

# Improvement in Track-to-Track Association from using an Adaptive Threshold

Lawrence D. Stone and Thy M. Tran

Metron Inc  
Reston, VA, USA  
[stone@metsci.com](mailto:stone@metsci.com)  
[Thy.Tran@metsci.com](mailto:Thy.Tran@metsci.com)

Mark L. Williams

Advanced Information Processing  
BAE Systems  
Filton, Bristol, England.  
[Mark.L.williams@baesystems.com](mailto:Mark.L.williams@baesystems.com)

**Abstract** – *This paper considers the performance of two track-to-track association algorithms. The first bases association decisions on a chi-squared distance between tracks and a fixed significance threshold to determine when no association is allowed. The second algorithm finds the maximum a posteriori probability (MAP) set of associations between tracks from two independent tracking systems. For tracks whose state estimates are characterized by Gaussian distributions, the second algorithm may be viewed as a version of the first algorithm with an adaptive threshold. This paper examines the performance of these two algorithms in terms of expected fraction of correct matches of tracks from system 1 to tracks from system 2 and finds that the adaptive threshold algorithm performs as well or better than the fixed threshold algorithm and that adjustments to the adaptive threshold generally produce little or no benefit.*

**Keywords:** Association, tracking

## 1 Introduction

In [1] and [2] Mori and Chong considered the problem of associating tracks from two independent tracking systems. They developed a formula for computing the posterior probability of an assignment of tracks from system 1 with those from system 2 being correct and an algorithm for finding the maximum a posteriori probability (MAP) assignment when the number of tracks held by the two systems may differ. This algorithm is a snapshot approach in which only the most recent state estimates (in terms of probability distributions) are used to compute the MAP assignment. Since system 1 may hold tracks on targets not held by system 2 and vice versa, the algorithm allows for the possibility that a track in one system may have no match in the other. The MAP algorithm in [2] is derived under the assumption that each system produces tracks with correct measurement to track associations and no false tracks. The number of real targets is assumed to have a Poisson distribution and the target states are distributed as i.i.d. draws from a common prior distribution. Under these conditions, [2] shows that finding the MAP association reduces to the solution of a linear programming problem even for general target state distributions.

In the case where the target state distributions are Gaussian, the linear programming solution method is very similar to the one derived in [3]. In that case the problem is formulated as minimizing a cost function defined in terms of the chi-squared distance between state distributions. To allow for the possibility that a track from system 1 has no match with a track from system 2, [3] sets a significance level. If the chi-squared distance between two tracks exceeds that significance level, no match is allowed.

In [4] the MAP algorithms were extended to include feature as well as kinetic information in computing association probabilities and finding the MAP assignment. The authors showed that adding feature information can improve on metric-only association performance. They also explored the possibility of adjusting the adaptive threshold and performed tests on simulated data that showed no adjustment is necessary when features are considered.

In subsequent papers Mori and Chong, [5] – [7] extended their results to the case where the distribution of target states is i.i.d. but the number of targets is not Poisson distributed. In [8] Ferry extended MAP to include target type information and to account for the possibility of missing feature measurements. Using this approach he showed that incorporating feature information always improves association performance. In [9] he finds exact solutions for the problem of joint bias removal and track-to-track association. In [13] Bar-Shalom and Chen take a somewhat different approach to incorporating features or attributes into the track-to-track association process.

The purpose of this paper is to return to the questions raised in [2] and [4] as to whether an adaptive threshold is better than a fixed one and whether the adaptive threshold can be improved. This paper reports on simulation studies that show that the adaptive threshold is better than a fixed (significance) threshold and that adjustments to the adaptive threshold generally provide little or no benefit. The measure of performance used in these studies is the fraction of correct matches. A correct match occurs when a track from system 1 is correctly matched with a track from

system 2 or when a track from either system is correctly identified as having no match in the other system's tracks.

In a sense, it is surprising that the MAP algorithm does so well using this measure of performance. Finding the MAP association involves finding the association  $a^*$  that maximizes the product in equation (7) below. In contrast maximizing the fraction of correct matches or equivalently maximizing the expected number of correct matches involves maximizing a sum of pair-wise association probabilities as is shown in section 2.3.3.

