMENT (4) =	1205.5
MOMENT (5) =	3942.1	MOMENT (5) =	3942.1
MOMENT (6) =	11463.	MOMENT (6) =	11463.
MOMENT (7) =	30278.	MOMENT (7) =	30278.
MOMENT (8) =	73760.	MOMENT (8) =	73760.
MOMENT (9) =	0.16761E+06	MOMENT (9) =	0.16761E+06
MOMENT (10) =	0.35837E+06	MOMENT (10) =	0.35837E+06

Figure 19. A case of four dimensional correlated populations with equal variance in each component and mean at (0,2.83,2.83,0).

NORMAL POPULATION					TEST POPULATION				
0	2.00	0.40	0.01	0.01	2.83	2.00	0.40	0.01	0.01
0	0.40	2.00	0.40	0.01	0.00	0.40	2.00	0.40	0.01
0	0.01	0.40	2.00	0.40	2.83	0.01	0.40	2.00	0.40
0	0.01	0.01	0.40	2.00	0.00	0.01	0.01	0.40	2.00

RSIM FROM B TO A		RSIM FROM A TO B	
RSIM (1) =	12.850	RSIM (1) =	12.850
RSIM (2) =	21.699	RSIM (2) =	21.699
RSIM (3) =	30.549	RSIM (3) =	30.549
RSIM (4) =	39.398	RSIM (4) =	39.398
RSIM (5) =	48.248	RSIM (5) =	48.248
RSIM (6) =	57.097	RSIM (6) =	57.097
RSIM (7) =	65.947	RSIM (7) =	65.947
RSIM (8) =	74.797	RSIM (8) =	74.797
RSIM (9) =	83.646	RSIM (9) =	83.646
RSIM (10) =	92.496	RSIM (10) =	92.496

MOMENT FROM B TO A		MOMENT FROM A TO B	
MOMENT (1) =	12.850	MOMENT (1) =	12.850
MOMENT (2) =	1791.4	MOMENT (2) =	1791.4
MOMENT (3) =	498.11	MOMENT (3) =	498.11
MOMENT (4) =	2157.5	MOMENT (4) =	2157.5
MOMENT (5) =	8009.0	MOMENT (5) =	8009.0
MOMENT (6) =	26329.	MOMENT (6) =	26329.
MOMENT (7) =	78361.	MOMENT (7) =	78361.
MOMENT (8) =	0.21447E+06	MOMENT (8) =	0.21447E+06
MOMENT (9) =	0.54618E+06	MOMENT (9) =	0.54618E+06
MOMENT (10) =	0.13059E+07	MOMENT (10) =	0.13059E+07

Figure 20. Another case of four dimensional correlated populations with equal variance in each component and mean at (2.83,0,2.83,0).

NORMAL POPULATION					TEST POPULATION				
0	2.00	0.40	0.01	0.01	0.00	2.00	0.40	0.01	0.01
0	0.40	2.00	0.40	0.01	2.83	0.40	2.00	0.40	0.01
0	0.01	0.40	2.00	0.40	0.00	0.01	0.40	2.00	0.40
0	0.01	0.01	0.40	2.00	2.83	0.01	0.01	0.40	2.00

RSIM FROM B TO A		RSIM FROM A TO B	
RSIM (1) =	12.850	RSIM (1) =	12.850
RSIM (2) =	21.699	RSIM (2) =	21.699
RSIM (3) =	30.549	RSIM (3) =	30.549
RSIM (4) =	39.398	RSIM (4) =	39.398
RSIM (5) =	48.248	RSIM (5) =	48.248
RSIM (6) =	57.097	RSIM (6) =	57.097
RSIM (7) =	65.947	RSIM (7) =	65.947
RSIM (8) =	74.797	RSIM (8) =	74.797
RSIM (9) =	83.646	RSIM (9) =	83.646
RSIM (10) =	92.496	RSIM (10) =	92.496

MOMENT FROM B TO A		MOMENT FROM A TO B	
MOMENT (1) =	12.850	MOMENT (1) =	12.850
MOMENT (2) =	1791.4	MOMENT (2) =	1791.4
MOMENT (3) =	498.11	MOMENT (3) =	498.11
MOMENT (4) =	2157.5	MOMENT (4) =	2157.5
MOMENT (5) =	8009.0	MOMENT (5) =	8009.0
MOMENT (6) =	26329.	MOMENT (6) =	26329.
MOMENT (7) =	78361.	MOMENT (7) =	78361.
MOMENT (8) =	0.21447E+06	MOMENT (8) =	0.21447E+06
MOMENT (9) =	0.54618E+06	MOMENT (9) =	0.54618E+06
MOMENT (10) =	0.13059E+07	MOMENT (10) =	0.13059E+07

Figure 21. A third case of four dimensional correlated populations with equal variance in each component and mean at (0,2.83,0,2.83), symmetric position to figure 20.

in different directions. The first two of these cases have different values for the RSIM, this differs from the uncorrelated figures 5 and 6 on pages 18 and 19. This results from the data distributions no longer being "circular" as before, thus all directions are not equivalent. Figures 20 and 21 give the same values for the RSIM; the means in these figures are in symmetric positions with respect to the eigenvectors of the covariance matrices.

Figure 22 approximates the cases of uniform expansion and contraction respectively of the covariance matrix of B with no change in the means. This corresponds to the uncorrelated case in figure 7 on page 22. The derivation of that result of the product of the pair of the n-th RSIM yielding the square of the dimension does not depend on the correlation status of the data. In figure 22 the expansion factor α is 1.5, and each successive RSIM (B-A) is about a factor of 1.5 times the previous one and each RSIM (A-B) is about two-thirds the previous RSIM. But the RSIM in this figure does not have the exact values because the matrices of the two populations are not precisely related by a scalar factor. The diagonal and adjacent elements are exactly proportional, but the rest of the off-diagonal elements are the same in both populations due to the way they are generated. This small difference causes less than a percent deviation from the exact values for most of the RSIM. The RSIM do have the exact values if all of the elements of the covariance matrix are related by α . This is another instance in which a threshold or some other measure of closeness (as described with figures 13-15 on pages 33-35) can be applied to recognize these RSIM as resulting from an almost uniform expansion.

NORMAL POPULATION

0	8.00	1.00	0.01	0.01
0	1.00	2.00	0.22	0.01
0	0.01	0.22	0.20	0.12
0	0.01	0.01	0.12	1.00

TEST POPULATION

0.00	12.00	1.50	0.01	0.01
0.00	1.50	3.00	0.33	0.01
0.00	0.01	0.33	0.30	0.18
0.00	0.01	0.01	0.18	1.50

RSIM FROM B TO A

RSIM (1) =	5.9985
RSIM (2) =	8.9954
RSIM (3) =	13.490
RSIM (4) =	20.230
RSIM (5) =	30.338
RSIM (6) =	45.498
RSIM (7) =	68.232
RSIM (8) =	102.33
RSIM (9) =	153.46
RSIM (10) =	230.15

RSIM FROM A TO B

RSIM (1) =	2.6674
RSIM (2) =	1.7787
RSIM (3) =	1.1862
RSIM (4) =	0.79100
RSIM (5) =	0.52749
RSIM (6) =	0.35177
RSIM (7) =	0.23459
RSIM (8) =	0.15644
RSIM (9) =	0.10433
RSIM (10) =	0.69575E-01

MOMENT FROM B TO A

MOMENT (1) =	5.9985
MOMENT (2) =	161.83
MOMENT (3) =	65.200
MOMENT (4) =	159.31
MOMENT (5) =	343.05
MOMENT (6) =	669.06
MOMENT (7) =	1203.5
MOMENT (8) =	2022.5
MOMENT (9) =	3206.2
MOMENT (10) =	4829.9

MOMENT FROM A TO B

MOMENT (1) =	2.6674
MOMENT (2) =	6.3278
MOMENT (3) =	5.7330
MOMENT (4) =	6.2289
MOMENT (5) =	5.9646
MOMENT (6) =	5.1729
MOMENT (7) =	4.1376
MOMENT (8) =	3.0921
MOMENT (9) =	2.1797
MOMENT (10) =	1.4601

Figure 22. An example of four dimensional correlated populations with the same means and uniform expansion in the covariance matrix of the test population.

Figure 23 illustrates the case of an approximately uniform contraction of the correlated test population covariance matrix with different means. A full analysis of this case is presented in the next chapter. It can be seen in the figure that the RSIM computed from the population with larger variance (A in the figure) increase with n , while the RSIM from the smaller to the larger decrease with n . As explained before, this phenomena is due to the fact the the RSIM involve only the inverse of the covariance matrix of one population and the uninverted matrix of the other population. If C_A has larger elements than C_B , then C_A^{-1} has smaller elements than C_B . This causes one set of RSIM to have distinctively larger values than the RSIM computed the other direction. This feature of the RSIM can easily be checked and recognized in a classification scheme.

Figure 24 represents the case of a contraction of the variance of only one component of the test population with identical means. This case is a correlated version of figure 9 on page 26. The contraction is in the first component of the variance of B in this case. With this one component shrunk, the RSIM (B-A) all have values close to three which is one less than the dimension of the patterns. Each RSIM (A-B) is about a factor of ten greater than the preceeding RSIM, both of these results are similar to the uncorrelated case. However since the off-diagonal elements are no longer zero, the result of the multiplication of two correlated matrices is not easily analyzed because the large diagonal and adjacent elements have an effect everywhere in the resultant matrix product. This makes it difficult to obtain quantitative information about the populations from the values of the RSIM.

NORMAL POPULATION

0	8.00	1.00	0.01	0.01
0	1.00	2.00	0.22	0.01
0	0.01	0.22	0.20	0.12
0	0.01	0.01	0.12	1.00

TEST POPULATION

4.00	4.00	0.50	0.01	0.01
1.00	0.50	1.00	0.11	0.01
2.50	0.01	0.11	0.10	0.06
0.30	0.01	0.01	0.06	0.50

RSIM FROM B TO A

RSIM (1) =	40.206
RSIM (2) =	39.430
RSIM (3) =	29.493
RSIM (4) =	19.694
RSIM (5) =	12.351
RSIM (6) =	7.4431
RSIM (7) =	4.3631
RSIM (8) =	2.5064
RSIM (9) =	1.4177
RSIM (10) =	0.79212

RSIM FROM A TO B

RSIM (1) =	83.962
RSIM (2) =	318.11
RSIM (3) =	933.23
RSIM (4) =	2453.9
RSIM (5) =	6069.7
RSIM (6) =	14438.
RSIM (7) =	33426.
RSIM (8) =	75854.
RSIM (9) =	0.16953E+06
RSIM (10) =	0.37435E+06

MOMENT FROM B TO A

MOMENT (1) =	40.206
MOMENT (2) =	31869.
MOMENT (3) =	11630.
MOMENT (4) =	0.12520E+06
MOMENT (5) =	0.11010E+07
MOMENT (6) =	0.82293E+07
MOMENT (7) =	0.53737E+08
MOMENT (8) =	0.31271E+09
MOMENT (9) =	0.16463E+10
MOMENT (10) =	0.79340E+10

MOMENT FROM A TO B

MOMENT (1) =	83.962
MOMENT (2) =	0.11213E+07
MOMENT (3) =	0.11216E+06
MOMENT (4) =	0.26571E+07
MOMENT (5) =	0.52106E+08
MOMENT (6) =	0.87901E+09
MOMENT (7) =	0.13095E+11
MOMENT (8) =	0.17557E+12
MOMENT (9) =	0.21488E+13
MOMENT (10) =	0.24275E+14

Figure 23. Four dimensional correlated populations with different means and uniform contraction in the covariance matrix of the test population.

NORMAL POPULATION

0	8.00	1.00	0.01	0.01
0	1.00	2.00	0.22	0.01
0	0.01	0.22	0.20	0.12
0	0.01	0.01	0.12	1.00

TEST POPULATION

0.00	0.80	0.28	0.01	0.01
0.00	0.28	2.00	0.22	0.01
0.00	0.01	0.22	0.20	0.12
0.00	0.01	0.01	0.12	1.00

RSIM FROM B TO A

RSIM (1) =	3.1419
RSIM (2) =	3.1002
RSIM (3) =	3.1399
RSIM (4) =	3.1896
RSIM (5) =	3.2423
RSIM (6) =	3.2973
RSIM (7) =	3.3549
RSIM (8) =	3.4149
RSIM (9) =	3.4777
RSIM (10) =	3.5432

RSIM FROM A TO B

RSIM (1) =	13.207
RSIM (2) =	107.98
RSIM (3) =	1079.7
RSIM (4) =	11040.
RSIM (5) =	0.11314E+06
RSIM (6) =	0.11596E+07
RSIM (7) =	0.11886E+08
RSIM (8) =	0.12183E+09
RSIM (9) =	0.12487E+10
RSIM (10) =	0.12799E+11

MOMENT FROM B TO A

MOMENT (1) =	3.1419
MOMENT (2) =	15.302
MOMENT (3) =	10.563
MOMENT (4) =	14.690
MOMENT (5) =	18.178
MOMENT (6) =	20.523
MOMENT (7) =	21.497
MOMENT (8) =	21.141
MOMENT (9) =	19.695
MOMENT (10) =	17.500

MOMENT FROM A TO B

MOMENT (1) =	13.207
MOMENT (2) =	9417.5
MOMENT (3) =	1277.0
MOMENT (4) =	10271.
MOMENT (5) =	75756.
MOMENT (6) =	0.52178E+06
MOMENT (7) =	0.33965E+07
MOMENT (8) =	0.21078E+08
MOMENT (9) =	0.12552E+09
MOMENT (10) =	0.72087E+09

Figure 24. A case of four dimensional correlated populations with the same means and contraction in a single component of the variance.

The larger the off-diagonal elements are relative to the diagonal elements, the less the effect of a change in the variance of one component is reflected in the RSIM. Figure 25 demonstrates an example of the off-diagonal elements having a large effect on the RSIM when the variance of one component has changed even more dramatically (the third component's variance is 100 times greater in the test population of figure 25). Since the adjacent to the diagonal elements are a function of the diagonal elements in this work, C_{23} and C_{34} of the test population are ten and twenty times larger respectively than the corresponding elements in the normal population. If in this case the matrices were uncorrelated, each RSIM (B-A) would be about 100 times the previous one and all of the RSIM computed the other direction would be close to three. But in this case the RSIM (B-A) all differ by a factor of about 120 and the RSIM (A-B) start out close to three then steadily increase. A classification algorithm with a very large threshold might be able to recognize this case, but no valid information about the populations could be determined from analyzing the RSIM values. And a larger threshold in a recognition algorithm always increases the probability of misclassification.

Figure 26 corresponds to the correlated version of the case of small changes presented in figure 15 on page 35. All of the RSIM in the current case have values close to four, the dimension of the data. If an algorithm is checked to see if all RSIM are within one (an arbitrary threshold) of the dimension, the test population in figure 26 (which has small differences in both the means and the covariance matrices) is only recognized with the threshold if no greater than the

NORMAL POPULATION

0	8.00	1.00	0.01	0.01
0	1.00	2.00	0.22	0.01
0	0.01	0.22	0.20	0.12
0	0.01	0.01	0.12	1.00

TEST POPULATION

0.00	8.00	1.00	0.01	0.01
0.00	1.00	2.00	2.20	0.01
0.00	0.01	2.20	0.00	2.10
0.00	0.01	0.01	2.10	1.00

RSIM FROM B TO A

RSIM (1) =	121.70
RSIM (2) =	14168.
RSIM (3) =	0.16859E+07
RSIM (4) =	0.20065E+09
RSIM (5) =	0.23881E+11
RSIM (6) =	0.28422E+13
RSIM (7) =	0.33828E+15
RSIM (8) =	0.40261E+17
RSIM (9) =	0.47917E+19
RSIM (10) =	0.57030E+21

RSIM FROM A TO B

RSIM (1) =	3.4700
RSIM (2) =	4.1363
RSIM (3) =	5.1222
RSIM (4) =	6.5634
RSIM (5) =	8.6697
RSIM (6) =	11.748
RSIM (7) =	16.248
RSIM (8) =	22.824
RSIM (9) =	32.437
RSIM (10) =	46.485

MOMENT FROM B TO A

MOMENT (1) =	121.70
MOMENT (2) =	0.10492E+09
MOMENT (3) =	0.14435E+07
MOMENT (4) =	0.12925E+09
MOMENT (5) =	0.10692E+11
MOMENT (6) =	0.82975E+12
MOMENT (7) =	0.61065E+14
MOMENT (8) =	0.42959E+16
MOMENT (9) =	0.29063E+18
MOMENT (10) =	0.18996E+20

MOMENT FROM A TO B

MOMENT (1) =	3.4700
MOMENT (2) =	24.902
MOMENT (3) =	14.994
MOMENT (4) =	23.866
MOMENT (5) =	33.941
MOMENT (6) =	44.182
MOMENT (7) =	53.501
MOMENT (8) =	60.965
MOMENT (9) =	65.935
MOMENT (10) =	68.129

Figure 25. The case of four dimensional correlated populations with the same means and expansion in a single component of the variance.

