

DS #2	g_1^1	g_2^1	$F(x,y) = \min(x,y)$					
$r(x_i, x_j)$	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8
x_1	1	0	0	0	0	0	0	0
x_2	0	1	0	0	0	0	0	0
x_3	0	0	1	0.1	0.1	0.1	0.1	0.1
x_4	0	0	0.1	1	0.2	0.2	0.1	0.2
x_5	0	0	0.1	0.2	1	0.4	0.1	0.7
x_6	0	0	0.1	0.2	0.4	1	0.1	0.4
x_7	0	0	0.1	0.1	0.1	0.1	1	0.1
x_8	0	0	0.1	0.2	0.7	0.4	0.1	1

Cluster # 1: $d_1^1 = 0.75$
 Cluster # 2: $d_2^1 = 0.75$
 $D^1 = 0.75$

DS #2	g_1^1	g_2^1	$F(x,y) = xy$					
$r(x_i, x_j)$	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8
x_1	1	0	0	0	0	0	0	0
x_2	0	1	0	0	0	0	0	0
x_3	0	0	1	0.5	0.11	0.11	0.13	0.14
x_4	0	0	0.5	1	0.22	0.22	0.13	0.29
x_5	0	0	0.11	0.22	1	0.8	0.2	0.78
x_6	0	0	0.11	0.22	0.8	1	0.25	0.78
x_7	0	0	0.13	0.13	0.2	0.25	1	0.2
x_8	0	0	0.14	0.29	0.78	0.78	0.2	1

Cluster # 1: $d_1^1 = 0.40$
 Cluster # 2: $d_2^1 = 0.45$
 $D^1 = 0.425$

DS #1	g_1^1	g_2^1	$F(x,y) = \max(x+y, 1.0)$					
$r(x_i, x_j)$	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8
x_1	1	0	0.8	0.8	0.1	0.1	0.1	0.3
x_2	0	1	0.1	0.1	0.5	0.6	0.8	0.5
x_3	0.8	0.1	1	0.9	0.2	0.2	0.3	0.4
x_4	0.8	0.1	0.9	1	0.3	0.3	0.2	0.5
x_5	0.1	0.5	0.2	0.3	1	0.9	0.6	0.8
x_6	0.1	0.6	0.2	0.3	0.9	1	0.7	0.8
x_7	0.1	0.8	0.3	0.2	0.6	0.7	1	0.6
x_8	0.3	0.5	0.4	0.5	0.8	0.8	0.6	1

Cluster # 1: $d_1^1 = 0.125$
 Cluster # 2: $d_2^1 = 0.125$
 $D^1 = 0.125$

IV. CONCLUDING REMARKS

We have generalized some previous results of Ruspini and others in fuzzy clustering, using the new concept of indistinguishability relation based on the concept of t -norm and also we have studied its metrical properties through the dual concept of t -conorm that leads to G -pseudometrics. From the concept of G -pseudometric we have defined fuzzy r -clusters and fuzzy cluster coverages. Finally, we have proposed a measure of cluster validity based on the concept of fuzzy coverage.

It is important to notice that the process of measuring the validity is carried out before any decision concerning the assignments of elements to the clusters. Therefore we can postpone the decision step until we have an acceptable cluster validity. That is, we have a sort of closed loop in the sense that a bad measure of validity obliges the user to reconsider a previous hypothesis, for example, the number of clusters, the values of the prototypes, etc. Right now we are studying this "close loop" aspect in the setting of different classification algorithms.

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A Test to Determine the Multivariate Normality of a Data Set

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Abstract—This correspondence describes a new test for multivariate normality useful in pattern recognition. The test is based on the Friedman-Rafsky multivariate extension of the Wald-Wolfowitz runs test. We perform Monte-Carlo experiments to determine if the test is reliable in high dimensions with moderate sample size. We compare the test to some other tests mentioned in the literature.

Index Terms—Covariance matrix, Friedman-Rafsky test, minimum spanning tree, Monte-Carlo simulations, multivariate normal distribution, pattern recognition.

I. INTRODUCTION

The use of the assumption that data follow the multivariate normal distribution is common in pattern recognition and clustering [3]. However, few tests are available for determining if such an assumption is statistically valid, especially for data residing in high (>2) dimensions, which are common in pattern recognition studies.