The algorithms discussed in this paper presume that measurement bias has been removed before they are applied. In general, the problems of bias removal and association must be solved jointly. There are a number of approximate algorithms for doing this such as the one given in [10]. Reference [9] provides an exact solution to this problem.

## 2 Track Association Algorithms

We assume that at time  $t$  there are  $I$  tracks from system 1 and  $J$  tracks from system 2. In general  $I \neq J$ . The tracks have been produced independently by the two systems, and the track estimates for time  $t$  are given in terms of Gaussian probability distributions on target (kinematic) state. The means and covariances of the tracks are

$$\begin{aligned} x_i^1 \text{ and } V_i^1 & \text{ for the } i\text{th track of system 1} \\ x_j^2 \text{ and } V_j^2 & \text{ for the } j\text{th track of system 2.} \end{aligned}$$

Let

$$\chi_{ij}^2 = (x_i^1 - x_j^2)^T (V_i^1 + V_j^2)^{-1} (x_i^1 - x_j^2) \quad (1)$$

denote the chi-squared distance between track  $i$  of system 1 and track  $j$  of system 2. Equation (1) assumes that state estimation errors in system 1 are independent of those from system 2. Reference [12] has shown this is not true when the underlying motion models used by the two systems are related. If that is the case, then  $V_i^1 + V_j^2$  in (1) must be replaced with  $V_i^1 + V_j^2 - V_{ij}^1 - V_{ji}^2$  where  $V_{ij}^1$  and  $V_{ji}^2$  are the cross covariances due to common process noise.

### 2.1 Definition of an Association

Following [2], we define a *track-to-track association* to be a 1-to-1 mapping  $a$  of a subset  $\text{Dom}(a) \subseteq \{1, \dots, I\}$  onto a subset  $\text{Rng}(a) \subseteq \{1, \dots, J\}$ . For  $i \in \text{Dom}(a)$ ,  $a(i)$  equals the index of the track from system 2 associated with track  $i$  from system 1. Tracks in  $\{1, \dots, I\} \setminus \text{Dom}(a)$  are not associated with any track from system 2. Correspondingly, tracks in  $\{1, \dots, J\} \setminus \text{Rng}(a)$  are not associated with any track from system 1.

### 2.2 Fixed Threshold Track Association Algorithm

As observed in [2], the conventional fixed threshold association algorithm [3] may be defined as follows. Let  $\bar{\chi}^2$  be the fixed threshold corresponding a chosen significance level. For example, the significance level 0.003 is used in [3]. Define the cost function  $C_{ij}$  by

$$C_{ij} = \begin{cases} \chi_{ij}^2 & \text{if } \chi_{ij}^2 < \bar{\chi}^2 \text{ and } (i, j) \in \{1, \dots, I\} \times \{1, \dots, J\} \\ \bar{\chi}^2 & \text{if } i \in \{1, \dots, I\} \text{ and } j = J + i \\ \infty & \text{otherwise} \end{cases} \quad (2)$$

Then finding the minimum cost track-to-track association  $a^*$  in [3] is equivalent to finding  $\xi^*$  that solves the following linear program.

$$\begin{aligned} \text{Minimize} \quad & \sum_{i=1}^I \sum_{j=1}^{I+J} C_{ij} \xi_{ij} \\ \text{Subject to} \quad & \xi_{ij} \in [0, 1] \text{ for } (i, j) \in \{1, \dots, I\} \times \{1, \dots, I+J\} \\ & \sum_{j=1}^{I+J} \xi_{ij} = 1 \text{ for } i \in \{1, \dots, I\} \\ & \sum_{i=1}^I \xi_{ij} \leq 1 \text{ for } j \in \{1, \dots, I+J\} \end{aligned} \quad (3)$$

In [3] it is shown that this linear program produces integer solutions, i.e.,  $\xi_{ij}^* \in \{0, 1\}$ . The association  $a^*$  is obtained by defining

$$a^*(i) = j \text{ when } \xi_{ij}^* = 1 \text{ for } (i, j) \in \{1, \dots, I\} \times \{1, \dots, J\}$$

If  $\xi_{ij}^* = 1$  for  $j = J + i$ , then the  $i$ th track from system 1 is not associated with any track from system 2. The effect of using the cost function in (2) is to force associations when there is a feasible one with chi-squared distance less than the threshold. The optimization does this in a fashion that minimizes overall cost.