NORMAL POPULATION

0	8.00	1.00	0.01	0.01
0	1.00	2.00	0.22	0.01
0	0.01	0.22	0.20	0.12
0	0.01	0.01	0.12	1.00

TEST POPULATION

0.00	8.05	1.00	0.01	0.01
0.02	1.00	1.98	0.22	0.01
0.10	0.01	0.22	0.21	0.12
0.00	0.01	0.01	0.12	0.99

RSIM FROM B TO A

RSIM (1) =	4.1066
RSIM (2) =	4.2245
RSIM (3) =	4.3547
RSIM (4) =	4.4982
RSIM (5) =	4.6559
RSIM (6) =	4.8291
RSIM (7) =	5.0188
RSIM (8) =	5.2266
RSIM (9) =	5.4536
RSIM (10) =	5.7016

RSIM FROM A TO B

RSIM (1) =	4.0132
RSIM (2) =	4.0236
RSIM (3) =	4.0314
RSIM (4) =	4.0371
RSIM (5) =	4.0409
RSIM (6) =	4.0432
RSIM (7) =	4.0441
RSIM (8) =	4.0440
RSIM (9) =	4.0429
RSIM (10) =	4.0412

MOMENT FROM B TO A

MOMENT (1) =	4.1066
MOMENT (2) =	35.621
MOMENT (3) =	20.942
MOMENT (4) =	35.059
MOMENT (5) =	51.735
MOMENT (6) =	69.151
MOMENT (7) =	85.255
MOMENT (8) =	98.211
MOMENT (9) =	106.73
MOMENT (10) =	110.23

MOMENT FROM A TO B

MOMENT (1) =	4.0132
MOMENT (2) =	32.402
MOMENT (3) =	19.519
MOMENT (4) =	31.898
MOMENT (5) =	45.941
MOMENT (6) =	59.924
MOMENT (7) =	72.087
MOMENT (8) =	81.016
MOMENT (9) =	85.886
MOMENT (10) =	86.521

Figure 26. The case of four dimensional correlated populations with only a small difference in both means and covariance matrices.

sixth RSIM is examined. As this figure shows, the use of the RSIM with thresholds or measures of closeness for recognition is independent of the state of correlation of the data.

These correlated cases demonstrate that the RSIM have many of the same features for correlated data as in the case of uncorrelated data. The RSIM are shown to possess distinct values for certain relationships of the parameters and these values or properties are often simpler to use in a pattern recognition system than the population parameters themselves. The next chapter provides a graphical framework for using these properties of the RSIM for pattern recognition.

CHAPTER IV

A GRAPHICAL REPRESENTATION OF THE REDUCED SEMI-INVARIANTS OF THE INTERCLASS MAHALANOBIS DISTANCE

This chapter deals with some ways the RSIM can be utilized for pattern recognition. The data is statistical in nature; and instead of dealing with each pattern vector (data point) individually, related patterns (usually in a temporal sense) are grouped together in a population and since a Gaussian distribution is assumed, the population is completely described by its mean vector and covariance matrix. The 'training set' or normal population is generated by collecting patterns of a normally operating system or well known situation and determining the mean vector and covariance matrix. Once these are known, nothing else needs to be done to this data unless there is a reason to update this population [according to well known techniques (10)]. If what is considered normal does not change with time and if enough data is contained in the training set to prevent statistical fluctuations, the parameters describing the normal population will not change.

A second set of data is collected at a later time and the mean and covariance matrix of this population are computed. The RSIM are then calculated. In effect this transforms the parameters of both populations into a new set of values, the RSIM. The RSIM have already been shown to contain many properties for recognition about the relationship of the populations.

Now this relationship can be represented as a single point in an "RSIM space". The value of every RSIM is not necessary for use in a pattern recognition system; the simple classifier described later in this work largely utilizes only the fifth and tenth pair of RSIM. This is done because, in the analysis of the RSIM, it is found that either the contribution from equation 8 or 9 begins to dominate the value by the fifth RSIM. The tenth is the highest RSIM computed and shows the most effect of any difference between the two populations. By using only two of the RSIM, the relationship can easily be expressed as a point on an X-Y plot.

n-n RSIM Space

The first RSIM space to consider has the n -th RSIM (B-A) plotted on the X-axis and the n -th RSIM (A-B) plotted on the Y-axis of a simple Cartesian coordinate system. The point (N,N) in this space indicates both populations have the same parameters, since the n -th RSIM is equal to N, the dimension of the data. This space has a number of interesting properties upon which a pattern recognition system can be rigorously developed. Two of the major changes which can occur to a second population relative to the first are a uniform expansion or contraction in all components of the covariance matrix and a radial change in the mean vector. This section details what effect these two changes have on the values of the RSIM and how they can be monitored in n -n RSIM space.

The expansion factor α (a scalar) is defined by:

$$\underline{C}_B = \alpha \underline{C}_A \quad \text{and} \quad \underline{C}_B^{-1} = \frac{1}{\alpha} \underline{C}_A^{-1} \quad (10)$$

α greater than one implies that $\underline{C}_B$ is expanded relative to $\underline{C}_A$; α less than one implies that $\underline{C}_B$ is contracted. The radial factor β (another scalar) is defined as:

$$\underline{M}_B = \beta \underline{M} \quad (11)$$

where $\underline{M}$ is a vector collinear with $\underline{M}_B$ and $\underline{M}_A$ (the origin of the data coordinate system is at $\underline{M}_A$). If β is equal to zero, then $\underline{M}_B$ is the same as $\underline{M}_A$. A third quantity needed for the analysis is:

$$R = \underline{M}^T \underline{C}_A^{-1} \underline{M} \quad (12)$$

This is the "unit" Mahalanobis distance in the direction of $\underline{M}$ in this system.

Substituting α and β into equation 6 gives:

$$\text{RSIM (B-A)} = \text{tr}(\underline{C}_A^{-1} \alpha \underline{C}_A)^n + n \beta \underline{M}^T \underline{C}_A^{-1} (\alpha \underline{C}_A \underline{C}_A^{-1}) \beta \underline{M} = \alpha^n N + n \alpha^{n-1} \beta^2 R \quad (13)$$

Substituting α and β into equation 7, the RSIM in the other direction:

$$\text{RSIM (A-B)} = \text{tr}(\underline{C}_A^{-1} \frac{1}{\alpha} \underline{C}_A)^n + n \beta \underline{M}^T \frac{1}{\alpha} \underline{C}_A^{-1} (\frac{1}{\alpha} \underline{C}_A \underline{C}_A^{-1})^{n-1} \beta \underline{M} = \alpha^{-n} N + n \alpha^{-n} \beta^2 R \quad (14)$$

If the n -th RSIM (B-A) is to be plotted on the X-axis and the n -th RSIM (A-B) is plotted on the Y-axis, X and Y are defined in this n -n RSIM space as:

$$X = \alpha^n N + n \alpha^{n-1} \beta^2 R \quad (15)$$

$$Y = \alpha^{-n}N + n\alpha^{-n}\beta^2R \quad (16)$$

To find the equation of a curve in this n - n RSIM space that corresponds to changes in β with no changes in α (i.e. test population moving away from normal population) equation 16 is multiplied by α^{2n-1} and is subtracted from equation 15 to remove β from the expression. This yields:

$$X = \alpha^{2n-1}Y - (\alpha^n - \alpha^{-n+1})N$$

or rearranging terms;

$$Y = \alpha^{1-2n}X + N(\alpha^{-n} - \alpha^{-n+1}) \quad (17)$$

This is the equation of a straight line with a slope of α^{1-2n} and a Y-intercept of $N(\alpha^{-n} - \alpha^{-n+1})$. In the case of $\alpha = 1$, (identical covariance matrices) equation 17 reduces to $Y = X$, the result derived in the case of equal covariance matrices (see figures 4, 17, and 18 on pages 16, 41, and 42). If α is greater than one (expansion), the slope of the line of equation 17 is less than one and the Y-intercept is negative. If α is less than one, the slope of this line is greater than one and the y-intercept is greater than zero. The line $Y = X$ partitions these two instances and no lines from equation 17 intersect at positive coordinates even though they are not parallel. To find the equation of a curve in this n - n RSIM space that corresponds to changes in α for a fixed β ; solving for α in equation 16 gives:

$$\alpha = \left(\frac{N + n\beta^2R}{Y} \right)^{1/n} \quad (18)$$

Substituting this expression for α into equation 15 and rearranging the terms yields:

$$XY = N^2 + Nn\beta^2R + Y^{1/n}(n\beta^2R)^{2n-1/n} \quad (19)$$

which is recognized as the equation of a hyperbola. In the case of β equals zero (identical mean vectors), equation 19 reduces to $XY = N^2$, the equation of an equilateral hyperbola, which is the same result associated with figures 7 and 22, pages 21 and 47 (uniform expansion). These hyperbolas and straight lines form the basis for a powerful system to analyze the RSIM.

Figure 27 is one of a series of computations of the RSIM of populations related by uniform expansion and a radial movement of the means in the (1,1) direction from the normal population. In this figure N (the dimension) is equal to two, and R (the unit Mahalanobis distance from the point (1,1) to the normal population) is defined as:

$$R = (1 \ 1) \begin{pmatrix} 1 & 0 \\ 0 & .8 \end{pmatrix}^{-1} \begin{pmatrix} 1 \\ 1 \end{pmatrix} = 2.25$$

Thus the β 's in this series of computations are 0, 2, and 3; and the α 's are 1., 0.75, and 1.25.

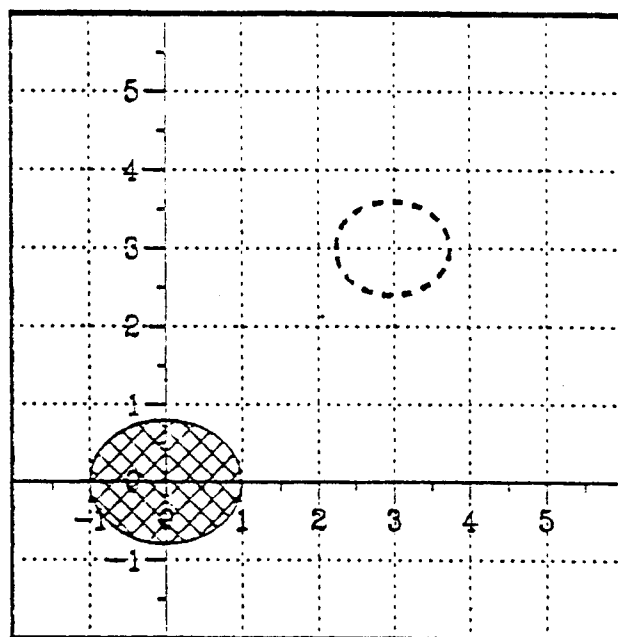
The values found for the RSIM should fit into equations 17 and 19. Using the fifth RSIM in figure 27 (which has the values for α and β of 0.75 and 3.0 respectively), equation 17, the line of constant α gives:

$$\begin{aligned} 435.09 &= (.75)^{1-2(5)}(32.511) + 2(.75^{-5}-.75^{-4}) \\ &= 13.32 \times 32.511 + 2(4.21-3.16) = 435.09 \end{aligned}$$

NORMAL POPULATION

$$\begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} 1.00 & 0.00 \\ 0.00 & 0.80 \end{pmatrix}$$

TEST POPULATION

$$\begin{pmatrix} 3.00 \\ 3.00 \end{pmatrix} \begin{pmatrix} 0.75 & 0.00 \\ 0.00 & 0.60 \end{pmatrix}$$


RSIM FROM B TO A

RSIM (1) =	21.750
RSIM (2) =	31.500
RSIM (3) =	35.016
RSIM (4) =	34.805
RSIM (5) =	32.511
RSIM (6) =	29.188
RSIM (7) =	25.495
RSIM (8) =	21.825
RSIM (9) =	18.396
RSIM (10) =	15.317

RSIM FROM A TO B

RSIM (1) =	29.667
RSIM (2) =	75.556
RSIM (3) =	148.74
RSIM (4) =	262.32
RSIM (5) =	435.09
RSIM (6) =	693.90
RSIM (7) =	1076.9
RSIM (8) =	1638.2
RSIM (9) =	2453.9
RSIM (10) =	3631.5

Figure 27. The case of two dimensional uncorrelated populations with $\alpha = 0.75$, $\beta = 3$.

Equation 19, the hyperbola of constant β gives:

$$\begin{aligned}
 32.511 &= 2\left(\frac{2+5 \times 3^2 \times 2.25}{435.09}\right) + 5 \times 3^2 \times 2.25 \left(\frac{2+5 \times 3^2 \times 2.25}{435.09}\right)^{\frac{5-1}{5}} \\
 &= 2(.237) + 101.25(.3164) \\
 &= 32.511
 \end{aligned}$$

The points for the third RSIM of the series of computations mentioned above are plotted in figure 28 using equation 17 with α 's of 0.75, 1.0, and 1.25 to draw the dashed lines. β 's of 0, 1, 2, and 3 are used in equation 19 to draw the solid lines. All of the points generated by the series of computations fall exactly at the intersection of the theoretical lines. Figure 29 is a blowup of figure 28, it has β 's of 0, 0.1, 0.2, 0.3 and 0.4. This figure shows that there is an area in n-n RSIM space between the hyperbola $XY = N^2$ and the axes in which no point may fall due to uniform expansion or radial movement.

This analysis directly leads to the foundation of a pattern recognition system for these features of the test population. The lines of radial movement of the means (with constant covariance) plus the hyperbolas of uniform expansion of the covariance (with constant means) define a curvilinear coordinate system. This coordinate system exists in the n-n RSIM space and can define (decide) the relationship of the populations.

The first use for this coordinate system is to determine if the two populations are related only by a radial movement of the means and uniform expansion of the test population's covariance matrix. Two

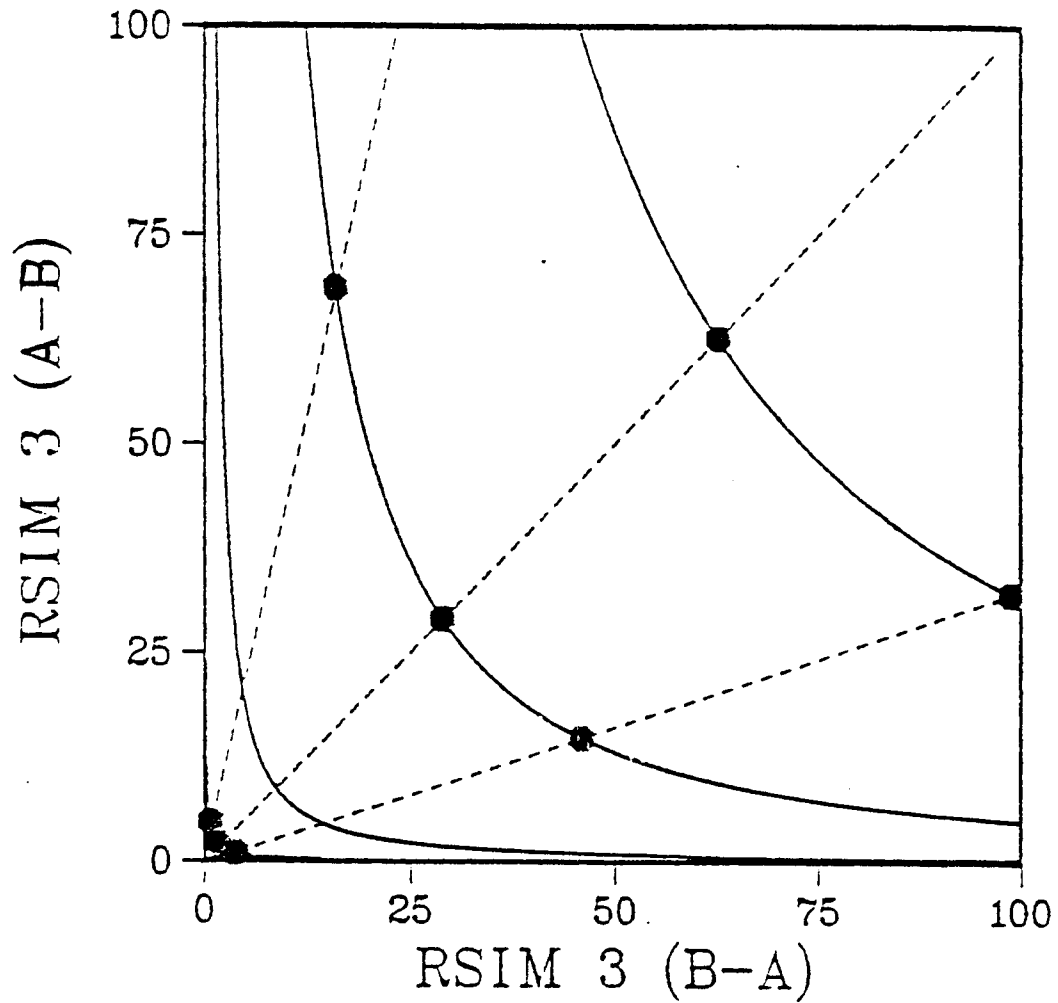


Figure 28. The results of α 's of 1, .75, 1.25 and β 's of 0, 2, 3, plotted on a grid of 3-3 RSIM space.