Tests for multivariate normality are few, but those that exist can be split into three categories: tests of marginal normality, tests for joint normality, and tests based on one-dimensional projections. The articles [1], [8], [7], and [9] and sections of the book [6] provide a good overview of such tests. However, little work has been done on the practical aspects of such tests. Cross, Wyse, and Jain [2] provide one example with a Monte-Carlo study of the sample size and dimensionality properties of a test proposed by Mardia. Our paper continues this program for the practical assessment of normality tests using a similar approach.

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II. THE FRIEDMAN-RAFSKY TEST

The Friedman-Rafsky test [4] was originally proposed as a multivariate extension of the classic Wald-Wolfowitz two-sample runs test, whose null hypothesis is that the two univariate samples have the same distribution. The meaning of "runs" for the multivariate extension is based on the minimal spanning tree (MST) of the pooled samples. The test statistic is the count of the number of edges in the MST linking points belonging to the two different samples. This is analogous to the univariate case, where the statistic is the total number of runs of elements from the same population in the sorted list of the pooled samples. In the multivariate extension, the MST is used to "sort" the elements of the samples, an operation that is conceptually obvious in one dimension, but ill-defined in higher dimensions.

More formally, let the N data points in one sample be labeled X and the M data points in the other sample be labeled Y . The MST of the pooled samples is computed. The number of edges in the MST linking a point labeled X to a point labeled Y is found. Denote this X -to- Y join count as T . Under the null hypothesis that X and Y are independent random samples from the same distribution, Friedman and Rafsky show that as $M, N \rightarrow \infty$ with M/N bounded away from 0 and ∞ , the distribution of

$$T' = \frac{T - E[T]}{\sqrt{(\text{Var}[T|C])}}$$

approaches the standard normal distribution for MST's computed using the Euclidean distance metric, where C is the number of edge pairs in the realized MST which share a common node, and

$$E[T] = \frac{2MN}{L}$$

$$\text{Var}[T|C] = \frac{2MN}{L(L-1)} \left(\frac{2MN-L}{L} + \frac{C-L+2}{(L-2)(L-3)} [L(L-1) - 4MN + 2] \right)$$

with $L = M + N$.

Note that the computational complexity for performing the Friedman-Rafsky test is $O(L^2)$. Computing the MST of L points in a space of dimensionality greater than 2 (using the classic algorithm by Prim [10]) is known to require $O(L^2)$ operations. The permutation parameter C , which is needed to compute the variance of the statistic, can be written as $\frac{1}{2} \sum_{i=1}^L d_i(d_i - 1)$ where d_i is the degree of the i th node in the MST. Given the MST representation returned by Prim's algorithm, finding the degree of each node requires $O(L)$ operations per node. Thus the computational complexity needed to determine C is also $O(L^2)$. Computation of the test statistic T' requires only $O(L)$ operations, since there are $L - 1$ edges in the MST.

Smith and Jain [13] have used the Friedman-Rafsky test to test a null hypothesis of uniformity against clustered alternatives. In [11] it was also shown that this test for the uniform distribution achieves high power against a multivariate swarm of points following the normal distribution, provided that the number of points is sufficiently large (about 200). A short note [12] contains some initial results leading to this current paper.

III. A MULTIVARIATE NORMALITY TEST

To test whether a given sample follows the normal distribution, we modify the Friedman-Rafsky procedure as follows. The sample of N points to be tested for normality is labeled X . The mean vector V_x and the covariance matrix C_x of X are estimated. A second sample Y of N points is generated from a multivariate normal distribution with parameters (V_x, C_x) . The Friedman-Rafsky test is then performed with X and Y taken as independent samples; the null hypothesis of normality of the sample X is rejected if $T' < Z(\alpha)$ where $Z(\alpha)$ is the α quantile of the standard normal distribution.

Small values of T' imply a spatial separation of X and Y while values larger than expected imply that the two samples are mixed "too much." Thus, the one-sided test is appropriate for detecting most common deviations from normality. As described below, assuming the normality of T' precludes the use of the two-sided test.

The test uses the assumption that the Y sample is independent of the X sample by relying on the asymptotic normality of T' . This assumption is clearly invalid since Y depends on V_x and C_x . Thus Y is "closer" to X than would be expected if both arose as independent samples. The effect of the dependency, made clear in the remaining section, is to make the one-sided test more conservative, i.e., to decrease its power against alternatives. We show, however, that the test still retains adequate power.

One way to remove the difficulty with the independence assumption is to derive a more reliable critical region of the test. One computational method for doing so is to perform a Monte-Carlo simulation. For our test, this procedure is as follows.