### 2.3 Adaptive Threshold (MAP) Algorithm

The MAP algorithm from [2] requires a more detailed model of the problem than the fixed threshold one above because we have to specify the probabilistic framework which will allow us to compute posterior association probabilities in a Bayesian manner.

#### 2.3.1 MAP Model

The MAP model of [2] assumes that there are no false tracks generated by the two systems. The number of true targets is Poisson distributed with mean  $\bar{\nu}$ . The target state space is a subset of Euclidean  $n$ -space,  $E^n$ . Typically, the target state will consist of position and velocity in a 2 or 3 dimensional space so that the state space is  $E^4$  or  $E^6$ . The prior state distribution for each target is defined by a common probability density function  $p^0$  on  $E^n$ . In other

words, the prior distribution on the number and state of the targets forms a Poisson Point Process [11]. A realization of the process may be obtained by first making a draw for  $N$ , the number of targets, from the Poisson distribution with mean  $\bar{\nu}$ , and then making  $N$  independent draws from the probability density  $p^0$  to determine the state of each of the  $N$  targets.

For system  $k$ , the probability of detecting a target in state  $x \in E^n$  is  $P_d^k(x)$  for  $k=1,2$ . Suppose that at time  $t$  the state distributions on the targets from systems 1 and 2 are given by

$$\{p_i^1; i=1, \dots, I\} \text{ and } \{p_j^2; j=1, \dots, J\}.$$

Define

$$L(i, j) = \begin{cases} \int_{E^6} \frac{p_i^1(x) p_j^2(x)}{\bar{\nu} p^0(x)} dx & \text{if } (i, j) \in \{1, \dots, I\} \times \{1, \dots, J\} \\ \int_{E^6} p_i^1(x) (1 - P_d^2(x)) dx & \text{if } i \in \{1, \dots, I\} \text{ and } j = 0 \\ \int_{E^6} p_j^2(x) (1 - P_d^1(x)) dx & \text{if } i = 0 \text{ and } j \in \{1, \dots, J\} \end{cases} \quad (4)$$

where  $j=0$  means that no track from system 2 is associated with track  $i$  from system 1 and  $i=0$  has the symmetric meaning. Let

$$\ell(i, j) = \frac{L(i, j)}{L(i, 0)L(0, j)} \text{ for } (i, j) \in \{1, \dots, I\} \times \{1, \dots, J\} \quad (5)$$

$$C_{ij} = \begin{cases} -2 \ln(\ell(i, j)) & \text{for } (i, j) \in \{1, \dots, I\} \times \{1, \dots, J\} \\ 0 & \text{for } i \in \{1, \dots, I\} \text{ and } j = J + i \\ \infty & \text{otherwise} \end{cases} \quad (6)$$

### 2.3.2 MAP Association

Mori and Chong [2] show that the posterior probability of an association  $a$  being correct is given by

$$\Pr\{a\} = K \prod_{i \in \text{Dom}(a)} \ell(i, a(i)) \quad (7)$$

where  $K$  does not depend on  $a$ . Thus finding the MAP association  $a^*$  in (7) is equivalent to finding  $\xi^*$  to solve the following linear program with  $C_{ij}$  defined by (6).

$$\begin{aligned} & \text{Minimize } \sum_{i=1}^I \sum_{j=1}^{J+I} C_{ij} \xi_{ij} \\ & \text{Such that } \xi_{ij} \in [0, 1] \text{ for } (i, j) \in \{1, \dots, I\} \times \{1, \dots, J+I\} \\ & \sum_{j=1}^{J+I} \xi_{ij} = 1 \text{ for } i \in \{1, \dots, I\} \\ & \sum_{i=1}^I \xi_{ij} \leq 1 \text{ for } j \in \{1, \dots, J+I\}. \end{aligned} \quad (8)$$