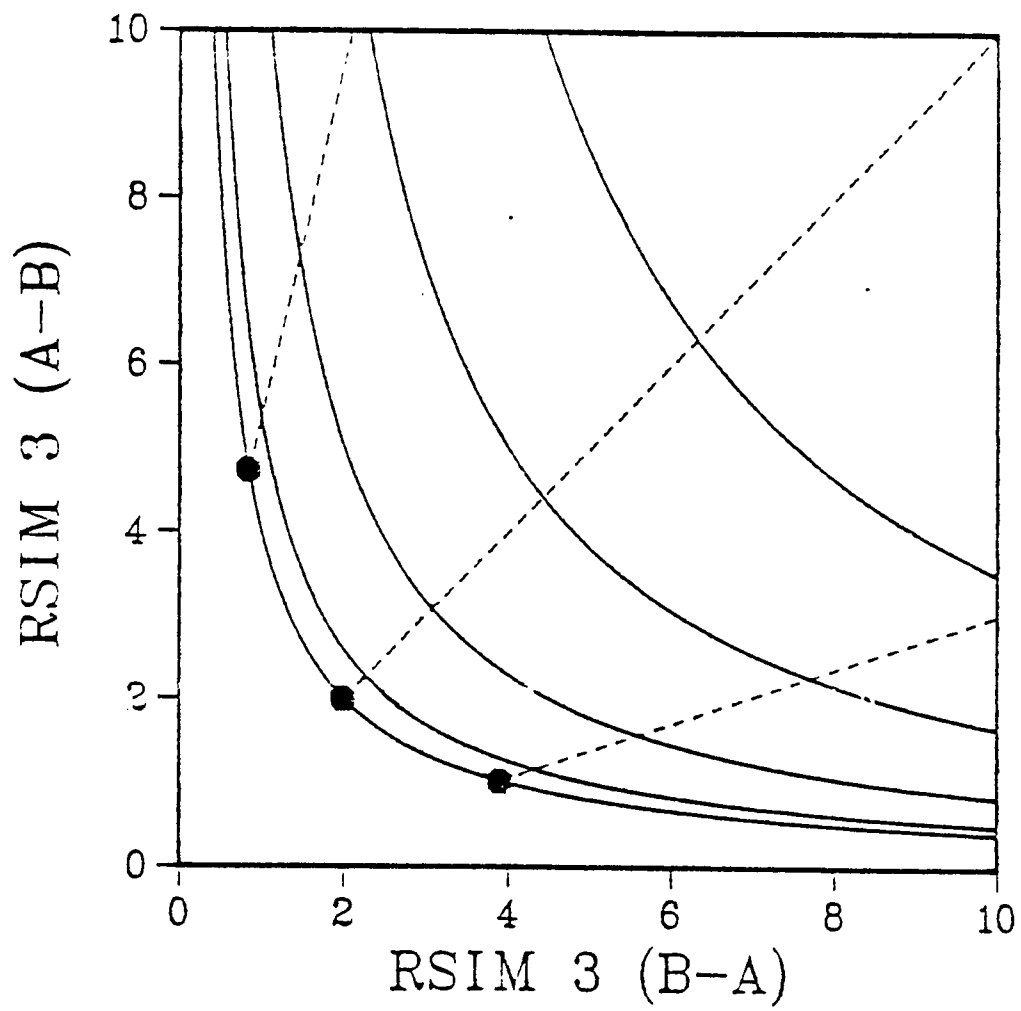


Figure 29. A blowup of figure 30 (3-3 RSIM space).

mean vectors are always collinear; a radial movement of the means implies that a certain direction from the mean vector has been specified. (The (1,1) direction was used in the above example.) One way for the direction to be specified is by a previous measurement having in a certain direction (e.g. another test population). This is valuable in an instance of a continuous monitoring problem. Third and later measurements can be found to be collinear or not with the first two populations since it can be determined if that the mean vector is in a certain direction. A second way a radial direction might be specified is that a direction could have a significance to the particular problem. This direction would be incorporated as part of the monitoring system. If the means of the test population are in this direction relative to the mean of the normal class, the recognition algorithm could determine this. The following technique determines if two populations satisfy the relationships of radial difference and uniform expansion. Both sets of RSIM are calculated. The unit Mahalanobis distance is defined in the radial direction to be checked. An n-n RSIM plot is made, e.g. the fifth RSIM is plotted as described above in the (linear) Cartesian coordinate system. Every point in this space has unique coordinates in the curvilinear space. The values of α and β are determined for this plotted point (by a one time computation of the curvilinear coordinate system for this fifth RSIM and the appropriate R). However any point in this space has α and β values whether or not the populations are related in the proper manner for these values to be correct. If they are related in the proper manner, then any other RSIM (e.g. the tenth) gives the same values for

α and β when the RSIM is plotted in that space. If different values for α and β are found in the second n - n RSIM space, then there is another difference in the populations than radial movement and uniform expansion. Figure 30 shows the curvilinear coordinate systems in 5,5 RSIM space with an R of 2., three dimensions, α 's of .7, .8, .9, 1., 1.1, 1.2, and 1.3, and β 's of 0., 1., 2., 3., and 4.0. Figure 31 shows the same grid in 10-10 RSIM space, the lines of constant β are farther from the line $Y = X$ than in 5-5 RSIM space, and the hyperbolas of constant α are also farther from the origin in 10-10 RSIM space. Figure 32 shows the effect of increasing the dimension of the data from three to nine in this figure. The hyperbolas of constant α are only slightly displaced outward with this increase in dimension. Figure 33 shows that an increase in R from 2.0 to 2.5 also results in pushing the hyperbolas outward in 5-5 RSIM space.

Another use of the n - n RSIM curvilinear coordinate system is in a surveillance system. The normal population is collected and a series of test populations are taken at later time intervals. If the test populations start out with the same parameters as the reference or normal population, the points plotted in n - n RSIM space fall at the point (N,N) . If the test populations begin to move radially along the direction being monitored or there is uniform expansion to the covariance matrix, the movement of the points in n - n RSIM space is along one of the "axial" directions of the curvilinear axes. If there is a movement in n - n RSIM space along both of these axes, then either a combination of the radial movement and expansion has occurred (verifiable by the previous technique) or another type of change has

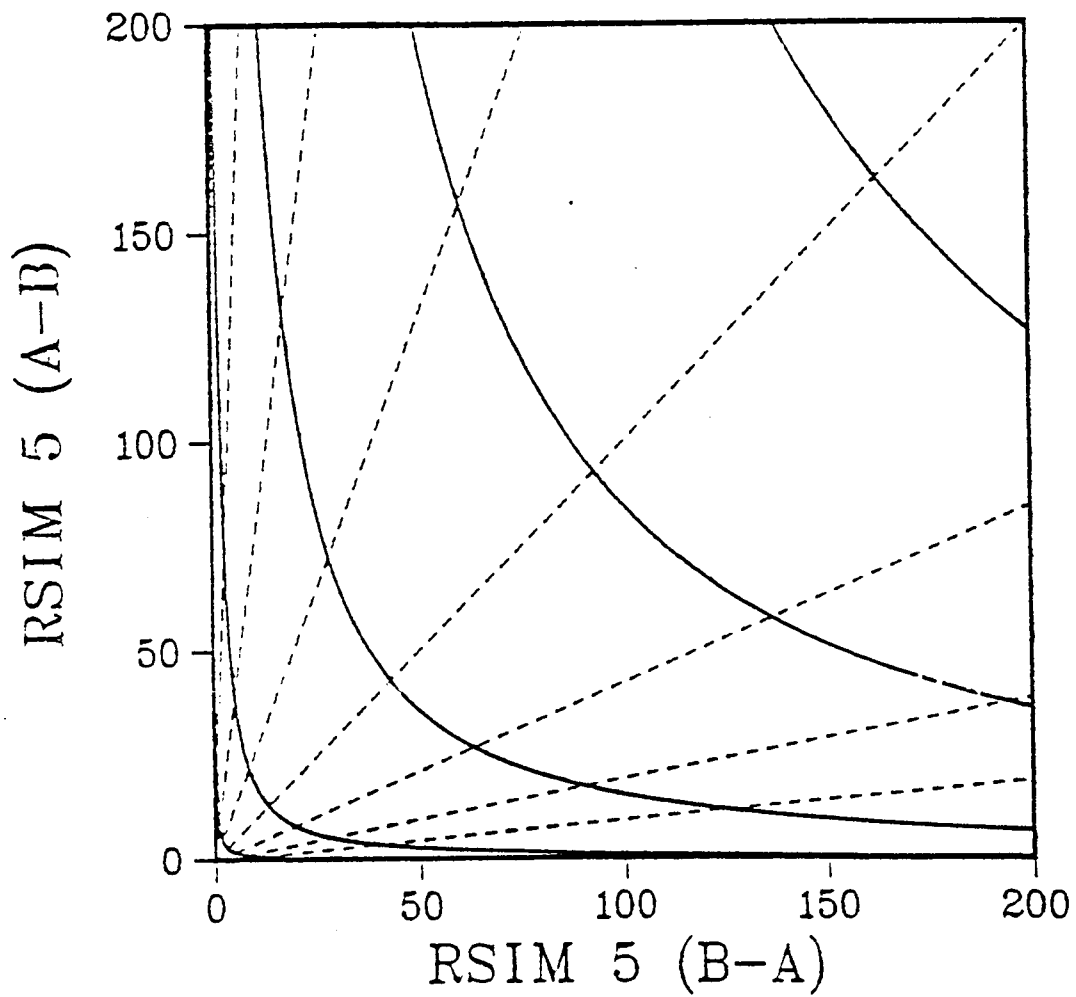


Figure 30. A plot of 5-5 RSIM space with $N = 3$,
 $R = 2$.

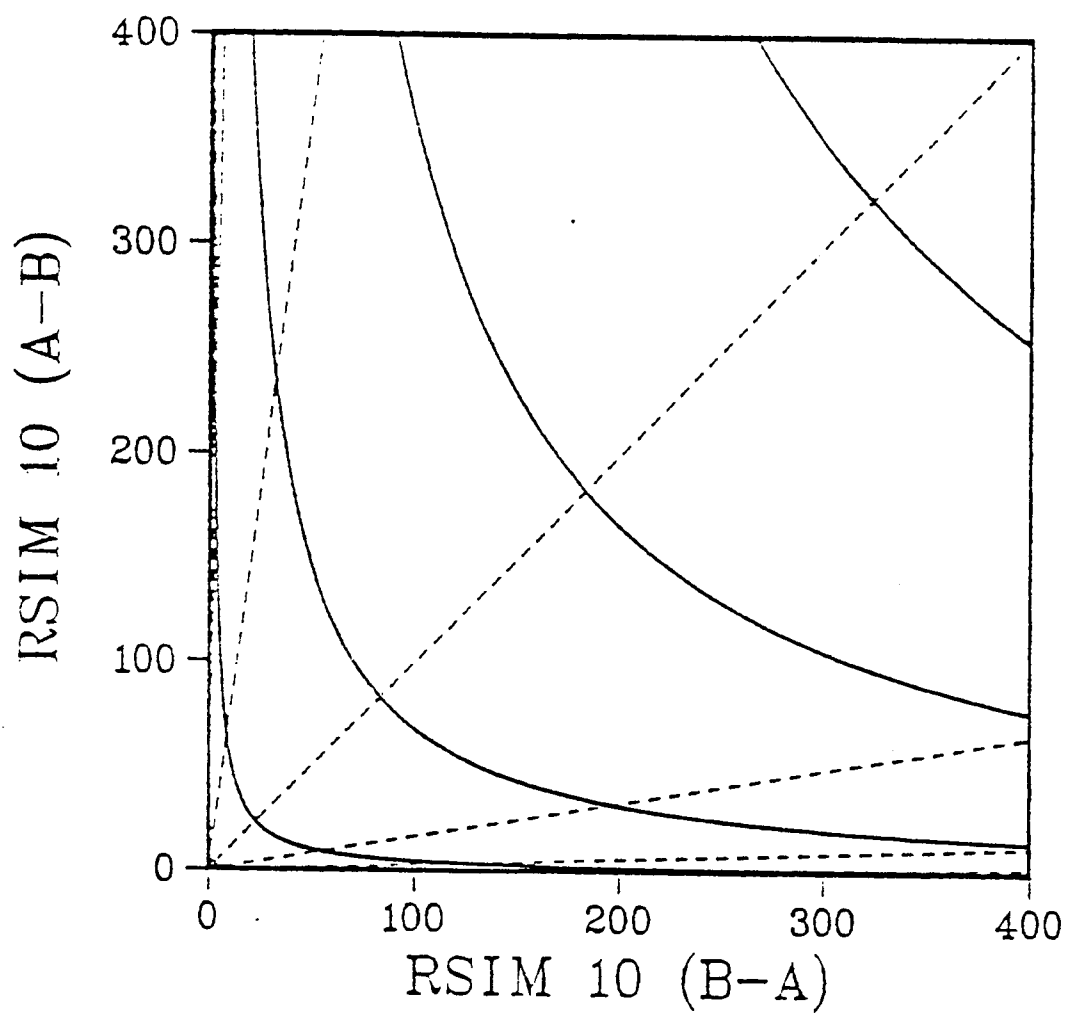


Figure 31. A plot of 10-10 RSIM space with $N = 3$, $R = 2$.

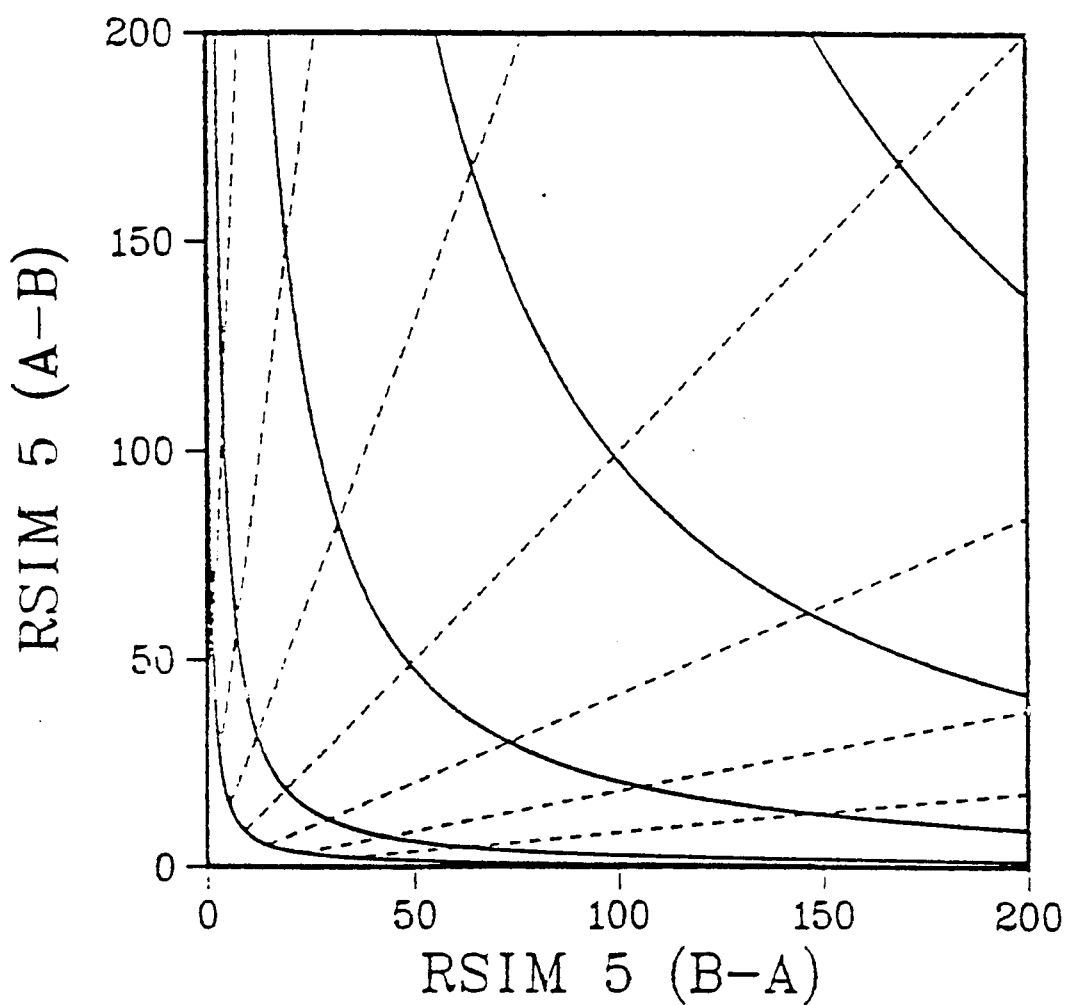


Figure 32. A plot of 5-5 RSIM space showing the effect of increasing the dimension of the data to 9.

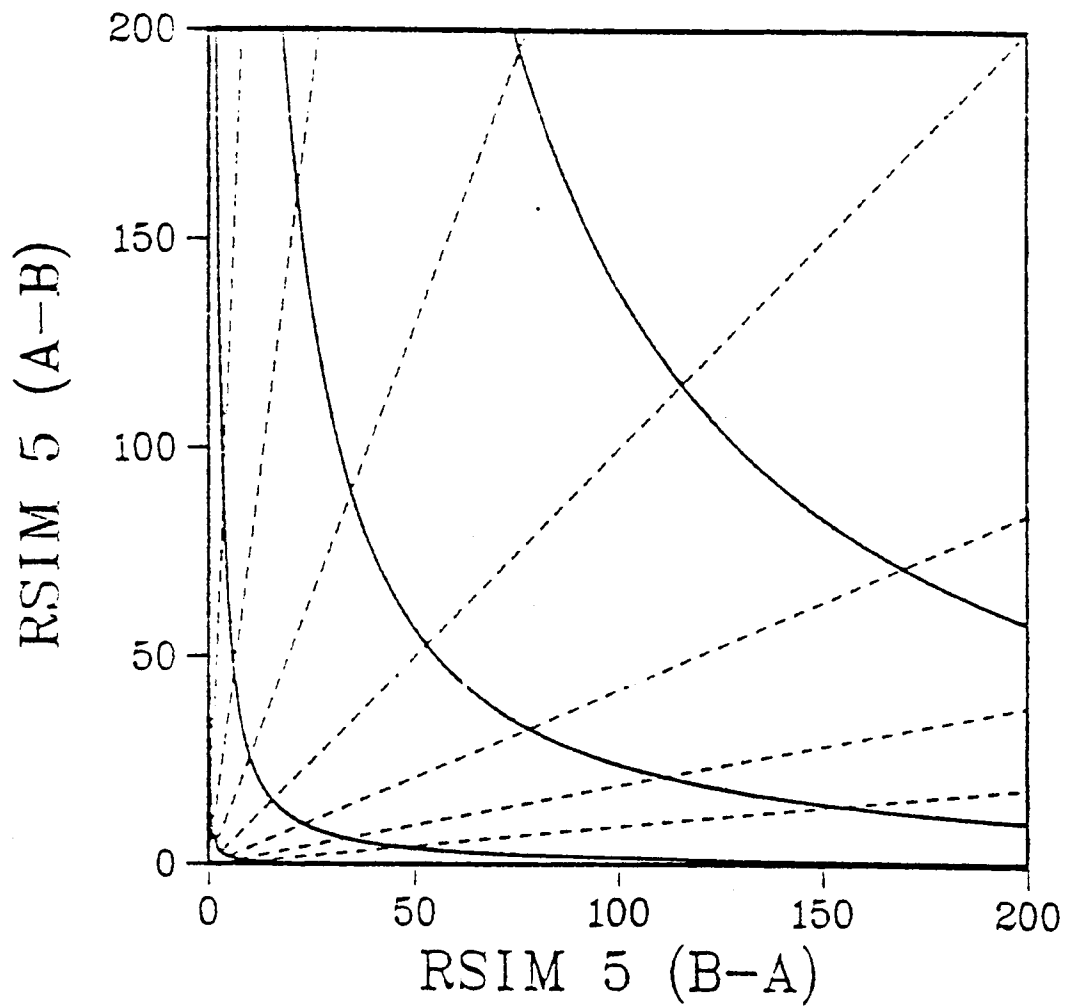


Figure 33. A plot of 5-5 RSIM space showing the effect of increasing R to 2.5.

occurred to the parameters. The history of the changes of the data can be mapped out by following the points in n - n RSIM space. As described in the next chapter, the computation of the RSIM is very fast; if the test populations can be collected rapidly enough, the resultant point in n - n RSIM space could be displayed on a CRT in real time. Certain bounds could be established for the monitoring system; if the expansion exceeds a given value or the means drift apart more than a given distance, the monitoring program could easily recognize this and perform the appropriate response. More than one radial direction can be monitored at a time by applying the check for radial movement in as many directions as desired. This greatly enhances the power of the monitoring system.

m - n RSIM Space

There are other useful graphical representations of the RSIM in addition to n - n RSIM space. There is no need to consider the n -th RSIM($B-A$) with the m -th RSIM($A-B$) (assuming $m \neq n$); due to the properties of the RSIM, in general no useful information can be obtained from a plot of this type. However, it can be useful to graph a pair of RSIM computed in the same direction. This section discusses graphical representations of this type and uses 5-10 RSIM($B-A$) space as an example.