1) As before, from the X and Y samples, determine T' . Call this value T'_0 .

2) Generate a sample X^* from $N(V_x, C_x)$. Then generate a Y^* sample from $N(V_x, C_x)$. Compute the test statistic from the X^* and Y^* samples and call its value T'_1 .

3) Repeat Step 2 $W - 2$ more times, giving T'_2, \dots, T'_{W-1} .

4) Let R be the rank order of T'_0 among the $W T'$ values. Reject the null hypothesis of normality of X at the α level if $R \leq \alpha W$.

In the remainder of this paper, we shall refer to the test using the normal critical region as the "normal" test and the test using a Monte-Carlo determined critical region as the "Monte-Carlo" test.

Besides the interdependence of the X and Y samples, two other problems arise with the proposed test. First, and most important, the computation of the test statistic depends on the generation of a normal random sample Y . Different realizations of Y will yield different test statistics. Practical use of the test demands that a number of test instances be carried out.

Another issue is choosing the cardinality of the Y sample the same as the cardinality of the given X sample; choosing a larger cardinality for Y might lead to a test with higher power. A later section will address this issue.

IV. EXPERIMENTAL RESULTS

To illustrate the proposed test, we now provide two examples of its use.

Fig. 1 shows 25 points following the standard normal distribution (points graphed with a filled-in circle). These points are to be tested for normality using our proposed test and make up the X sample. Also shown in Fig. 1 are the 25 test points making up the Y sample (points graphed with a hollow triangle), which were generated from a normal distribution with the mean and covariance matrix estimated from the X sample. Finally, in the figure, we show the MST formed using these pooled samples. There are 26 edges in the MST linking points in samples X and Y . This yields a test statistic value of $T' = 0.218$ and gives a significance level > 0.33 using the "normal" test.

Likewise, Fig. 2 shows 25 points from a well-separated Gaussian mixture (the bimodal distribution with $\Delta = 7.5$, described in a following section of the paper), 25 test points for the Y sample (points graphed with a hollow triangle) generated from a normal distribution with the mean and covariance matrix estimated from the X sample, and the MST formed using these pooled samples. There are 18 edges in the MST linking points in samples X and Y . This yields a test statistic value of $T' = -1.968$ and gives a significance level < 0.025 .

A. The Size of the Test

The first question with the proposed test is whether the size of the test can be set by relying on the asymptotic normality of T' given that the sample size is finite and that the Y sample is not independent of the X sample.

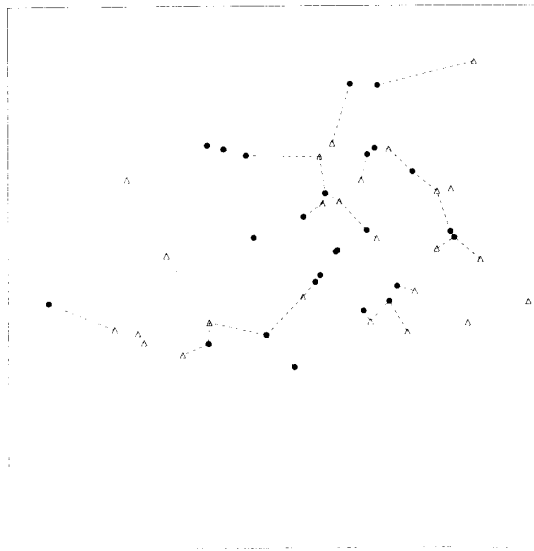


Fig. 1. Twenty-five points following the standard normal distribution, 25 points generated as a testing sample, and the MST formed when using these two samples. This yields $T' = 0.281$, giving a significance level >0.33 .

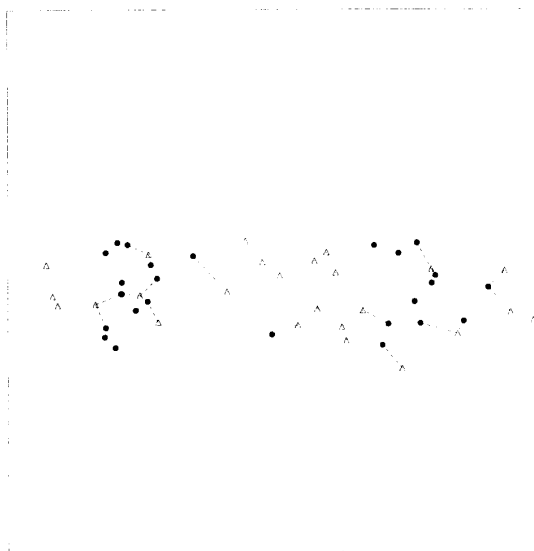


Fig. 2. Twenty-five points following the bimodal distribution with $\Delta = 7.5$, 25 points generated as a testing sample, and the MST formed when using these two samples. This yields $T' = -1.968$, giving a significance level <0.025 .