When the target state distributions are Gaussian, i.e.,

$$p_i^1 \sim N(x_i^1, V_i^1) \text{ and } p_j^2 \sim N(x_j^2, V_j^2),$$

$p^0(x) = \rho$  over a finite region, and  $P_d^1$  and  $P_d^2$  are constant, we have

$$C_{ij} = \chi_{ij}^2 - A_{ij} \text{ for } (i, j) \in \{1, \dots, I\} \times \{1, \dots, J\} \quad (9)$$

where

$$A_{ij} = -\ln \left[ (\bar{\nu} \rho (1 - P_d^1)(1 - P_d^2))^2 \det(2\pi(V_i^1 + V_j^2)) \right] \quad (10)$$

Clearly we still obtain the MAP solution from (8) if we add  $A_{ij}$  to definition of  $C_{ij}$  in (6) and (9) to obtain

$$C_{ij} = \begin{cases} \chi_{ij}^2 & \text{for } (i, j) \in \{1, \dots, I\} \times \{1, \dots, J\} \\ A_{ij} & \text{for } i \in \{1, \dots, I\} \text{ and } j = J + i \\ \infty & \text{otherwise} \end{cases} \quad (11)$$

Comparing (11) and (2) we see that finding the MAP association is equivalent to replacing the fixed threshold  $\bar{\chi}^2$  with the adaptive one  $A_{ij}$ .

### 2.3.3 Expected Number of Correct Pairwise Associations

When we compare the performance of track-to-track association algorithms, we will do so in terms of the fraction of correct pair-wise associations defined as follows. For  $i \in \{1, \dots, I\}$  and  $j \in \{1, \dots, J\}$ , let

$$\psi(i, j) = \begin{cases} 1 & \text{if } i \text{ is correctly associated with } j \\ 0 & \text{otherwise} \end{cases}$$

$$\psi(i, 0) = \begin{cases} 1 & \text{if } i \text{ is correctly not associated with any track} \\ 0 & \text{otherwise} \end{cases}$$

$$\psi(0, j) = \begin{cases} 1 & \text{if } j \text{ is correctly not associated with any track} \\ 0 & \text{otherwise.} \end{cases}$$

Then, the number of correct pairwise associations for the association  $a$  is

$$N_C(a) = \sum_{i \in \text{Dom}(a)} \psi(i, a(i)) + \sum_{i \notin \text{Dom}(a)} \psi(i, 0) + \sum_{j \in \text{Rng}(a)} \psi(0, j) \quad (12)$$

Suppose we run a number of Monte Carlo trials where each trial represents a realization of the model in section 2.3.1, and for each trial we compute the MAP association  $a^*$  and  $N_C(a^*)$ . The average of  $N_C(a^*)$  over these trials is an estimate of  $E[N_C(a^*)]$ . We can see from (12) that  $E[N_C(a^*)]$  is equal to a sum of pair-wise association

probabilities. We can perform the same computation for a fixed threshold association algorithm and compare the results with those from the MAP algorithm. Dividing  $N_c(a)$  by the number of correct matches we obtain the fraction of correct matches.

### 3 Comparing the Fixed and Adaptive Threshold Associations

This section describes simulation results in which we compare the performance of the fixed and adaptive threshold algorithms in terms of fraction of correct matches.

#### 3.1 Description of Simulation

Following reference [2], we simulated the posterior distributions of 40 targets. We set the detection probability to be  $P_d^1$  for the system 1 and  $P_d^2$  for the system 2 for all target states. For each of the 40 targets we made an independent draw with success probability  $P_d^1$  to determine if it is detected by system 1 and another independent draw with probability of success  $P_d^2$  to determine if it is detected by system 2.