A plot of this type is presented in figure 34. This 5-10 RSIM plot has the value of the fifth RSIM on the X-axis and the value of the tenth plotted on the Y-axis. As shown in the cases of figures 1 and 16, on pages 11 and 40, if the two populations are identical, the

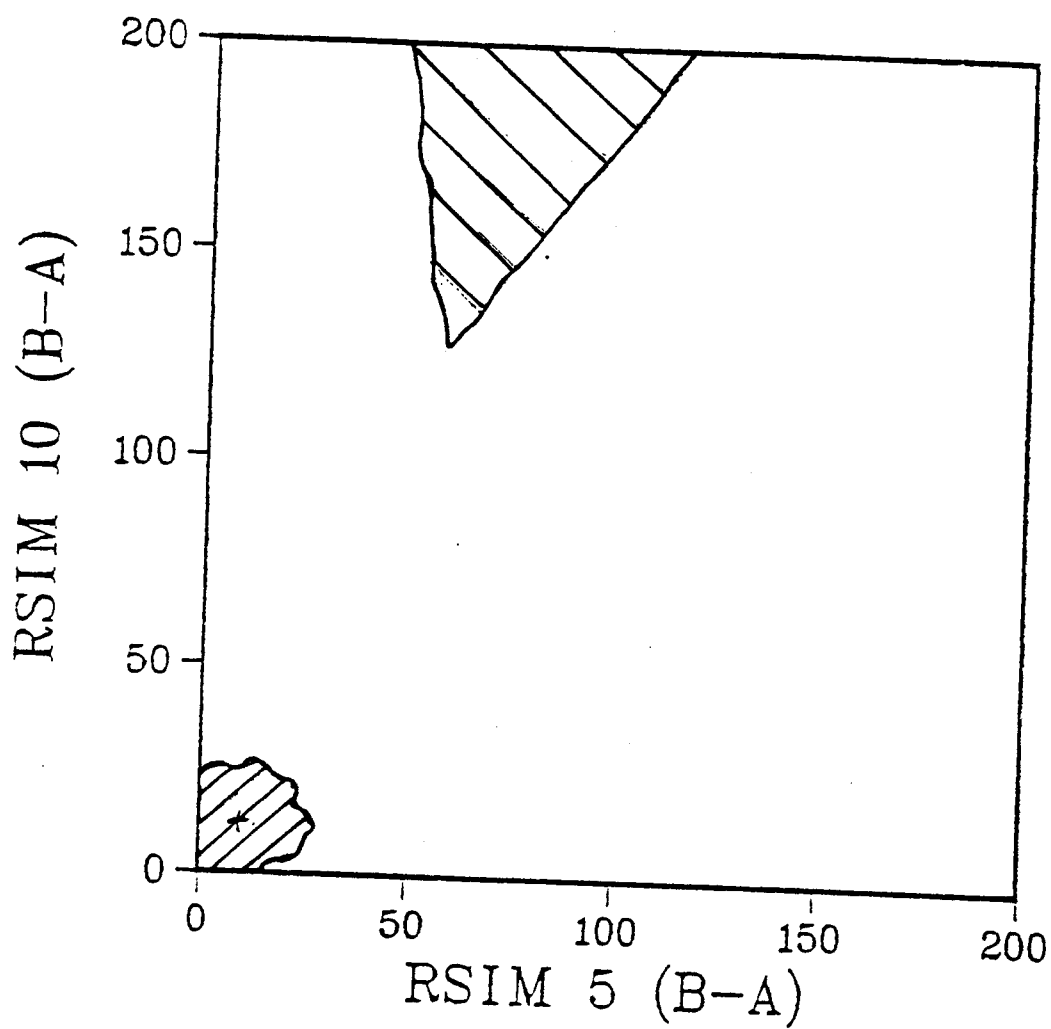


Figure 34. A plot of 5-10 RSIM (B-A) space.

corresponding point is plotted in 5-10 RSIM space at (N,N) where N is the dimension of the original pattern space. The test population is indistinguishable from "normal" and is likely to be assigned to the same class as the training set to which it is being compared when a point is at (N,N) . If the populations are only slightly different in their parameters (figures 13-15, 26, pages 33-35, 53) the point occurs in 5-10 RSIM space at $(N+dx, N+dy)$ where dx and dy are rather small. Although it is not necessarily true for all problems, this type of test population would probably be classified as belonging to the same class as the training set. This implies that there exists a region about the point (N,N) in RSIM space in which any point indicates membership of the two populations in the same class. This region is indicated in figure 34 around the point $(10,10)$. The size and exact shape of this area is dependent on the particular problem and can be determined by trial and error if not enough a priori information exists. In the simple classifier presented later in this study, this region is a square centered on the point (N,N) with side of length two times "T" (where T is an input parameter with a value of 0.5). Alternately a circular or any other shaped region could have been selected. But for any given problem, this region can have a very irregularly shaped boundary.

In the case of the covariance matrices being similar, with increasing distance between the means, the tenth RSIM increases much more rapidly than the fifth. In RSIM space, this corresponds to a set of points far from the origin in an almost vertical direction. This defines a second region in this RSIM space (also indicated in figure 34).

A point in this area is recognized as indicating a definite difference in the means of the two populations. An example of this is the fifth and tenth RSIM (B-A) of figure 4 on page 16. Another region of interest in this space is the area under a line from the origin to the point (N,N). This area indicates that the tenth RSIM (B-A) is less than the fifth and there is little difference in their means. As discussed with figure 7 on page 22, this occurs when there is contraction in the spread of the test population B relative to the normal population A, and equation 9 does not contribute significantly to the sum. This region is indicated in figure 35, a 5-10 RSIM space with a different scale than figure 34. The same region corresponds to expansion in B if the fifth and tenth RSIM from A to B are plotted instead.

This graphical analysis forms the basis for the classifier presented in chapter six. The values of the RSIM are fed into a routine which examines the fifth and tenth RSIM pairs to decide if they belong to one of these special regions.

Multiclass Recognition

In the above discussion, it is assumed that there is only a normal class and a test is being made to determine whether or not a another population belongs to the normal class. But since there is a certain structure to RSIM space, it is possible to divide a "not normal" condition (e.g. point farther than given distance from N,N) into various classes, depending on either the area of RSIM space or what caused the abnormality. In effect, this extends the analysis to a more than two class pattern recognition problem.

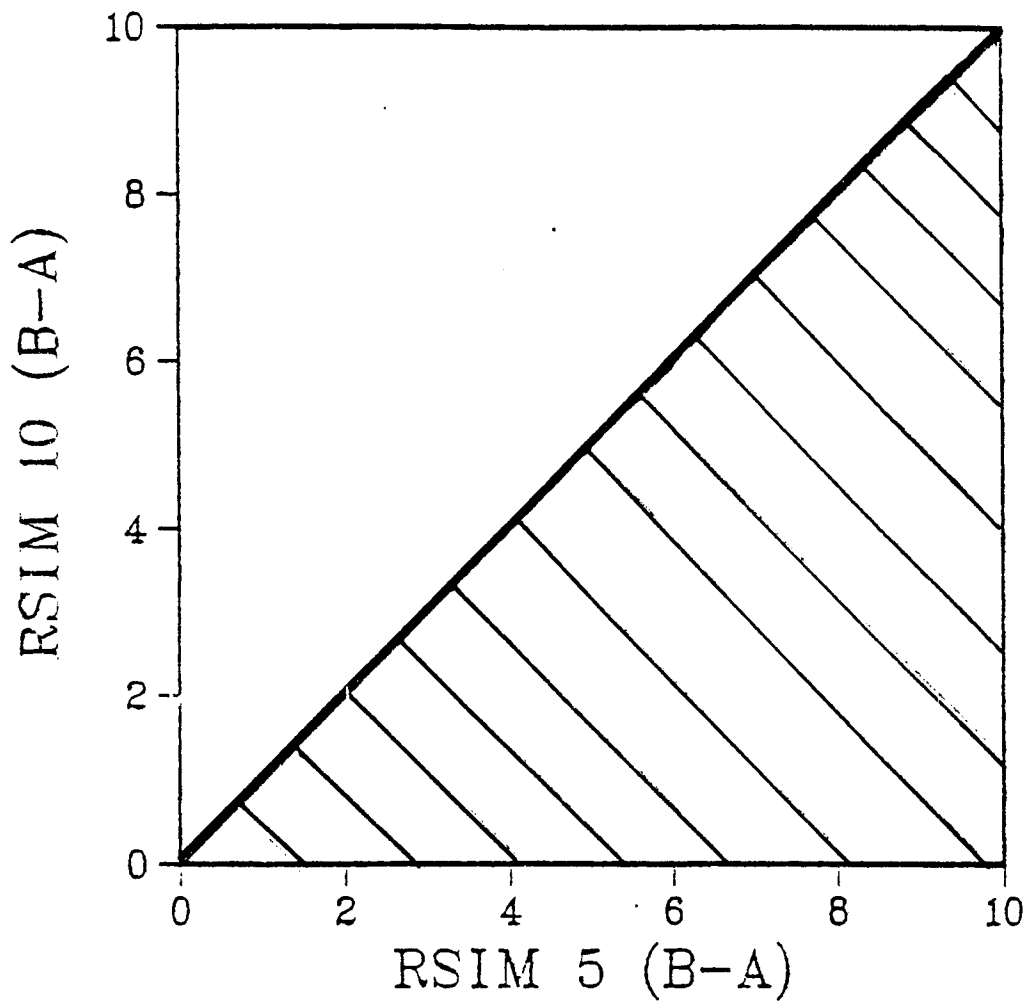


Figure 35. A blowup of 5-10 RSIM (B-A) space showing the area near the point (N,N).

One approach to the multiclass problem is as follows.

Populations representative of all of the classes are used to generate the means and covariance matrices for every class. The RSIM from the test population to be classified are computed to every class and the point in RSIM space closest to (N,N) corresponds to the overall greatest similarity between the test population and that class. An example of this is presented in figure 36. Of the points plotted, C is closest to $(10,10)$ and indicates membership of the test population in the same class as the normal population used for this RSIM computation. A decision function of this type is a minimum distance classifier in RSIM space.

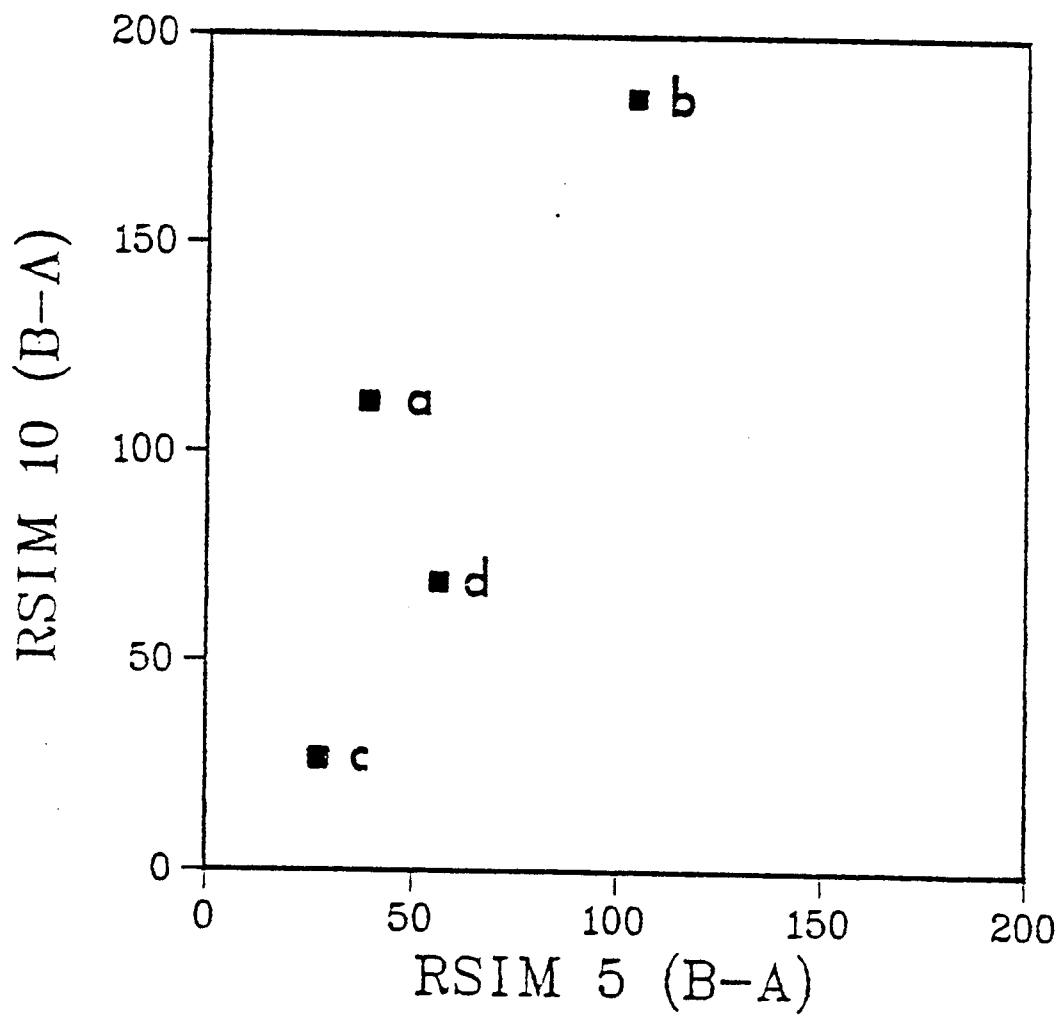


Figure 36. An example of multiclass recognition in 5-10 RSIM space.

CHAPTER V

IMPLEMENTATION AND RESULTS

An interactive program written in Fortran on a PDP 11/34 minicomputer (using an RSX-11M operating system) computes the RSIM and moments and analyzes the RSIM. The interactive nature of the program is helpful in gaining empirical insight into the properties of the RSIM. After finding an interesting property of the RSIM having a possible implication for pattern recognition, the verification and extent of this result can be quickly checked with this program.