To check the null distribution of the test, we perform a Monte-Carlo study. In each Monte-Carlo run, N points following the standard normal distribution are generated, the "normal" normality test is performed on that sample, and the number of rejections at various levels α are tabulated. To check the test for sample size dependence, we let N be 100, 500, or 1000. For a given sample size, samples of normal data in 2, 5, and 10 dimensions are used. In all cases the number of Monte-Carlo runs is 2000.

Tables I-III show the results for each of the sample sizes. As can be seen, the number of rejections of the null hypothesis for the normal data is not significant. However, the results are all under

TABLE I
"NORMAL" TEST NULL REJECTION RATES FOR VARIOUS DIMENSIONS WHEN $N = 100$

True Rate	Dimension		
	2	5	10
0.01	0.009	0.002	0.000
0.02	0.020	0.005	0.001
0.05	0.042	0.016	0.005
0.10	0.084	0.035	0.010
0.20	0.178	0.115	0.041

TABLE II
"NORMAL" TEST NULL REJECTION RATES FOR VARIOUS DIMENSIONS WHEN $N = 500$

True Rate	Dimension		
	2	5	10
0.01	0.008	0.003	0.004
0.02	0.015	0.007	0.008
0.05	0.036	0.031	0.015
0.10	0.080	0.063	0.037
0.20	0.167	0.139	0.089

TABLE III
"NORMAL" TEST NULL REJECTION RATES FOR VARIOUS DIMENSIONS WHEN $N = 1000$

True Rate	Dimension		
	2	5	10
0.01	0.007	0.005	0.002
0.02	0.016	0.008	0.006
0.02	0.023	0.012	0.012
0.05	0.046	0.027	0.024
0.10	0.088	0.071	0.046
0.20	0.195	0.164	0.098

TABLE IV
"MONTE-CARLO" TEST NULL REJECTION RATES FOR VARIOUS DIMENSIONS WHEN $N = 100$

True Rate	Dimension		
	2	5	10
0.01	0.009	0.015	0.007
0.02	0.015	0.030	0.017
0.05	0.042	0.065	0.045
0.10	0.115	0.115	0.110
0.20	0.205	0.225	0.215

the true rejection rates. This is especially true when the number of dimensions is large and/or when N is small. Thus the "normal" test for normality is a conservative test.

Table IV repeats Table I, but for the "Monte-Carlo" test. These simulations confirm the expected result that the size is properly set in the "Monte-Carlo" test for normality.

B. A Power Study

To study the power of the proposed test against a deviation from normality, we use random samples of size N from the bimodal distribution studied in [2]. This distribution generates samples containing an equal number of points from two normal populations. One population contains points from a normal distribution which has a zero mean vector and an identity covariance matrix; the other population consists of points from a normal distribution also with

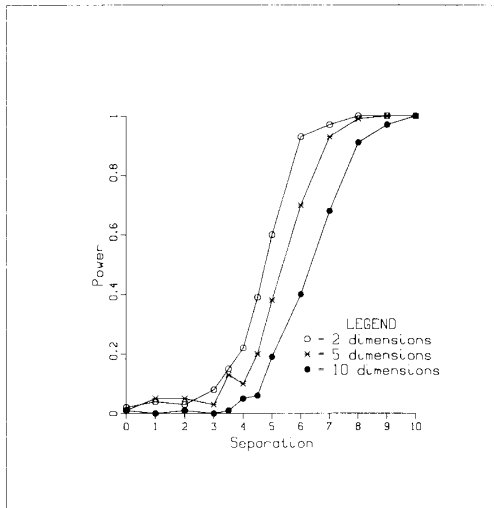


Fig. 3. Power versus Δ for bimodal distribution in various dimensions when $N = 100$.