The target state space is 6D position-velocity. The track posteriors are Gaussian in position-velocity space. We specify base covariances  $\mathbf{V}_1$  and  $\mathbf{V}_2$  for the system 1 and system 2 tracks respectively. The target density  $\rho\bar{v}$  was chosen to equal 5 targets per  $3\sigma$  hyper volume corresponding to the covariance matrix  $\mathbf{V}_1 + \mathbf{V}_2$ . The true position of each target was chosen from the uniform density  $\rho$  over a region of volume  $H$  such that  $\rho\bar{v}H = 40$ . To obtain the posterior position-velocity distribution of a system 1 target we randomly varied the lengths of the axes of the base covariance  $\mathbf{V}_1$  over plus or minus 10% and randomly rotated the axes over plus or minus 1 degree to produce the posterior covariance. The mean of the target state distribution was obtained by taking a draw from the Gaussian distribution with mean 0 and covariance  $\mathbf{V}_1$  and then adding this draw to the actual target state. The same procedure was followed for system 2 targets using the base covariance  $\mathbf{V}_2$ .

To test the performance of the fixed versus adaptive algorithms, we generated 100 sets of tracks for system 1 and system 2 using the procedure described above. For each set of tracks we applied the MAP algorithm and the fixed threshold algorithm using 0.1, 0.01, 0.003, and 0.001 significance levels to determine the fixed threshold  $\bar{\chi}^2$ . For each set we computed the fraction of correct matches (associations). We then computed the average fraction of correct matches over the 100 sets. Recall that a correct match occurs if a track from system 1 is correctly associated with a track from system 2, or when a track from system 1 is correctly **not** matched with a track from system 2 and vice versa.

#### 3.2 Results

For the first set of results, we set  $P_d^1 = P_d^2$  and let the detection probability vary from 0.9 to 0.5. The results are shown in Figure 1. One can see that the performance of the MAP algorithm is consistently as good or better than any of the fixed threshold algorithms. The performance of the MAP algorithm dominates all the fixed threshold algorithms for all detection probabilities. This is a striking demonstration of the superiority of the adaptive threshold algorithm over fixed threshold algorithms.

Note that the standard fixed threshold algorithm, which is based on the 0.003 significance level, does substantially worse than MAP except when the detection probability is 0.9. In addition the fixed threshold algorithm corresponding to significance level 0.01 is consistently better than the one for the 0.003 significance level.

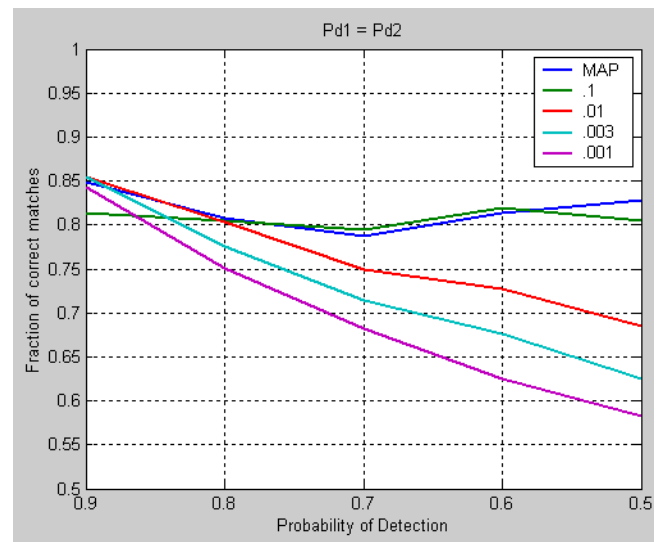


Figure 1. Comparison of the Adaptive vs Fixed Threshold Algorithms when  $P_d^1 = P_d^2$ .

In [2] Mori and Chong compared the performance of fixed threshold algorithms using a simulation similar to ours in which the number of targets detected on both systems was taken to be 80% of the actual targets present. They observed a similar effect. Namely, that using the 0.1 significance level threshold produced better results than the 0.003 significance level threshold. They explained the result by noting that the smaller significance level (higher threshold) tends to force more associations between tracks that should not have been matched. However, in their results, MAP did not perform as well as the fixed threshold algorithm using the using the 0.1 or 0.03 significance level thresholds. MAP did perform better than algorithms using the 0.01 and 0.001 significance level thresholds.