Main Program

The program consists of a main routine, three major subroutines, and eight other subroutines. The main program first queries the user about the nature of the calculation, determining the dimension of the populations and the correlation of the data. The program handles up to thirty-two dimensional data. The dimension controls the amount of input in a later step and is needed for the calculation. The correlation controls the values of the off-diagonal elements of the covariance matrices. If the reply to uncorrelated data is yes, then all off-diagonal elements of both covariance matrices are set equal to zero. If the answer is no, then the off-diagonal elements are all non-zero. Then the diagonal elements of the "normal" population (A) are input, one for each dimension. The mean of A is assumed to be at the origin as described in the second chapter. The off-diagonal elements of both covariance matrices are initialized as zero. If there

is correlation of the data, then these elements are changed. The elements adjacent to diagonal elements, e.g. C_{ij} with $i=j\pm 1$, are set equal to the sum of C_{ij} and C_{ji} divided by ten. The other non-adjacent elements are given the value 0.01, relatively small compared to the diagonal elements used in this study. The values are chosen to roughly correspond to typical PSD's involved in noise analysis studies, and are automatically generated to avoid the tedious task of entering every element of both matrices. Then an essentially non-terminating loop is entered in which first the mean vector of the test population (B) is input. Next the diagonal elements of the covariance matrix of B are input and if necessary the off-diagonal elements of C_B are set with the same algorithm used with C_A . The subroutine SEMINV is called ten times to compute the first through the tenth RSIM from B to A. Subroutine MOMENT is then called using these RSIM to compute the first through the tenth moments of the Mahalanobis distance from B to A. Then SEMINV is called to compute the ten RSIM from A to B. And MOMENT is called again to compute the moments of these RSIM. These values are then output to the user and the third major subroutine ANALYZ is called to monitor the values of the RSIM and infer the relationship of the two populations. Finally control is transferred in the main program to the top of the loop to input a new mean vector for B. The flow of the main program is diagrammed in figure 37. The time required for one set of calculations (not counting IO) is less than one second and therefore can be done in a real-time environment. To apply this program to a particular problem, the IO portion of the main program would be replaced and

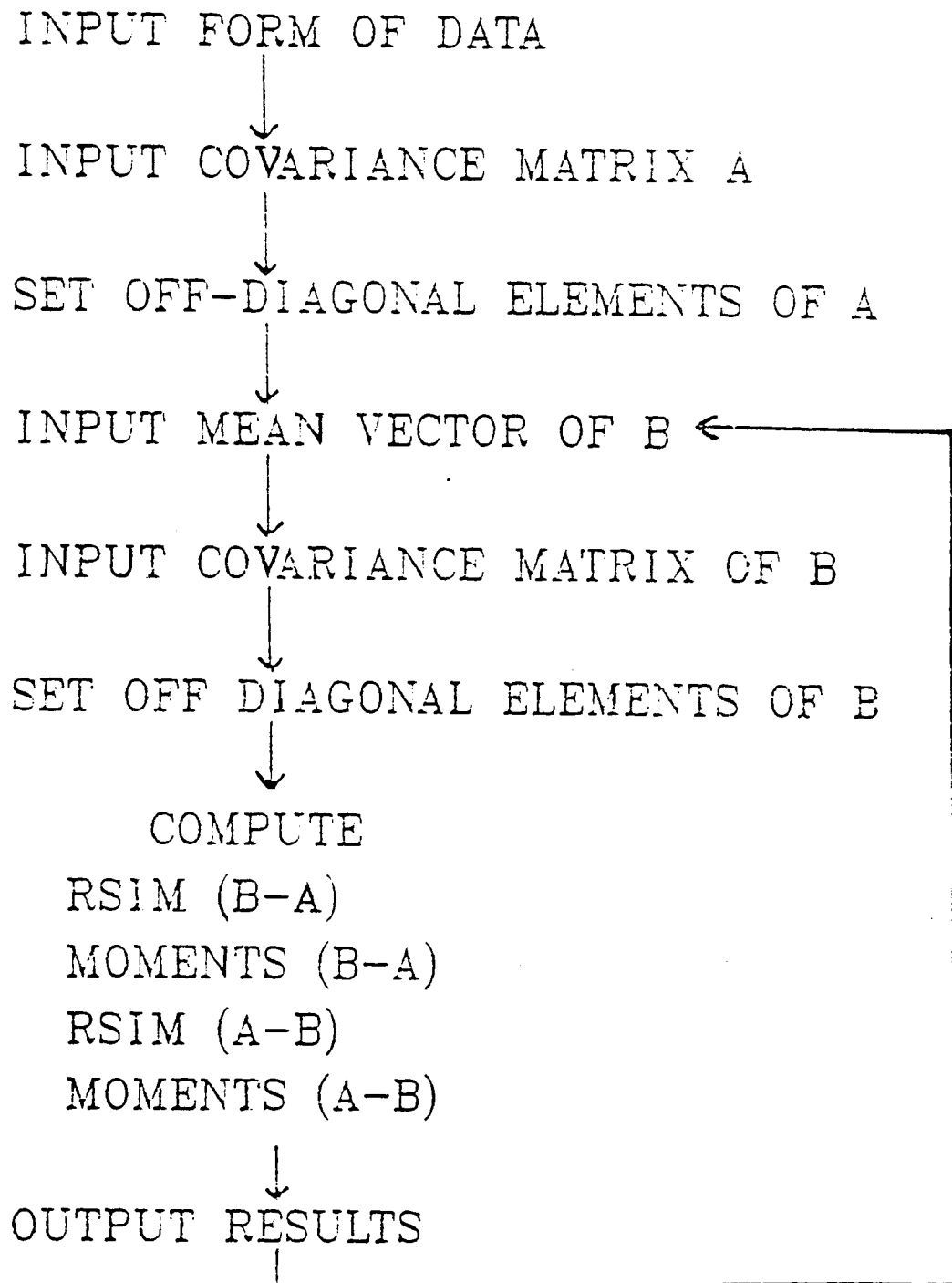


Figure 37. Flow diagram of the main program of the RSIM calculation.

ANALYZ would be adopted to fit the monitoring situation, but the heart of the calculation would remain the same as presented here.

RSIM Calculation

SEMINV computes the RSIM by solving equation 6. The inputs to the routine are n, the number of the RSIM being calculated, the mean and covariance matrix of the population being computed to, the same parameters of the population being computed from, and N, the dimension of the populations. The routine returns the value of the n-th RSIM. The computation is very straightforward; equation 8 (the trace term) is calculated first, then equation 9 is calculated and both terms are added. The flow of SEMINV is diagrammed in figure 38. The routine calls upon a number of modular subroutines to accomplish the computation. These are:

VEKSUB - takes the difference of two vectors (the means of A and B in this case) and stores the result as an N by 1 matrix

INVERS - transforms a matrix to vector form, calls MINV, and then transforms the result of MINV back to matrix form

MINV - old IBM SSP routine for matrix inversion

MMULT - multiplies two matrices together

INIT - initializes a matrix to the identity matrix (note: this is also the result of any matrix taken to the zeroth power)

TRACE - sums the diagonal elements of a matrix

FACT - returns the factorial of a number

TRANSP - takes the transpose of a matrix.

TAKE DIFFERENCE OF
MEANS AND TRANSPOSE

↓
TAKE INVERSE OF A

↓
CALCULATE $A^{-1} B$

↓
RAISE TO n'th POWER

↓
TAKE TRACE OF RESULT

↓
CALCULATE BA^{-1}

↓
 $n = 1 ?$

↓
N

RAISE TO $n-1$ POWER

SET TO IDENTITY MATRIX

↓
MULTIPLY OUT 2'nd TERM ←

↓
ADD TO TRACE FOR RESULT

Figure 38. Flow diagram of SEMINV, the routine to compute the RSIM.

The source listings of these routines as well as those of the main routines are included in the appendix.

Moment Calculation

The moments about zero of the interclass Mahalanobis distance are directly computable from the populations of the classes according to a method given by Gonzalez and Wagner. This technique involves the computation of a transformation matrix for each moment calculation. This can become computationally expensive. Another problem with this approach is the scaling considerations of some of the parameters; raising a large number to the power necessary to compute the moment may exceed the capacity of the computer.

However, the moments can also be computed directly from the semi-invariants χ_n . The n -th central moment w is given by:

$$w_n = \sum \frac{n!}{a_1! a_2! \dots a_n!} \left(\frac{\chi_1}{1!} \right)^{a_1} \left(\frac{\chi_2}{2!} \right)^{a_2} \dots \left(\frac{\chi_n}{n!} \right)^{a_n} \quad (20)$$

where the a 's (non-negative integers) are given by the expression:

$$a_1 + 2a_2 + 3a_3 + \dots + na_n = n \quad (21)$$

and the summation is over all of the possible sets of a_i . The implementation of equation 20 is straightforward except for the problem of being able to generate all solutions to equation 21 for each n .

Equation 21 is a linear Diophantine equation. Diophantus (1) was a Greek of the third century who studied indeterminate equations with many solutions (usually restricted to be in integers). Through

the centuries many others, including Pisano, Paoli, Hermite, the Chinese and the Arabs, wrote manuscripts on this subject. The normal solution to a Diophantine equation of the type:

$$a_1x_1 + a_2x_2 + \dots + a_kx_{k-1} = m \quad (k > 2) \quad (22)$$

is to reduce it to the form: $A X + B Y = C$ by assuming that the greatest common denominator of the a_i 's divides c with no remainder and rewriting the coefficients of the x_{k-1} and x_k terms, redefining x_{k-1} and x_k into a new single variable. This is done recursively until the desired form in two unknowns is obtained.

Equation 21 fits this form; all of the a_i 's are relatively prime with respect to each other and their greatest common divisor (one) evenly divides any integer. For each n in equation 21, there will be a different set of solutions and the set of a_i for the case of $n+1$ are not easily generated from the set of a_i 's for n . An example for a given n , two obvious solutions are $a_1=n$ and $a_n=1$ (with all other $a_i=0$). In the case of $n+1$, $a_1=n+1$ and $a_{n+1}=1$ are solutions as well as $a_n=1$, $a_1=1$; but there are other solutions not as obvious as these. A net effect of adding one to the sum of any group of a_i 's (more than just a pair) will also be a solution. There is no easy way to generate all of the solutions for $n+1$ from the solution set for n .

A third approach to solve this problem, an iterative method is used to generate all of the sets of a_i . The technique is illustrated in the flow diagram presented in figure 39. A trial set of a_i 's excluding

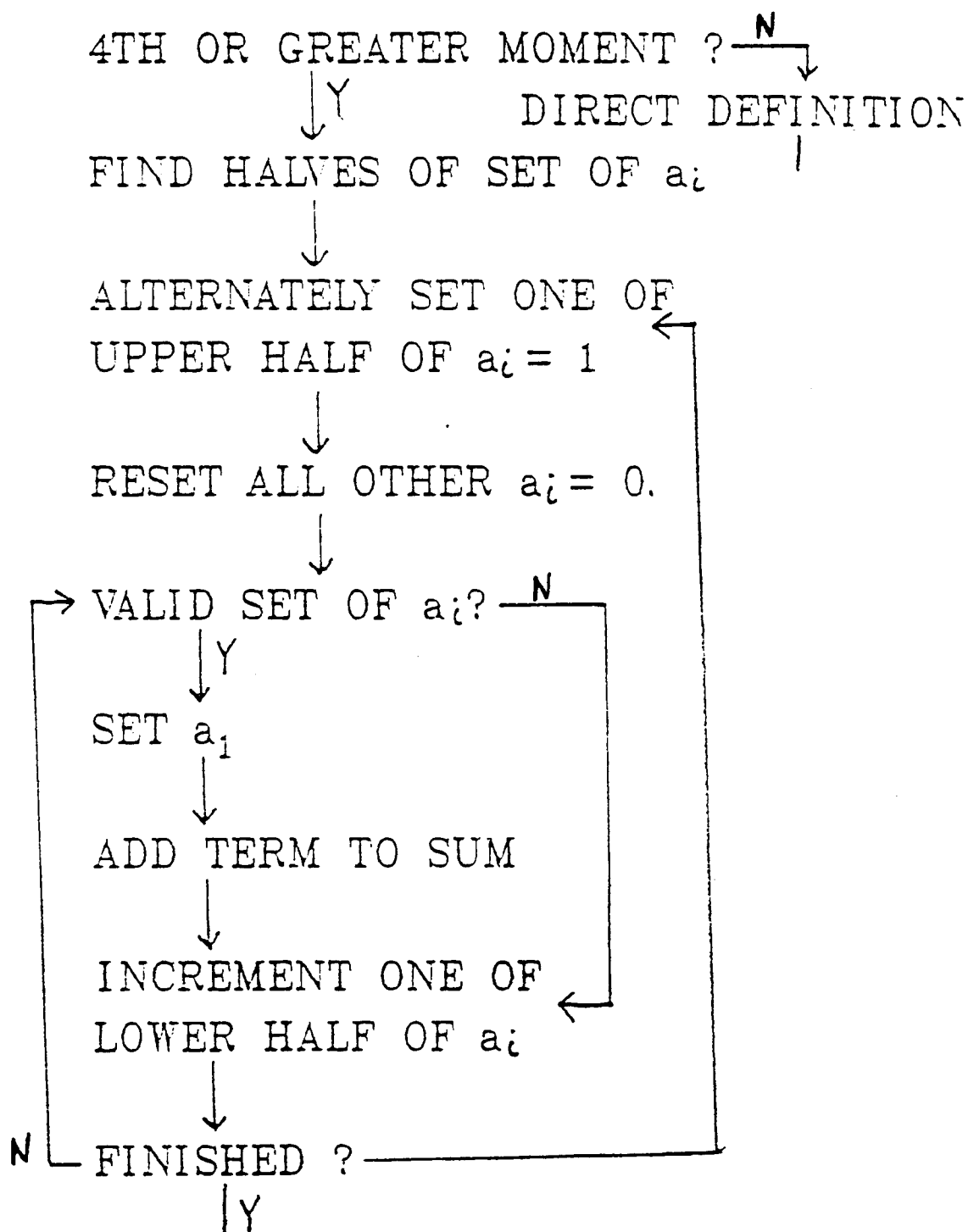


Figure 39. Flow diagram of MOMENT, the routine to compute the moments from the RSIM.

a_1 is selected and if the set can yield a solution, a_1 is a dependent variable and is given the appropriate value. If the set of a_i 's is valid, the term is added to the sum. In either case, another set of a_i 's is then selected. In a completely brute force approach, the number of iterations required is exceedingly large and this technique is not practical. It is completely unreasonable to try any number for a_i larger than n ; this could not possibly give a solution. This method would require $(n+1)^n$ iterations (n variables taking $n+1$ values); this would become virtually impossible for n greater than five or six. However, several refinements are made which significantly reduce the number of iterations required. First of all as stated above, there are really only $n-1$ independent variables; a_1 is considered the dependent variable and its value can only be a function of the other a_i in a solution and therefore does not have to be iterated. This reduces the computation to n^n iterations. More important to reducing iterations is consideration of the maximum value each a_i can assume. a_1 can have any value up to n . The coefficient of a_2 is two and any value greater than $n/2$ is too large for a_2 . The maximum value for a_3 is $n/3$. Generally, the maximum value a_j can assume is n/j where n/j is an integer division. This infers that any a_i with i greater than $n/2$ can only take on the values zero or one. And furthermore, only one of these a_i can have the value of one at a given time. Implementing this eliminates many of the iterations necessary to find all solutions. Half of the a_i 's, those from $i = n/2$ to n no longer need to be iterated but can alternately be set to one and the iterations performed only on the a_i 's from $i=2$ to $n/2$. These can

easily be iterated only up to their maximum allowed value. The resulting number of iterations is now reduced to

$$\left(\frac{n}{2} + 1\right) \prod_{i=1}^{\frac{n}{2}-2} \left(\frac{n}{(i+1)} + 1\right) \quad (23)$$

which is significantly less than n^n . (Note: all divisions in the formula are integer divisions.)

This technique is implemented in subroutine MOMENT. Since the "reduced" semi-invariants are being used, the resulting moments are also "reduced". Also the factor of $n^{\pm}$ in equation 20 is common to all moments and is left out of the calculation. This further reduces the value of the moments, but as in the case of the RSIM does not change any recognition information in them. However, since the RSIM prove to be very valuable for pattern recognition and are calculated first, the moments are not analyzed in terms of their pattern recognition capabilities in this study.

MOMENT is passed the array of RSIM and n , the number of the moment to be computed. If n is less than four, the reduced moment w is computed directly from the RSIM from the following relationships:

$$\begin{aligned} w_1 &= x_1 \\ w_2 &= (x_2 + x_1^2)/2 \\ w_3 &= (x_3 + 3x_1x_2 + x_1^3)/6 \end{aligned} \quad (24)$$

These come directly from equation 20 (with the $n^{\pm}$ left out) and are necessary to be computed separately due to the nature of the algorithm.

The fourth and higher moments are obtained by using this special iterative algorithm. The range of the "upper" half of the a_i 's is found by the integer division of n by two and adding one. Only one of these a_i 's can be non-zero at a time as described above. The outside loop of the algorithm alternately sets each a_i in this range to one (resetting all others to zero) and finally does one pass with all set to zero. The inside loop then checks if the entire set of a_i give a result equal to or less than n , if so, then a_1 is given the proper value to yield a solution and the term is added to the summation. If the above check fails, no term is added. Then at the bottom of this inside loop the a_i 's from $i=2$ to $n/2$ are appropriately incremented and the new set is checked again at the top of the inside loop. This incrementing at the bottom of the loop is the key trick in implementing the solution. Each a_i goes from 0 to n/i as needed and programming this takes only four lines of code.

Figure 40 presents the results of the algorithm for the eighth moment. Each line corresponds to a set of a_i found to yield a solution to the Diophantine equation. The validity of any of these sets can easily be checked by taking the summation of the product of the number of the a_i (the i of a) with its value. For example the second solution to the eighth moment gives the value $(1*1)+(2*1)+(5*1) = 8$ and thus is a valid solution. The number of iterations necessary for each moment is also presented with the figure. This number of iterations is the number of times a set of a_i 's is checked and therefore represents the number of times the innermost loop is executed. This is proportional to the execution time of the subroutine MOMENT minus the

MOMENT # 8

A1=3	A2=0	A3=0	A4=0	A5=1	A6=0	A7=0	A8=0
A1=1	A2=1	A3=0	A4=0	A5=1	A6=0	A7=0	A8=0
A1=0	A2=0	A3=1	A4=0	A5=1	A6=0	A7=0	A8=0
A1=2	A2=0	A3=0	A4=0	A5=0	A6=1	A7=0	A8=0
A1=0	A2=1	A3=0	A4=0	A5=0	A6=1	A7=0	A8=0
A1=1	A2=0	A3=0	A4=0	A5=0	A6=0	A7=1	A8=0
A1=0	A2=0	A3=0	A4=0	A5=0	A6=0	A7=0	A8=1
A1=8	A2=0	A3=0	A4=0	A5=0	A6=0	A7=0	A8=0
A1=6	A2=1	A3=0	A4=0	A5=0	A6=0	A7=0	A8=0
A1=4	A2=2	A3=0	A4=0	A5=0	A6=0	A7=0	A8=0
A1=2	A2=3	A3=0	A4=0	A5=0	A6=0	A7=0	A8=0
A1=0	A2=4	A3=0	A4=0	A5=0	A6=0	A7=0	A8=0
A1=5	A2=0	A3=1	A4=0	A5=0	A6=0	A7=0	A8=0
A1=3	A2=1	A3=1	A4=0	A5=0	A6=0	A7=0	A8=0
A1=1	A2=2	A3=1	A4=0	A5=0	A6=0	A7=0	A8=0
A1=2	A2=0	A3=2	A4=0	A5=0	A6=0	A7=0	A8=0
A1=0	A2=1	A3=2	A4=0	A5=0	A6=0	A7=0	A8=0
A1=4	A2=0	A3=0	A4=1	A5=0	A6=0	A7=0	A8=0
A1=2	A2=1	A3=0	A4=1	A5=0	A6=0	A7=0	A8=0
A1=0	A2=2	A3=0	A4=1	A5=0	A6=0	A7=0	A8=0
A1=1	A2=0	A3=1	A4=1	A5=0	A6=0	A7=0	A8=0
A1=0	A2=0	A3=0	A4=2	A5=0	A6=0	A7=0	A8=0

MOMENT # 8 SOLVED IN 225 ITERATIONS

Figure 40. The set of solutions to equation 21 for the eighth moment calculation.

overhead involved. The execution time for the 225 iterations of the eighth moment takes well less than a second on the 11/34 and therefore seems instantaneous to the interactive user. However, if none of the methods to reduce the number of iterations are employed, 9^8 iterations could be required. This many operations would take a significant time on most computers. This great reduction in iterations certainly justifies the iterative algorithm used in solving the Diophantine equation.