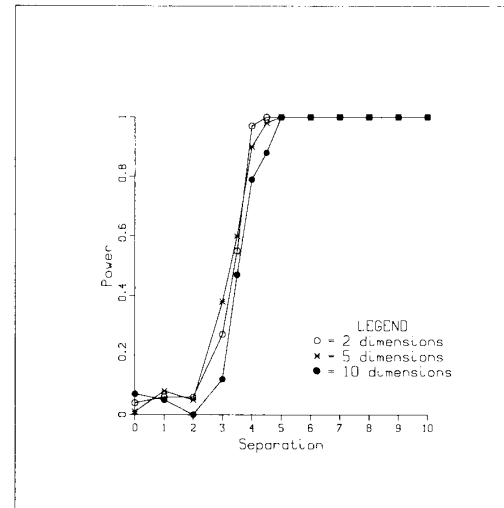


Fig. 5. Power versus Δ for bimodal distribution in various dimensions when $N = 1000$.

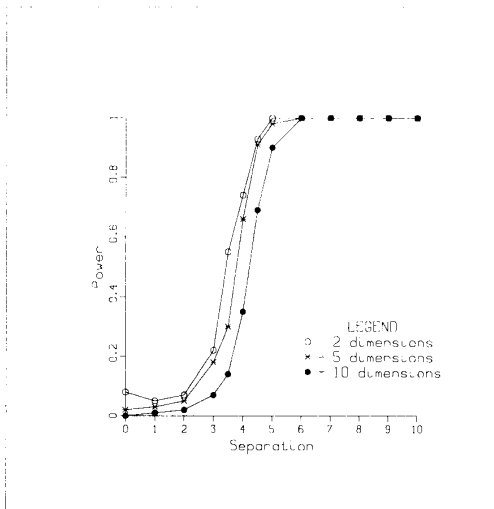


Fig. 4. Power versus Δ for bimodal distribution in various dimensions when $N = 500$.

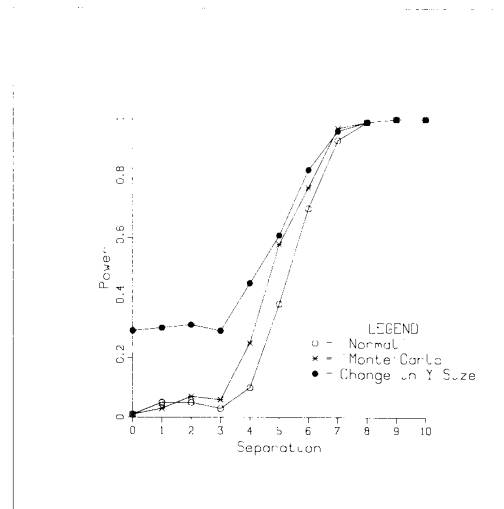


Fig. 6. Power versus Δ for bimodal distribution in five dimensions when $N = 100$ for various tests.

identity covariance matrix but with a mean vector of length Δ . Thus the means of the two mixture densities are separated by a distance of Δ . When Δ is zero, an N point sample from the bimodal distribution follows the multivariate standard normal distribution, whereas increasing Δ gives a mixture distribution with increasing bimodal deviation from normality.

We study the power of the "normal" normality test against the bimodal alternative by Monte-Carlo simulation. Each Monte-Carlo run consists of generating N points following the bimodal distribution and performing the normality test. To check the test for sample size dependence, we let N be 100, 500, or 1000. For a given sample size, samples of bimodal data in 2, 5, and 10 dimensions are taken with the mean separation parameter, Δ , ranging over integer values from 0 to 10, inclusive. In all cases the number of Monte-Carlo runs is 100 and α is 0.05.

Fig. 3 shows the results for dimensions 2, 5, and 10 with $N = 100$. Figs. 4 and 5 show the results for these dimensions when N is 500 and 1000, respectively.

We will compare these power results to other tests in the next section. For now, note that power appears to monotonically increase with increasing Δ . Also, as N increases, the effect of the

dimensionality of the data is less important. An interesting conjecture is that there is some asymptotic power cure.

We can now compare the power results of the "normal" test to its variation when the cardinality of the Y sample is chosen much larger than that of the X sample and also to the "Monte-Carlo" test. Fig. 6 shows these comparisons for five dimensions and $N = 100$. The curve labeled with the hollow circle is the baseline "normal" test curve, repeated from Fig. 3. As above, 100 simulations are used to generate the other curves for integer values of Δ .

The curve marked with an asterisk in Fig. 6 is the power curve generated for the "Monte-Carlo" test. The number of trials W to determine the critical region in the "Monte-Carlo" test is 102. Note that, as expected from the conservative nature of the "normal" test, the power for the "Monte-Carlo" test is larger than the power for the "normal" test. However, the decrease in power for the "normal" test is not large.