We discussed this discrepancy with the authors of [2], but were not able to determine why their results differed from ours. Since the software code used to perform the

simulations in [2] was not available at the time we had the discussions, we were not able to determine the cause of the differences.

For the second set of results, we considered situations in which  $P_d^1 \neq P_d^2$ . We set  $P_d^1 = 0.9$  and let  $P_d^2$  vary from 0.9 to 0.5. The results are shown in Figure 2. Again one can see that the adaptive threshold performs as well or better than any of the fixed threshold algorithms and that the 0.003 significance-level fixed threshold algorithm is suboptimal except when  $P_d^1 = P_d^2 = 0.9$ .

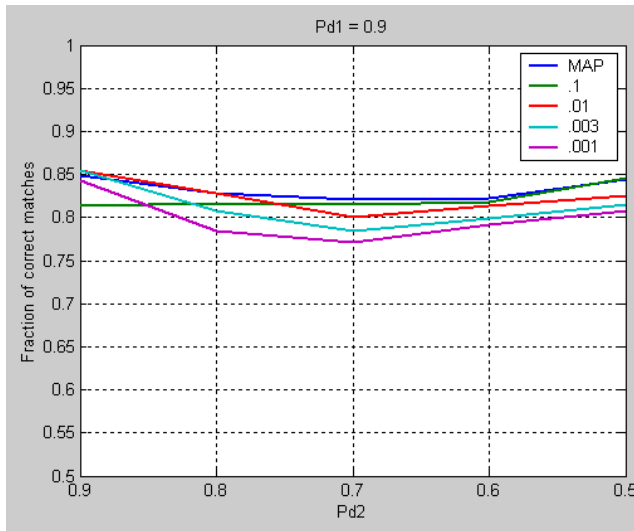


Figure 2. Comparison of the Adaptive vs Fixed Threshold Algorithms when  $P_d^1 \neq P_d^2$ .

## 4 Adjustments to the Adaptive Threshold

Recall that MAP is not designed to maximize fraction of correct associations. It produces the association with the highest posterior probability so there is reason to believe that one can do better than MAP when using that measure of performance. With this in mind we considered the modifications of MAP that are obtained by adding a constant to the adaptive threshold from MAP. This produces an adjusted adaptive threshold.

Specifically, we modified the adaptive threshold  $A_{ij}$  in (10) by adding a constant value  $\hat{A}$  to obtain the adjusted adaptive threshold  $\hat{A}_{ij} = A_{ij} + \hat{A}$ . We call  $\hat{A}$  the additional threshold. We then used the same simulated data as described above for the  $P_d^1 = P_d^2 = 0.9$  case but applied the MAP algorithm with the adjusted adaptive threshold. We let the additional threshold values vary from -10 to +10. Figure 3 shows the results. For this discussion, we consider solely the metric-only case, the black line in Figure 3. One can see that an additional threshold between 1 and 2 produces slightly better results than no adjustment,  $\hat{A} = 0$ . (The lines for SNR 1 through 64 refer to the effect of adding certain feature information to the metric

information. They do not concern us here.) For this case, using  $\hat{A} = 0$  produced 99% or better of the correct matches that are obtained at the optimum threshold adjustment.