Some examples of the values of the reduced moments were presented with the correlated data in Chapter 3. The most important aspect of the moment calculation is the solution of equation 21. This is accomplished in an efficient way with the iterative algorithm presented here. The algorithm is thoroughly documented as an aid to solving other problems of a similar nature. The crucial aspect of the implementation of the computation of the RSIM is that it is done in a flexible manner. It is set up to operate interactively at first, but due to its modular nature, it can easily be adapted to any specific problem.

RSIM Analyzed

A routine is presented in this section which recognizes the relationship of the two populations by examining the values of the RSIM. The subroutine ANALYZ is a modular routine which performs the recognition process. ANALYZ is called each time both sets of RSIM are computed. These values are input to ANALYZ in addition to N, the dimension of the data, and T, a threshold value. ANALYZ then makes a

series of tests on the values of the RSIM to determine the relationship of the populations from the information contained in the RSIM. This series of tests are based on the structure in the RSIM and the analysis of RSIM spaces.

The first test recognizes if the populations have the exact same parameters. This test is based on the fact that a point at (N,N) in 5-10 RSIM space or a point at (N,N) in 10-10 RSIM space indicates that the populations are identical. The way this is accomplished is by comparing the fifth RSIM (B-A), the tenth RSIM (B-A) and the tenth RSIM (A-B) to N. If the fifth and tenth RSIM (B-A) both equal N, the point in 5-10 RSIM space for the populations is at (N,N). If both tenth RSIM are also equal to N, another check of the identity condition is provided (although redundant). In implementing this test, it was found that the computation of the RSIM involved some round-off error. This error prevents a logical compare from having a true (equal) result. A standard fix for this is to subtract the two quantities and compare the absolute value of this to some very small number. ANALYZ assumes that any difference less than 1×10^{-5} in two quantities is not meaningful; therefore results of operations are compared to this value for checking equality. If the populations are identical, this fact is printed out and control is returned to the main program. Two identical populations is the most specific result in the hierarchy of this pattern recognition system. In this condition the RSIM contain the most structure; in other words both the means and covariance matrix of the test population are completely defined in terms of the normal population and no other test can reveal more

information using these RSIM. A negative response in this test indicates that there is some difference in the populations, and the next test is performed in ANALYZ.

If both populations are not identical, the next test recognizes if they are close to identical. The foundation of this test is the determination whether the computation of the RSIM yield values near the point (N,N) in 5-10 RSIM space. This test is implemented in a manner similar to the first test. The dimension N is subtracted from the fifth and tenth RSIM (in both directions for redundancy) and the absolute value of these four results are compare to T , the threshhold of 0.5. If all four values are less than T , ANALYZ recognizes that the populations are close to identical and prints out this fact along with the value of the threshhold used in this test. The region of nearly identical populations in this test is a square in 5-10 RSIM space centered on the point (N,N) with a side of length twice T . Any other size or shape of region which is applicable to a particular problem can also be employed. This test could also be repeated with a series of different threshhold values. A series of tests could quantify how close the two populations are by monitoring which threshholds accept the RSIM point. This also introduces the possiblilty of recognizing only populations differing by more than a minimum threshhold but less than some maximum bound. This is analogous to a band-pass filtering on the test populations. This test checks for a condition which can exist simultaneously with other conditions. Two populations may be close to identical and have other special relationships as identical covariance matrices or matrices

related by a scalar multiple. Therefore, after this test execution continues in ANALYZ with the next test.

The third test is for equal covariance matrices. A decision is made whether the values of the RSIM lie on the line $Y=X$ in both 5-5 and 10-10 RSIM space. If the fifth RSIM are the same whether computed from B to A or from A to B and the same condition holds for the tenth RSIM, then both populations have the same covariance matrix and this fact is printed out by ANALYZ. This test is checking for the cases presented with figures 4, page 16 (uncorrelated), and 16, page 40 (correlated). If the covariance matrices are equal, control is returned to the main program since now the covariance matrices are fully determined and the negative response of the first test has already indicated that the means are not the same. If this test is negative, the next test is performed by ANALYZ.

The next test recognizes if there is uniform expansion or contraction of the covariance matrix of the test population with no difference of the mean vectors of the two populations. The basis of this test is an examination of the values of the RSIM as described with figures 7, 22, and 23 on pages 22, 47, and 49. The value of α is computed in four ways in the implementation of this test. α is found by the division of the fifth by the fourth RSIM (B-A) and the tenth by the ninth of the same RSIM. The other two α are generated by the division of the fourth by the fifth RSIM (A-B) and the ninth by the tenth of this RSIM. If there is uniform expansion (with identical means) all four of these α are equal (within the roundoff error). If the difference of all of the pairs of α are less than the roundoff number,

ANALYZ prints the success of this test and the value of α . Control reverts back to the main program if the test is successful since a positive result of this test precludes any further successes in the following tests.

The last two tests check for expansion or contraction in one component of the variance with a difference of means in this same component. The foundation of this test is the presentation made with figures 8 and 9 on pages 25 and 26. The first of these tests is made to decide if one component has a greater variance. If it does, the tenth RSIM (A-B) has a value of one less than the dimension of the data. This is true independent of the mean value of this component. If the mean of this component has the same value in the test and normal populations, then the $n+1$ RSIM (B-A) is related to the n -th by a constant multiplicative factor for all n . Since this test is monitoring for a difference in that component of the means, if the RSIM (B-A) are not related by a constant factor and RSIM (A-B) equal $N-1$, ANALYZ recognizes that the populations are related in this special way and the expansion message is printed. The test for contraction in the variance of one component with a different mean is similar to the expansion test except that in this test the tenth RSIM (B-A) is checked for $N-1$ and RSIM (A-B) are checked for the constant factor. The structure of ANALYZ is presented in figure 41 which lists the tests in the order in which they are performed.

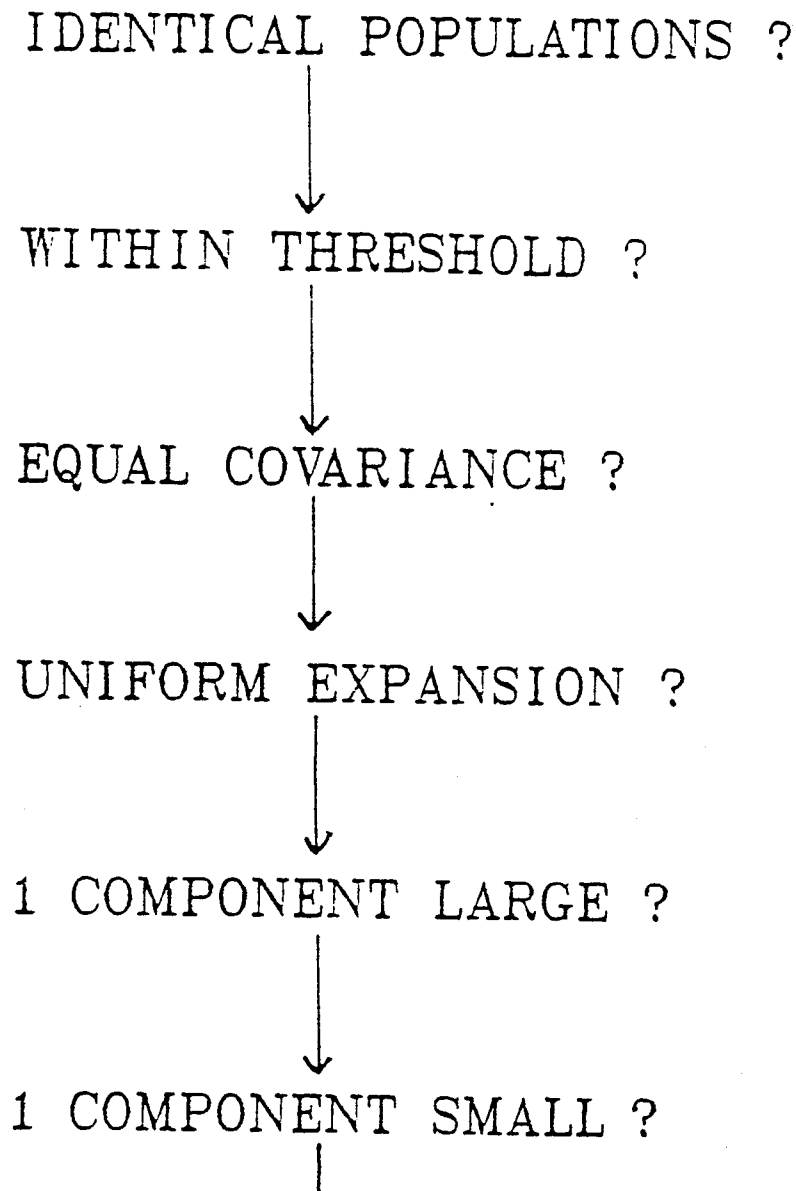


Figure 41. The flow diagram of ANALYZ, listing the tests.

Results of ANALYZ

The results of this monitoring routine ANALYZ on some simple data are presented in the following set of figures. Three dimensional data is used, some of it is correlated and some is uncorrelated for the tests which are designed for uncorrelated data. The performance of ANALYZ is excellent in recognizing the relationships of the population parameters. This is due to the distinctive properties of the RSIM which make the recognition process almost trivial.

Figure 42 is the case of identical correlated population parameters. It is easily recognized as fulfilling the conditions of the first test in ANALYZ. Figure 43 does not pass this first test; two components of the mean of the test population are not zero. Since the fifth and tenth pairs of RSIM are pairwise equal and less than 3.5 ($T=0.5$), the second test for almost identical populations is positive as is the third test for equal covariance matrices. If the covariance matrices are not quite equal as shown in the case of figure 44 (the third component of the variance differing by less than one percent), the test for equal covariance matrices fails since the RSIM are no longer pairwise equal. The populations are still within the threshold in figure 44 and this is successfully identified by the second test. Figure 45 is an opposite case of sorts to figure 44; the covariance matrices are identical and recognized as such, but due to the larger difference in the means, the populations are recognized as not being close (within the threshold) to each other.

NORMAL POPULATION

0	2.00	1.00	0.01
0	1.00	3.00	0.90
0	0.01	0.90	1.50

TEST POPULATION

0.00	2.00	1.00	0.01
0.00	1.00	3.00	0.90
0.00	0.01	0.90	1.50

RSIM FROM B TO A

RSIM (1) =	3.0000
RSIM (2) =	3.0000
RSIM (3) =	3.0000
RSIM (4) =	3.0000
RSIM (5) =	3.0000
RSIM (6) =	3.0000
RSIM (7) =	3.0000
RSIM (8) =	3.0000
RSIM (9) =	3.0000
RSIM (10) =	3.0000

RSIM FROM A TO B

RSIM (1) =	3.0000
RSIM (2) =	3.0000
RSIM (3) =	3.0000
RSIM (4) =	3.0000
RSIM (5) =	3.0000
RSIM (6) =	3.0000
RSIM (7) =	3.0000
RSIM (8) =	3.0000
RSIM (9) =	3.0000
RSIM (10) =	3.0000

TEST POPULATION IDENTICAL TO NORMAL POPULATION

Figure 42. The first test case; identical populations.

NORMAL POPULATION

0	2.00	1.00	0.01
0	1.00	3.00	0.90
0	0.01	0.90	1.50

TEST POPULATION

0.10	2.00	1.00	0.01
0.20	1.00	3.00	0.90
0.00	0.01	0.90	1.50

RSIM FROM B TO A

RSIM (1) =	3.0165
RSIM (2) =	3.0330
RSIM (3) =	3.0495
RSIM (4) =	3.0660
RSIM (5) =	3.0825
RSIM (6) =	3.0989
RSIM (7) =	3.1154
RSIM (8) =	3.1319
RSIM (9) =	3.1484
RSIM (10) =	3.1649

RSIM FROM A TO B

RSIM (1) =	3.0165
RSIM (2) =	3.0330
RSIM (3) =	3.0495
RSIM (4) =	3.0660
RSIM (5) =	3.0825
RSIM (6) =	3.0989
RSIM (7) =	3.1154
RSIM (8) =	3.1319
RSIM (9) =	3.1484
RSIM (10) =	3.1649

TEST POPULATION WITHIN THRESHHOLD 0.500
OF NORMAL POPULATION

EQUAL COVARIANCE MATRICES

Figure 43. The second test case; small difference in means.

NORMAL POPULATION

0	2.00	1.00	0.01
0	1.00	3.00	0.90
0	0.01	0.90	1.50

TEST POPULATION

0.00	2.00	1.00	0.01
0.20	1.00	3.00	0.90
0.00	0.01	0.90	1.49

RSIM FROM B TO A

RSIM (1) =	3.0131
RSIM (2) =	3.0262
RSIM (3) =	3.0393
RSIM (4) =	3.0525
RSIM (5) =	3.0657
RSIM (6) =	3.0790
RSIM (7) =	3.0922
RSIM (8) =	3.1055
RSIM (9) =	3.1189
RSIM (10) =	3.1322

RSIM FROM A TO B

RSIM (1) =	3.0277
RSIM (2) =	3.0554
RSIM (3) =	3.0833
RSIM (4) =	3.1112
RSIM (5) =	3.1392
RSIM (6) =	3.1673
RSIM (7) =	3.1955
RSIM (8) =	3.2237
RSIM (9) =	3.2521
RSIM (10) =	3.2805

TEST POPULATION WITHIN THRESHHOLD 0.500
OF NORMAL POPULATION

Figure 44. The third test case; small difference in both the means and covariance matrices.

NORMAL POPULATION

0	2.00	1.00	0.01
0	1.00	3.00	0.90
0	0.01	0.90	1.50

TEST POPULATION

3.22	2.00	1.00	0.01
0.19	1.00	3.00	0.90
1.96	0.01	0.90	1.50

RSIM FROM B TO A

RSIM (1) =	14.089
RSIM (2) =	25.178
RSIM (3) =	36.267
RSIM (4) =	47.356
RSIM (5) =	58.445
RSIM (6) =	69.534
RSIM (7) =	80.623
RSIM (8) =	91.712
RSIM (9) =	102.80
RSIM (10) =	113.89

RSIM FROM A TO B

RSIM (1) =	14.089
RSIM (2) =	25.178
RSIM (3) =	36.267
RSIM (4) =	47.356
RSIM (5) =	58.445
RSIM (6) =	69.534
RSIM (7) =	80.623
RSIM (8) =	91.712
RSIM (9) =	102.80
RSIM (10) =	113.89

EQUAL COVARIANCE MATRICES

Figure 45. The fourth test case; identical covariance matrices.

Figure 46 shows the results of ANALYZ with a uniform expansion (doubling in this case) of the covariance matrix of the test population with no change in means. This is successfully recognized by the fourth test (the first three failing as they should) since the n -th RSIM (B-A) is twice the $n-1$ RSIM (B-A) as well as the condition of each RSIM (A-B) being half the value of the previous RSIM also true. The contraction in figure 47 ($\alpha = 0.2$) is also properly identified by ANALYZ. Figure 48 demonstrates the sensitivity of this test; the second component of the variance is almost doubled as the other two components exactly are. The test fails in this figure (along with all of the other tests,) but if some type of threshold were applied in this case, it would be possible to recognize the occurrence of almost uniformly expanded covariance matrices. In figure 48, note that each RSIM (B-A) is very close to being double the previous value.

Figure 49 is an instance of an increase in the variance of the component with a different mean. As discussed above, this is a very important case in reactor noise monitoring. By finding the tenth RSIM (A-B) equal to one less than the dimension of the data and the RSIM (B-A) not related by a constant multiplicative factor, the test for increased variance in a single component is found to be positive. In figure 50, the identical means cause each RSIM (B-A) to be six times (six is the difference in the component of the variance) the previous value and thus is rejected by this test. An additional test could easily recognize this condition by checking for a constant factor in the RSIM (B-A). Figure 51 is the case of a contraction

NORMAL POPULATION

0	2.00	0.00	0.00
0	0.00	3.00	0.00
0	0.00	0.00	1.50

TEST POPULATION

0.00	4.00	0.00	0.00
0.00	0.00	6.00	0.00
0.00	0.00	0.00	3.00

RSIM FROM B TO A

RSIM (1) =	6.0000
RSIM (2) =	12.000
RSIM (3) =	24.000
RSIM (4) =	48.000
RSIM (5) =	96.000
RSIM (6) =	192.00
RSIM (7) =	384.00
RSIM (8) =	768.00
RSIM (9) =	1536.0
RSIM (10) =	3072.0

RSIM FROM A TO B

RSIM (1) =	1.5000
RSIM (2) =	0.75000
RSIM (3) =	0.37500
RSIM (4) =	0.18750
RSIM (5) =	0.93750E-01
RSIM (6) =	0.46875E-01
RSIM (7) =	0.23438E-01
RSIM (8) =	0.11719E-01
RSIM (9) =	0.58594E-02
RSIM (10) =	0.29297E-02

IDENTICAL MEANS WITH SPREAD
IN TEST POPULATION 2.00 * NORMAL

Figure 46. The fifth test case; uniform expansion in covariance matrix, same means.