The curve marked with the filled in circle is the power curve generated by modifying the "normal" test by setting the size of the Y sample to 500 points rather than 100 points. It is clear that the size of this test suffers (29 percent rejects with $\Delta = 0.0$) without a corresponding large increase in power. Further study supports

that this arises due to poor normalization of T to produce T' , using the asymptotic value for $\text{Var}[T|C]$. This might be corrected by applying the Monte-Carlo procedure described for the "Monte-Carlo" test to the original T values. However, this does not look worthwhile, as the power of the test with large Y does not appear significantly greater than that for its nominally chosen size.

C. Comparisons to Other Tests

We can compare the Monte-Carlo results of our proposed test to the study done in [2] on Mardia's test. In [2], the authors studied Mardia's test on the bimodal density when $N = 100$ in both two and five dimensions. In five dimensions, Mardia's test yielded spurious rejections of true normal data with this sample size. Additional results in [2] show that problem of spurious rejections is even worse as dimensionality increases. These problems do not occur with our proposed test.

Comparing the two-dimensional results of both tests shows that Mardia's test is able to detect small deviations from normality (Δ of approximately 2.0) more easily than the "normal" version of our proposed test. At $\Delta = 5.0$, both tests are at a power of 0.60. Our test rejects all realizations of the bimodal density when $\Delta > 8.0$ but this level of performance is not achieved for Mardia's test until $\Delta > 13.0$, even allowing its spurious rejections of the null hypothesis.

We can also compare our results to the theoretically derived results of Fukunaga and Flick [5]. Tables I and II in [5] contain results for our bimodal density. In our notation, their separation constant α is just $\Delta/2$. Fukunaga and Flick do not give any statistical information about their test and we must rely on the concept of a "minimal detectable" change in Δ from zero, which is not well defined in practice. Their results show that at a sample size of 100 in two dimensions, the minimum detectable Δ should be 1.14. In this case, our "normal" test can detect deviation from normality when $\Delta > 2$. With $N = 100$ in 10 dimensions, our test detects deviation from normality for $\Delta > 4.0$. Fukunaga and Flick's theoretical results in 8 dimensions at the same N show that their test can reject the null hypothesis when $\Delta > 4.58$. However, their results assume that the mean vector and the covariance matrix of the Gaussian distribution for the null hypothesis is known. The behavior of their test when these parameters are to be estimated is not known.

V. CONCLUSIONS

We have performed a modest simulation study of the applicability of the Friedman-Rafsky test to determine the multivariate normality of sample data. The test data are combined with a multivariate swarm of points following the normal distribution generated with mean vector and covariance matrix estimated from the test data. The minimal spanning tree of this resultant ensemble of points is computed and the count of the interpopulation edges in the MST is used as a test statistic. The simulation studied both the null case of the test and one simple deviation from normality.

Two conclusions can be made from this study. First, the test can be conservatively applied by using the asymptotic normality of the test statistic, even for small sample sizes. Second, the power of the test appears reasonable, especially in high dimensions.

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Computing the Width of a Set

MICHAEL E. HOULE AND GODFRIED T. TOUSSAINT

Abstract—Given a set of points $P = \{p_1, p_2, \dots, p_n\}$ in three dimensions, the width of P , $W(P)$, is defined as the minimum distance between parallel planes of support of P . It is shown that $W(P)$ can be computed in $O(n \log n + I)$ time and $O(n)$ space, where I is the number of antipodal pairs of edges of the convex hull of P , and in the worst case $I = \Omega(n^2)$. For convex polyhedra, the time complexity becomes $O(n + I)$. If P is a set of points in the plane, the complexity can be reduced to $O(n \log n)$. Finally, for simple polygons linear time suffices.

Index Terms—Algorithms, antipodal pairs, artificial intelligence, computational geometry, convex hull, geometric complexity, geometric transforms, image processing, minimax approximating line, minimax approximating plane, pattern recognition, rotating calipers, width.

I. INTRODUCTION

The width of a set of points P (or a simple polygon P) in two dimensions is the minimum distance between parallel lines of support of P (or P). In three dimensions, it is the minimum distance between parallel planes of support. This notion of width is closely related to that of diameter (the maximum distance between parallel lines or planes of support), and the methods that will be presented reflect this. Computation of the width has applications in collision-avoidance problems [1], and in approximating polygonal curves [11]-[13].

The two-dimensional width problem has received some attention

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