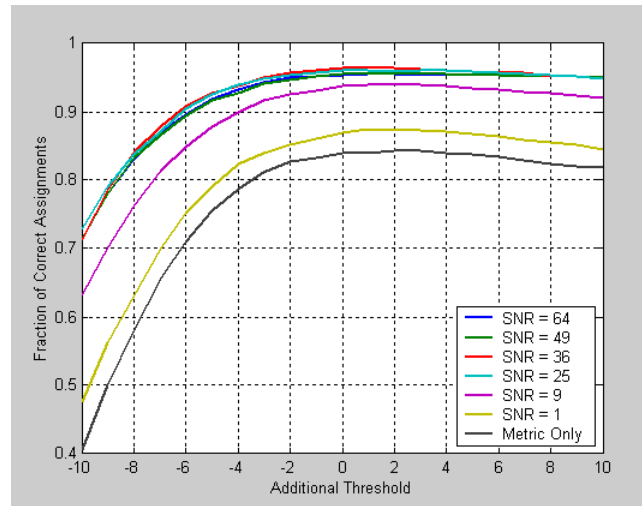


Figure 3. Results of Threshold Adjustment when  $P_d^1 = P_d^2 = 0.9$ . The Adjusted Adaptive Threshold is  $A_{ij} = A_{ij} + \hat{A}$  where  $\hat{A}$  is the Additional Threshold.

### 4.1 Additional Simulations with $P_d^1 = P_d^2$

In additional simulations we varied the mean number of targets, the target density  $\rho$ , and the detection probabilities  $P_d^1$  and  $P_d^2$ . In these runs we used only the 3D position information for the target state. Figures 4 – 6 show the results of varying the number of true targets and the target density when  $P_d^1 = P_d^2 = 0.9, 0.7, \text{ and } 0.5$ .

Figure 4 shows that for  $P_d^1 = P_d^2 = 0.9$ ,  $\hat{A} = 0$  performs almost as well as any other adjustment for a range of target densities. Figures 5 and 6 compare performance of the additional thresholds when  $P_d^1 = P_d^2 = 0.7$ , and 0.5.

In Figures 5 and 6, we see that performance of the algorithm corresponding to  $\hat{A} = 0$  degrades somewhat compared to negative additional thresholds at high target densities. Recall that higher thresholds tend to force associations. It appears that, in high density cases, reducing the threshold produces an advantage. However, the target densities are very high.

### 4.2 Additional Simulations with $P_d^1 \neq P_d^2$

Figures 7 – 9 show the results of considering unequal detection probabilities for the two systems under same conditions as in section 4.1 but limited to the case of 40 targets and a target density of 5 objects per 3sigma hyper ellipsoid.

Looking at Figures 7 – 9 we see that in most cases no threshold adjustment produces results almost as good as or better than any adjusted adaptive threshold.