NORMAL POPULATION

0	2.00	0.00	0.00
0	0.00	3.00	0.00
0	0.00	0.00	1.50

TEST POPULATION

0.00	0.40	0.00	0.00
0.00	0.00	0.50	0.00
0.00	0.00	0.00	0.30

RSIM FROM B TO A

RSIM (1) =	0.60000
RSIM (2) =	0.12000
RSIM (3) =	0.24000E-01
RSIM (4) =	0.48000E-02
RSIM (5) =	0.96000E-03
RSIM (6) =	0.19200E-03
RSIM (7) =	0.38400E-04
RSIM (8) =	0.76800E-05
RSIM (9) =	0.15360E-05
RSIM (10) =	0.30720E-06

RSIM FROM A TO B

RSIM (1) =	15.000
RSIM (2) =	75.000
RSIM (3) =	375.00
RSIM (4) =	1875.0
RSIM (5) =	9375.0
RSIM (6) =	46875.
RSIM (7) =	0.23438E+06
RSIM (8) =	0.11719E+07
RSIM (9) =	0.58594E+07
RSIM (10) =	0.29297E+08

IDENTICAL MEANS WITH SPREAD
IN TEST POPULATION 0.200 * NORMAL

Figure 47. The sixth test case; uniform contraction in covariance matrix, same means.

NORMAL POPULATION

0	2.00	0.00	0.00
0	0.00	3.00	0.00
0	0.00	0.00	1.50

TEST POPULATION

0.00	4.00	0.00	0.00
0.00	0.00	5.99	0.00
0.00	0.00	0.00	3.00

RSIM FROM B TO A

RSIM (1) =	5.9967
RSIM (2) =	11.987
RSIM (3) =	23.960
RSIM (4) =	47.894
RSIM (5) =	95.734
RSIM (6) =	191.36
RSIM (7) =	382.51
RSIM (8) =	764.61
RSIM (9) =	1528.4
RSIM (10) =	3055.1

RSIM FROM A TO B

RSIM (1) =	1.5008
RSIM (2) =	0.75084
RSIM (3) =	0.37563
RSIM (4) =	0.18792
RSIM (5) =	0.94012E-01
RSIM (6) =	0.47032E-01
RSIM (7) =	0.23529E-01
RSIM (8) =	0.11771E-01
RSIM (9) =	0.58889E-02
RSIM (10) =	0.29461E-02

NOTHING SPECIAL FOUND

Figure 48. The seventh test case; almost uniform expansion in covariance matrix.

NORMAL POPULATION

0	2.00	0.00	0.00
0	0.00	3.00	0.00
0	0.00	0.00	1.50

TEST POPULATION

2.50	12.00	0.00	0.00
0.00	0.00	3.00	0.00
0.00	0.00	0.00	1.50

RSIM FROM B TO A

RSIM (1) =	11.125
RSIM (2) =	75.500
RSIM (3) =	555.50
RSIM (4) =	3996.0
RSIM (5) =	26025.
RSIM (6) =	0.19246E+06
RSIM (7) =	0.13005E+07
RSIM (8) =	0.66780E+07
RSIM (9) =	0.57317E+08
RSIM (10) =	0.37539E+09

RSIM FROM A TO B

RSIM (1) =	2.6875
RSIM (2) =	2.2014
RSIM (3) =	2.0460
RSIM (4) =	2.0104
RSIM (5) =	2.0021
RSIM (6) =	2.0004
RSIM (7) =	2.0001
RSIM (8) =	2.0000
RSIM (9) =	2.0000
RSIM (10) =	2.0000

NON-ZERO COMPONENT OF MEAN HAS LARGE VARIANCE

Figure 49. The eighth test case; expansion in component of variance with different mean component.

NORMAL POPULATION

0	2.00	0.00	0.00
0	0.00	3.00	0.00
0	0.00	0.00	1.50

TEST POPULATION

0.00	12.00	0.00	0.00
0.00	0.00	3.00	0.00
0.00	0.00	0.00	1.50

RSIM FROM B TO A

RSIM (1) =	8.0000
RSIM (2) =	38.000
RSIM (3) =	218.00
RSIM (4) =	1298.0
RSIM (5) =	7778.0
RSIM (6) =	46652.
RSIM (7) =	0.27994E+06
RSIM (8) =	0.16796E+07
RSIM (9) =	0.10078E+08
RSIM (10) =	0.60466E+08

RSIM FROM A TO B

RSIM (1) =	2.1667
RSIM (2) =	2.0278
RSIM (3) =	2.0046
RSIM (4) =	2.0008
RSIM (5) =	2.0001
RSIM (6) =	2.0000
RSIM (7) =	2.0000
RSIM (8) =	2.0000
RSIM (9) =	2.0000
RSIM (10) =	2.0000

NOTHING SPECIAL FOUND

Figure 50. The ninth test case; expansion in one component of variance, identical means.

NORMAL POPULATION

0	2.00	0.00	0.00
0	0.00	3.00	0.00
0	0.00	0.00	1.50

TEST POPULATION

0.00	2.00	0.00	0.00
3.50	0.00	0.00	0.00
0.00	0.00	0.00	1.50

RSIM FROM B TO A

RSIM (1) =	6.1033
RSIM (2) =	2.1637
RSIM (3) =	2.0049
RSIM (4) =	2.0001
RSIM (5) =	2.0000
RSIM (6) =	2.0000
RSIM (7) =	2.0000
RSIM (8) =	2.0000
RSIM (9) =	2.0000
RSIM (10) =	2.0000

RSIM FROM A TO B

RSIM (1) =	256.17
RSIM (2) =	22919.
RSIM (3) =	0.16563E+07
RSIM (4) =	0.10633E+09
RSIM (5) =	0.66927E+10
RSIM (6) =	0.39844E+12
RSIM (7) =	0.23112E+14
RSIM (8) =	0.13151E+16
RSIM (9) =	0.73731E+17
RSIM (10) =	0.40853E+19

NON-ZERO COMPONENT OF MEAN HAS SMALL VARIANCE

Figure 51. The tenth test case; contraction in component of variance with different mean component.

in one component of the variance and is properly recognized by the final test in ANALYZ in a similar manner to the case of figure 49. Figure 52 demonstrates that this test is sensitive to even a much smaller difference in the mean vector.

These eleven figures show the excellent performance of the basic monitoring and recognition routine ANALYZ on a wide assortment of data. Most of its tests are based on the analysis of RSIM spaces presented in the preceding chapter. In a real monitoring situation (e.g. reactor noise surveillance), the most important type of test would be for nearly identical populations; a test shown to be very easy and definitive with the proper threshold. ANALYZ is just an example of a simple implementation of a pattern recognition system using the RSIM. A more sophisticated version could easily be implemented to meet the needs of a particular problem.

NORMAL POPULATION

0	2.00	0.00	0.00
0	0.00	3.00	0.00
0	0.00	0.00	1.50

TEST POPULATION

0.00	2.00	0.00	0.00
0.10	0.00	0.06	0.00
0.00	0.00	0.00	1.50

RSIM FROM B TO A

RSIM (1) =	2.0233
RSIM (2) =	2.0005
RSIM (3) =	2.0000
RSIM (4) =	2.0000
RSIM (5) =	2.0000
RSIM (6) =	2.0000
RSIM (7) =	2.0000
RSIM (8) =	2.0000
RSIM (9) =	2.0000
RSIM (10) =	2.0000

RSIM FROM A TO B

RSIM (1) =	52.167
RSIM (2) =	2518.7
RSIM (3) =	0.12625E+06
RSIM (4) =	0.63333E+07
RSIM (5) =	0.31771E+09
RSIM (6) =	0.15936E+11
RSIM (7) =	0.79946E+12
RSIM (8) =	0.40104E+14
RSIM (9) =	0.20117E+16
RSIM (10) =	0.10091E+18

NON-ZERO COMPONENT OF MEAN HAS SMALL VARIANCE

Figure 52. The eleventh test case; contraction in component of variance with slightly different mean, showing sensitivity of test.

CHAPTER VI

SUMMARY

A statistical pattern recognition system can easily identify the relationship of two Gaussian populations by testing the values of the reduced semi-invariants of the interclass Mahalanobis distance (RSIM) which are computable from the parameters of the populations. The interactive program for computing the RSIM described in the last chapter is very useful for verifying the properties of the RSIM. These properties presented in chapter three are the distinctive values that the RSIM have when the populations are related in certain ways (e.g. identical, only differ in one component of the means and variance, etc.). Most of these properties can be given a graphical representation by the development of RSIM spaces as presented in the fourth chapter. These graphical representations form the framework for a system to monitor (recognize) the relationship of the populations as demonstrated in the end of the previous chapter. The real benefit of using the RSIM instead of the population parameters is that the RSIM express in a few values the relative condition of two populations. The recognition system is much more direct, simpler, and can operate on as few as four values of the RSIM independent of the dimension of the original data. For example, in the case of monitoring for uniform expansion of the covariance matrix of a 32 dimensional test population, more than one thousand comparisons have to be made using the parameters directly to determine if the expansion is

exactly uniform. This greatly contrasts with the four comparisons necessary when using the RSIM. The computation of the RSIM is a powerful transformation for the purposes of recognition and future work in this area is expected to further explore the potentials of the RSIM spaces.

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APPENDIX

** DL1:(200,125)A.FTN:3 -- Last written 29-DEC-82 19:59:22 **

C**-

```
C      Module name: MAIN PROGRAM FOR THESIS
C
C      Version X01.00 Last edit: 29-DEC-82 19:56
C      Status: Development/Debugging
C
C      Revision history:
C
C          Version X01.00 30-APR-82 17:55 - 29-DEC-82 19:56
C          Created by: JIM BARHORST
C
C**-
```

C*****

```
C      MAIN PROGRAM OF THE MASTER'S THESIS OF JIM BARHORST
C      THIS PROGRAM DEFINES THE MEAN AND COVARIANCE MATRIX OF THE NORMAL
C      POPULATION (YM & CY) AND THEN GOES INTO A LOOP IN WHICH THE USER
C      INTERACTIVELY ENTERS THE MEAN AND COVARIANCE MATRIX OF THE TEST
C      POPULATION (XM & CX). THE PROGRAM THEN COMPUTES THE SEMI-INVARIANTS
C      AND MOMENTS OF THE MAHALANOBIS DISTANCE BETWEEN THE TWO POPULATIONS.
```

```
      DIMENSION CX(32,32),CY(32,32),XM(32),YM(32),X(20),A(20)
      DIMENSION Z(20),B(20)
```

```
      TYPE 510
```

```
510  FORMAT ('OWELCOME TO THE MAIN PROGRAM OF THE THESIS OF JIM',
1     ' BARHORST',///)
```

```
      TYPE 511
```

```
511  FORMAT ('SHOW MANY DIMENSIONS WILL YOU BE WORKING IN ? ')
      ACCEPT 512, N
```

```
512  FORMAT (I2)
```

```
      TYPE 513
```

```
513  FORMAT ('SDD YOU WISH STATISTICAL INDEPENDENCE OF TEST DATA? ')
      ACCEPT 514, SI
```

```
514  FORMAT (A1)
```

```
C      INITIALIZE YM AND COVARIANCE MATRICES
```

```
      DO 20 I=1,N
      YM(I)=0.
      DO 20 J=1,N
      CY(I,J)=0.
      CX(I,J)=0.
      IF (SI.EQ.'Y') GO TO 20
      CX(I,J)=0.01
      CY(I,J)=0.01
20  CONTINUE
```

```
C      INPUT DIAGONAL ELEMENTS OF THE NORMAL CLASS
```

```
3     TYPE 203
      DO 22 I=1,N
      TYPE 505, I,I
505  FORMAT ('SCY(',I1,',',I1,') = ')
      ACCEPT 504, CY(I,I)
22  CONTINUE
      IF (SI.EQ.'Y') GO TO 1
```

```
C      SET NEXT-TO-DIAGONAL ELEMENTS IF NOT STATISTICALLY INDEPENDENT
```

```
      DO 23 I=1,N
      DO 23 J=1,N
      IF (IABS(I-J).EQ.1) CY(I,J)=(CY(I,I)+CY(J,J))/5.
23  CONTINUE
```

```
1     TYPE 203
      DO 24 I=1,N
      TYPE 506, I
506  FORMAT ('$XM(',I1,') = ')
      ACCEPT 504, XM(I)
24  CONTINUE
```

```

DO 26 I=1,N
TYPE 507, I,I
507 FORMAT ('SCX(',I1,',',I1,') = ')
ACCEPT 504, CX(I,I)
504 FORMAT (E13.5)
26 CONTINUE
IF (S1.EQ.'Y') GO TO 31
DO 27 I=1,N
DO 27 J=1,N
IF (IABS(I-J).EQ.1) CX(I,J)=(CX(I,I)+CX(J,J))/5.
27 CONTINUE

31 TYPE 203
PRINT 517
517 FORMAT (1H1,/////////)
PRINT 516
516 FORMAT (1H0,13X,'NORMAL POPULATION',14X,'TEST POPULATION')
PRINT 515, ((CY(I,J),J=1,N),XM(I),(CX(I,J),J=1,N),I=1,N)
515 FORMAT (/<N>(15X,'0',2X,<N>(F5.2),<6+(4-N)*5>X,
1 F4.2,2X,<N>(F5.2),/))
PRINT 203
PRINT 204
204 FORMAT (///)

C FIND SEMI-INVARIANTS OF THE MAHALANOBIS DISTANCE FROM X TO Y

DO 10 L=1,10
10 CALL SEMINU (L,YM,CY,XM,CX,N,X(L))

C FIND THE MOMENTS OF THE MAHALANOBIS DISTANCE FROM X TO Y

DO 12 L=1,10
CALL MOMENT (X,L,A(L))
TYPE 502, L,X(L),L,A(L)
502 FORMAT (11X,'S-I (',I2,') = ',G12.5,5X,
1 'MOMENT (',I2,') = ',G12.5)
12 CONTINUE

TYPE 203
203 FORMAT (/)

C FIND SEMI-INVARIANTS OF THE MAHALANOBIS DISTANCE FROM X TO Y

DO 14 L=1,10
14 CALL SEMINU (L,XM,CX,YM,CY,N,Z(L))

C FIND MOMENTS OF THE MAHALANOBIS DISTANCE FROM Y TO X

DO 16 L=1,10
CALL MOMENT (Z,L,B(L))
TYPE 502, L,Z(L),L,B(L)
16 CONTINUE
TYPE 203

C SEND SEMI-INVARIANTS TO LINE PRINTER TO MAKE IN FIGURE

PRINT 509
509 FORMAT (15X,'RSIM FROM B TO A',16X,
1 'RSIM FROM A TO B',/)
PRINT 508, (L,X(L),L,Z(L),L=1,10)
508 FORMAT (/,10(13X,'RSIM (',I2,') = ',G12.5,9X,
1 'RSIM (',I2,') = ',G12.5,/))

```

** DL1:[200,125]SEMINUAR.FTN;5 -- Last written 04-NOV-82 19:24:04 **

C x x -

```
C      module name: SEMI-INVARIANT
```

C

C Version X01.00 Last edit: 04-NOV-62 19:12

C Status: Development/Debugging

C

C Revision history:

C

C Version X01.00 30-APR-82 16:06 - 04-NOV-82 19:13

C Created by: JIM BARHORST

C

C**x-

● 2019年12月10日，中国银保监会发布《关于规范商业银行互联网贷款业务的通知》，要求商业银行互联网贷款业务应当符合以下要求：(1) 坚持小额、分散原则，合理控制贷款集中度；(2) 坚持依法合规原则，不得违规开展业务；(3) 坚持风险可控原则，加强风险管理；(4) 坚持公平竞争原则，不得恶性竞争；(5) 坚持消费者权益保护原则，不得损害消费者权益。

SUBROUTINE SEMINU (N,YM,CY,XM,CX,M,X)

C ROUTINE TO COMPUTE 'X', THE N'TH RSIM

C YM IS THE MEAN OF THE 'NORMAL' CLASS (M-DIMENSIONAL)

CY IS THE COVARIANCE MATRIX OF THE "NORMAL" CLASS (M BY M)

C $\bar{x}_m$ IS THE MEAN OF THE CLASS BEING EXAMINED (M-DIMENSIONAL)

C CX IS THE COVARIANCE MATRIX OF THE CLASS BEING EXAMINED (M BY M)

C X IS GIVEN BY :

$$C \quad \text{TR}((CY' * CX) * N) + N * (XM - YM)' * CY' * (CX * CY') * (N - 1) * (XM - YM)$$

C WHERE:

C TR INDICATES THE TRACE OF

C T INDICATES TRANSPOSE

C ' INDICATES INVERSE

C ONE AND RESULT ARE WORKING MATRICES

```

DIMENSION YM(32),CY(32,32),XM(32),CX(32,32)

```

```

DIMENSION CXY(32,32), ONE(32,32), RESULT(32,32), CYP(32,32)

```

```

DIMENSION XMY(32,1),XMYT(32,32),A1X1(1,1)

```

```
C      GET XMY = XM-YM AND XMYT = XMY TRANSPOSE
```

CALL VEKSUB (XM, YM, XMY, M)

CALL TRANSP (XMY,XMYT,M,1)

```
C      GET CYP = CY INVERSE
```

CALL INVERS (CY,CYP,M)

```
C      GET TR = TRACE((CY'*CX)**N)
```

C CXY = CYF * CX

CALL MMULT (CYP,CX,CXY,M,M,M)

CALL INIT (ONE,M)

C TAKE CXY TO THE N'TH POWER

```
DO 20 ICOUNT=1,N
```

CALL MMULT (ONE,CXY,RESULT,M,M,M)

```
C    PUT PARTIAL RESULT BACK IN ONE
```

DO 20 I=1,M

DO 20 J=1,M

```
20 ONE(I,J)=RESULT(I,J)
```

CALL TRACE (RESULT,M,TR)

```

C   GET (CX*CY')**(N-1) WITH CXY = CX*CYP
      CALL MMULT (CX,CYP,CXY,M,M,M)
      CALL INIT (ONE,M)
      IF (N.EQ.1) GO TO 40

C   TAKE CXY TO THE N-1 POWER
      DO 30 ICOUNT=1,N1
      CALL MMULT (ONE,CXY,RESULT,M,M,M)
C   PUT PARTIAL RESULT BACK IN ONE
      DO 30 I=1,M
      DO 30 J=1,M
30   ONE(I,J)=RESULT(I,J)

C   GET SECOND TERM BY MULTIPLYING OUT
40   CALL MMULT (XMYT,CYP,RESULT,1,M,M)
      CALL MMULT (RESULT,ONE,CYX,1,M,M)
      CALL MMULT (CYX,XMY,A1X1,1,M,1)

C   ADD THE TERMS TO GET THE N'TH RSIM
      X=TR+N*A1X1(1,1)

      RETURN
      END

```

```

C*****

```

** DL1:[200,125]MOMENT.FTN;11 -- Last written 04-NOV-82 19:31:58 **

```

C***-
C      Module name: MOMENTS OF MAHALANOBIS DISTANCE
C
C      Version X01.00 Last edit: 04-NOV-82 19:26
C      Status: Development/Debugging
C
C      Revision history:
C
C          Version X01.00 07-MAY-82 16:27 - 04-NOV-82 19:26
C          Created by: JIM BARHORST
C***-
C*****
C      SUBROUTINE MOMENT (X,N,AM)
C
C      ROUTINE TO COMPUTE THE N'TH CENTRAL MOMENT OF THE MAHALANOBIS
C      DISTANCE "AM" FROM THE RSIM - X.
C      AM = SUM (PRODUCT(((X(I)/I!)*A(I))/A(I)!))
C      WHERE:
C      A(1)+2*A(2)+3*A(3)+...+N*A(N) = N
C
C      DIMENSION X(20),IA(21)
C
C      INITIALIZE AM AND DETERMINE IF MOMENTS ARE TO BE GIVEN OR COMPUTED
C
C      AM=0.
C      IF (N-2) 10,20,30
C
C      FIRST MOMENT
C 10  AM=X(1)
C      RETURN
C
C      SECOND MOMENT
C 20  AM=X(2)*X(1)**2/2.
C      RETURN
C
C      THIRD MOMENT
C 30  IF (N.GT.3) GO TO 40
C      AM=X(3)+3.*X(1)*X(2)+X(1)**3
C      AM=AM/6.
C      RETURN
C
C      FOURTH OR HIGHER MOMENT
C      BASED ON SPECIAL ITERATIVE METHOD FOR OBTAINING THE SET OF A'S
C
C 40  NP1=N+1
C      ND2=N/2
C      ND2P1=N/2+1
C
C      ITERATE HIGHER HALF OF A'S
C
C      DO 43 J=ND2P1,NP1
C
C      RESET ALL A'S TO ZERO
C      DO 42 I=1,N
C 42  IA(I)=0
C
C      SET APPROPRIATE HIGH A TO 1 (IF ANY)
C      IA(J)=1

```

C TOP OF LOOP; CHECKING FOR A VALID SET OF A'S

```

44  ISUM=0
    DO 45 I=2,N
45  ISUM=ISUM+IA(I)*I
    IF (ISUM.GT.N) GO TO 48

```

C GOOD SET OF A'S FOUND; SET A(1) & COMPUTE MOMENT

```

    IA(1)=N-ISUM
    AF=1
    AMI=1.

    DO 46 I=1,N
    CALL FACT (IA(I),FIA)
    AF=AF*FIA
    CALL FACT (I,FI)
    AMI=AMI*(X(I)/FI)**IA(I)
46  CONTINUE

```

AM=AM+AMI/AF

48 CONTINUE

C INCREMENT SET OF A'S PROPERLY

```

    DO 47 I=2,ND2
    IA(I)=IA(I)+1
    IF (IA(I).LE.N/I) GO TO 44
    IA(I)=0
47  CONTINUE

```

43 CONTINUE

RETURN
END

C*****

** DL:([200,125)ANALYZE.FTN;11 -- Last written 29-DEC-82 19:56:00 **

```

C***-
C      Module name: ANALYZE.FTN
C
C      Version X01.00  Last edit: 29-DEC-82 19:53
C      Status: Development/Debugging
C
C      Revision history:
C
C          Version X01.00 29-SEP-82 17:22 - 29-DEC-82 19:53
C          Created by: JIM BARHORST
C***-

```

C*****

SUBROUTINE ANALYZ (SIA,SIB,N,T)

```

C      ROUTINE TO ANALYZE THE SEMI-INVARIANTS SIA AND SIB
C      N IS THE DIMENSION OF THE PATTERN SPACE AND
C      T IS A THRESHHOLD FOR CLASSIFICATION.

      DIMENSION SIA(20),SIB(20)
      PRINT 59
59      FORMAT (////)
      ZERO=1.E-5

C      TEST FOR IDENTICAL POPULATIONS

      IF (.NOT.(ABS(SIA(5)-N).LT.ZERO
1      .AND.ABS(SIA(10)-N).LT.ZERO
2      .AND.ABS(SIB(10)-N).LT.ZERO)) GO TO 10
      PRINT 60
60      FORMAT ('0',18X,'TEST POPULATION IDENTICAL TO NORMAL POPULATION')
      RETURN

C      TEST FOR ALMOST IDENTICAL POPULATIONS

10     IF (.NOT.(ABS(SIA(10)-N).LT.T
1     .AND.ABS(SIA(5)-N).LT.T
2     .AND.ABS(SIB(10)-N).LT.T
3     .AND.ABS(SIB(5)-N).LT.T)) GO TO 12
      PRINT 61, T
61     FORMAT ('0',18X,'TEST POPULATION WITHIN THRESHHOLD',G10.3, /
1     19X,'OF NORMAL POPULATION')

C      TEST FOR EQUAL COVARIANCE MATRICES

12     IF (.NOT.(SIA(5).EQ.SIB(5)
1     .AND.SIA(10).EQ.SIB(10))) GO TO 14
      PRINT 62
62     FORMAT ('0',18X,'EQUAL COVARIANCE MATRICES')
      RETURN

```

```

C   TEST FOR UNIFORM CONTRACTION/EXPANSION OF COVARIANCE MAT.

14  ALF1A=SIA(5)/SIA(4)
    ALF2A=SIA(10)/SIA(9)
    ALF1B=SIB(4)/SIB(5)
    ALF2B=SIB(9)/SIB(10)
    IF (.NOT.(ABS(ALF1A-ALF1B).LT.ZERO
1      .AND.ABS(ALF2A-ALF2B).LT.ZERO
2      .AND.ABS(ALF2A-ALF1A).LT.ZERO)) GO TO 16
    PRINT 63, ALF1A
63  FORMAT ('0',1BX,'IDENTICAL MEANS WITH SPREAD',1BX,
1      ' IN TEST POPULATION',G10.3,' * NORMAL')
    RETURN

C   TEST FOR ONE COMPONENT OF MEAN HAVING LARGE VARIANCE

16  CONTINUE

    IF (.NOT.(ABS(SIA(10)/SIA(9)-SIA(9)/SIA(8)).GT.ZERO
1      .AND.SIB(10)-(N-1).LT.0.01)) GO TO 18
    PRINT 64
64  FORMAT ('0',1BX,'NON-ZERO COMPONENT OF MEAN HAS LARGE VARIANCE')
    RETURN

C   TEST FOR ONE COMPONENT OF MEAN HAVING SMALL VARIANCE

18  CONTINUE
    IF (.NOT.(ABS(SIB(10)/SIB(9)-SIB(9)/SIB(8)).GT.ZERO
1      .AND.(SIA(10)-(N-1).LT.0.01))) GO TO 20
    PRINT 65
65  FORMAT ('0',1BX,'NON-ZERO COMPONENT OF MEAN HAS SMALL VARIANCE')
    RETURN

20  PRINT 600
600  FORMAT ('0',1BX,'NOTHING SPECIAL FOUND')
    RETURN
END

```

** DL1:[200,125]VECTORSUB.FTN;3 -- Last written 04-NDU-B2 19:07:51 **

C***-

C Module name: VECTOR SUBTRACTION

C

C Version X01.00 Last edit: 04-NDU-B2 19:06

C Status: Development/Debugging

C

C Revision history:

C

C Version X01.00 21-APR-82 17:37 - 04-NDU-B2 19:06

C

C Created by: JIM BARHORET

C

C***-

C*****

 SUBROUTINE VEKSUB (A,B,R,N)

C ROUTINE TO COMPUTE N COMPONENTS OF THE VECTOR (A - B)

C AND STORE IT IN AN N BY 1 MATRIX "R"

 DIMENSION A(1),B(1),R(32,32)

 DO 10 I=1,N

10 R(I,1)=A(I)-B(I)

 RETURN

 END

C*****

** DL1:([200,125]MINVERSE.FTN;4 -- Last written 04-NOV-82 19:03:57 **

C***-

C Module name: MATRIX INVERSE SETUP

C

C Version X01.00 Last edit: 04-NOV-82 19:01

C Status: Development/Debugging

C

C Revision history:

C

C Version X01.00 30-APR-82 16:47 - 04-NOV-82 19:01

C Created by: JIM BARHORST

C

C***-

C*****

 SUBROUTINE INVERS (A,B,N)

C ROUTINE TO SET UP B(N,N) = A(N,N) INVERSE

C ACTUAL INVERSION DONE BY I.B.M. SSP ROUTINE 'MINU'

C C IS VECTOR REPRESENTATION OF MATRIX NEEDED BY MINU

C LL & MM ARE WORK VECTORS FOR MINU

 DIMENSION A(32,32),B(32,32),C(1024),LL(32),MM(32)

C SET UP 1-D VECTOR FOR MINU

 L=0

 DO 10 J=1,N

 DO 10 I=1,N

 L=L+1

10 C(L)=A(I,J)

C GET INVERSE

 CALL MINU (C,N,D,LL,MM)

C PUT BACK IN MATRIX FORM

 L=0

 DO 20 J=1,N

 DO 20 I=1,N

 L=L+1

20 B(I,J)=C(L)

 RETURN

 END

C*****

** DL1:[200,125]MINU.FTN:2 -- Last written 24-AUG-82 16:23:34 **

```
C***-
C      Module name: MINU
C
C      Version X01.00 Last edit: 30-APR-82 17:33
C      Status: Development/Debugging
C
C      Revision history:
C
C          Version X01.00 30-APR-82 16:57 - 30-APR-82 17:33
C          Created by: I.B.M. MANY MANY MOONS AGO!
C***-
```

```
      SUBROUTINE MINU (A,N,D,L,M)
      DIMENSION A(1),L(1),M(1)
      D=1.
      NK=-N
      DO 80 K=1,N
      NK=NK+N
      L(K)=K
      M(K)=K
      KK=NK+K
      BIGA=A(KK)
      DO 20 J=K,N
      IZ=N*(J-1)
      DO 20 I=K,N
      IJ=IZ+I
10      IF (ABS(BIGA)-ABS(A(IJ))) 15,20,20
15      BIGA=A(IJ)
      L(K)=I
      M(K)=J
20      CONTINUE
      J=L(K)
      IF (J-K) 35,35,25
25      KI=K-N
      DO 30 I=1,N
      KI=KI+N
      HOLD=-A(KI)
      JI=KI-K+J
      A(KI)=A(JI)
30      A(JI)=HOLD
35      I=M(K)
      IF (I-K) 45,45,38
38      JP=N*(I-1)
      DO 40 J=1,N
      JK=NK+J
      JI=JP+J
      HOLD=-A(JK)
      A(JK)=A(JI)
40      A(JI)=HOLD
45      IF (BIGA) 48,46,48
46      D=0.
      RETURN
```

```

48   DO 55 I=1,N
      IF (I-K) 50,55,50
50   IK=NK-I
      A(IK)=A(IK)/(-BIGA)
55   CONTINUE
      DO 65 I=1,N
        IK=NK-I
        HOLD=A(IK)
        IJ=I-N
        DO 65 J=1,N
          IJ=IJ+N
          IF (I-K) 60,65,60
60   IF (J-K) 62,65,62
62   KJ=IJ-I+K
          A(IJ)=HOLD*A(KJ)+A(IJ)
65   CONTINUE
          KJ=K-N
          DO 75 J=1,N
            KJ=KJ+N
            IF (J-K) 70,75,70
70   A(KJ)=A(KJ)/BIGA
75   CONTINUE
          D=D*BIGA
          A(KK)=1.0/BIGA
80   CONTINUE
          K=N
100  K=K-1
          IF (K) 150,150,105
105  I=L(K)
          IF (I-K) 120,120,108
108  JQ=N*(K-1)
          JR=N*(I-1)
          DO 110 J=1,N
            JK=JQ+J
            HOLD=A(JK)
            JI=JR+J
            A(JK)=-A(JI)
110  A(JI)=HOLD
120  J=M(K)
          IF (J-K) 100,100,125
125  KI=K-N
          DO 130 I=1,N
            KI=KI+N
            HOLD=A(KI)
            JI=KI-K+J
            A(KI)=-A(JI)
130  A(JI)=HOLD
          GO TO 100
150  RETURN
      END

```

== DL1:[200,125]MATRXMULT.FTN;3 -- Last written 04-NOV-82 19:05:54 ==

```
C==
C      Module name: MATRIX MULTIPLICATION
C
C      Version X01.00. Last edit: 04-NOV-82 19:04
C      Status: Development/Debugging
C
C      Revision history:
C
C          Version X01.00 21-APR-82 17:15 - 04-NOV-82 19:04
C          Created by: JIM BARHORST
C
C==
```

C*****

SUBROUTINE MMULT (A,B,R,N,M,L)

```
C      ROUTINE TO MULTIPLY TWO MATRICES:
C          "A" - N ROWS BY M COLUMNS
C          "B" - M ROWS BY L COLUMNS
C          THE RESULT IS STORED IN:
C          "R" - N ROWS BY L COLUMNS

C          DIMENSION A(32,32),B(32,32),R(32,32)

C          DO 10 I=1,N
C              DO 10 J=1,L
C                  CALCULATE THE VALUE OF THE I-TH ROW & J-TH COLUMN
C                  R(I,J)=0.
C                  DO 10 K=1,M
C                      10 R(I,J)=R(I,J)+A(I,K)*B(K,J)

C          RETURN
C          END
```

C*****

** DL1:[200,125]IDENTMTRX.FTN;7 -- Last written 24-AUG-82 16:23:35 **

```
C**-
C      Module name: IDENTITY MATRIX
C
C      Version X01.00 Last edit: 06-MAY-82 16:27
C      Status: Development/Debugging
C
C      Revision history:
C
C          Version X01.00 19-APR-82 17:11 - 06-MAY-82 16:27
C          Created by: JIM BARHORST
C**-
```

C*****

SUBROUTINE INIT (A,N)

C ROUTINE TO SET AN N BY N MATRIX A TO THE IDENTITY MATRIX

DIMENSION A(32,32)

DO 10 I=1,N

DO 10 J=1,N

A(I,J)=0.

IF (I.EQ.J) A(I,J)=1.

10 CONTINUE

RETURN

END

C*****

** DL1:[200,125]TRACE.FTN:2 -- Last written 24-AUG-82 16:23:35 **

C***-

C Module name: TRACE OF MATRIX

C

C Version X01.00 Last edit: 06-MAY-82 16:28

C Status: Development/Debugging

C

C Revision history:

C

C Version X01.00 19-APR-82 17:22 - 06-MAY-82 16:28

C Created by: JIM BARHORST

C***-

C*****

 SUBROUTINE TRACE (A,N,TR)

C ROUTINE TO COMPUTE TR = SUM OF 1ST N DIAGONAL ELEMENTS OF MATRIX A

 DIMENSION A(32,32)

 TR=0.

 DO 10 I=1,N

10 TR=TR+A(I,I)

 RETURN

 END

C*****

** DL1:[200,125]FACTORIAL.FTN;1 -- Last written 24-AUG-82 16:23:33 **

```

C**
C      Module name: FACTORIAL.FTN
C
C      Version X01.00 Last edit: 19-APR-82 13:31
C      Status: Development/Debugging
C
C      Revision history:
C
C          Version X01.00 19-APR-82 13:31 - 19-APR-82 13:31
C          Created by: JIM BARHORST
C**
C*****
C
C      SUBROUTINE FACT (N,F)
C
C      ROUTINE TO COMPUTE F = N-FACTORIAL
C
C          F=1.
C          DO 10 I=1,N
10      F=F*I
C
C          RETURN
C          END
C
C*****

```

** DL1:[200,125]TRANSPDSE.FTN:2 -- Last written 24-AUG-62 16:23:25 **

C**-

C Module name: MATRIX TRANSPDSE

C

C Version X01.00 Last edit: 06-MAY-62 16:29

C Status: Development/Debugging

C

C Revision history:

C

C Version X01.00 21-APR-62 17:24 - 06-MAY-62 16:29

C Created by: JIM BARHORST

C

C**-

C*****

 SUBROUTINE TRANSP (A,B,N,L)

C ROUTINE TO TAKE THE TRANSPDSE OF AN N ROW BY L COLUMN
C MATRIX "A" AND STORE THE RESULT IN "B" (L BY N)

 DIMENSION A(32,32),B(32,32)

 DO 10 I=1,N

 DO 10 J=1,L

10 B(J,I)=A(I,J)

 RETURN

 END

C*****

VITA

James F. Barhorst was born on September 6, 1953 in St. Louis, Missouri. He graduated from St. Louis University High in May of 1971 having become a National Merit Finalist. He entered St. Louis University on a scholarship the following September. In May of 1974, he graduated on the Dean's List with a B.A. in Physics. After living almost one year in Springfield, Missouri, during which time he married the former Karen Elizabeth Schrader of St. Louis, he took a position as a Scientific Assistant at Argonne National Laboratory located near Chicago, Illinois. After three years there, he accepted a position with Oak Ridge National Laboratory as a Research Associate in the Solid State Division. He enrolled at The University of Tennessee, Knoxville, in the Fall of 1979 and began study towards a Master's degree while continuing to work full time. The Barhorst's first child, Thomas William, was born on January 21, 1981. The Master of Science degree in computer science was awarded to Jim on March 18, 1983.