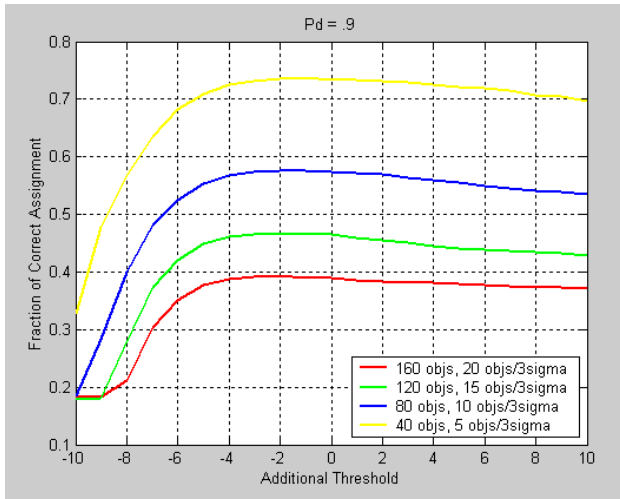


Figure 4. Adjusted Threshold Performance,  $P_d^1 = P_d^2 = 0.9$

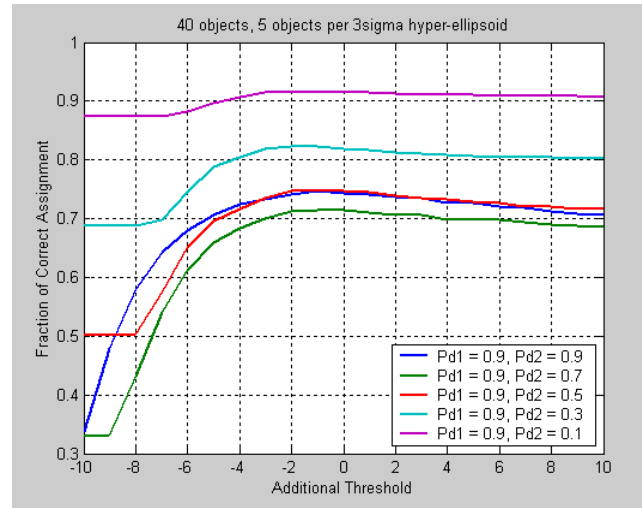


Figure 7. Adjusted Threshold Performance when  $P_d^1 = 0.9$

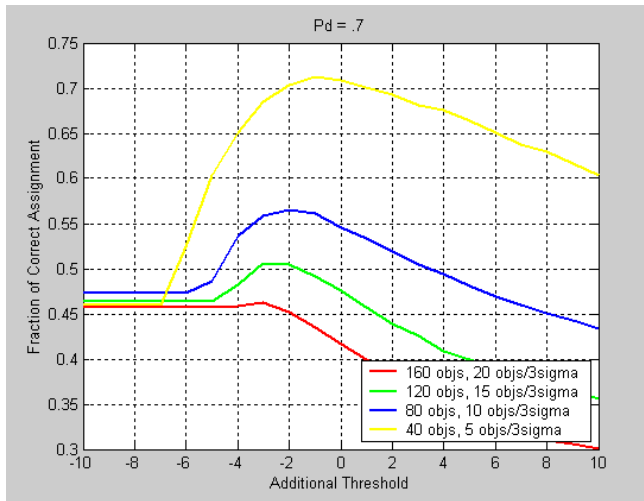


Figure 5. Adjusted Threshold Performance,  $P_d^1 = P_d^2 = 0.7$

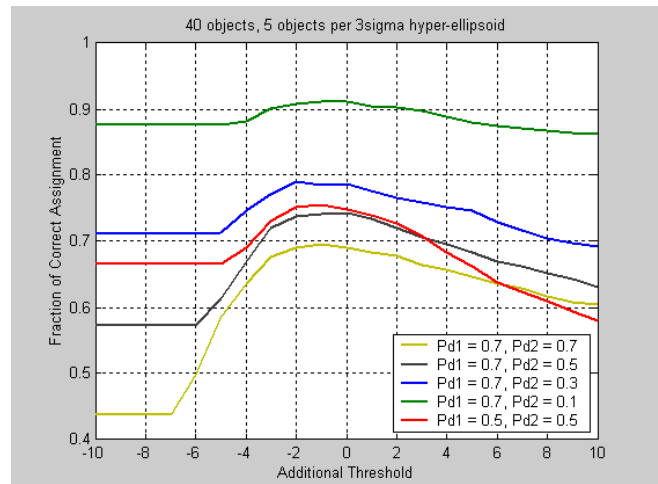


Figure 8. Adjusted Threshold Performance when  $P_d^1 \neq P_d^2$

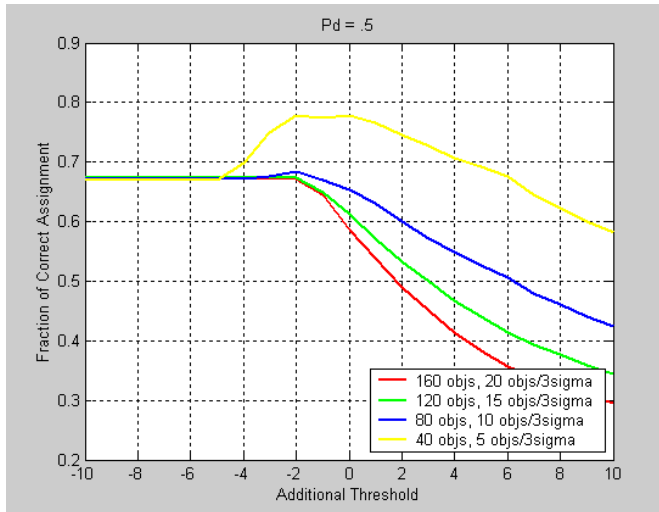


Figure 6. Adjusted Threshold Performance,  $P_d^1 = P_d^2 = 0.5$

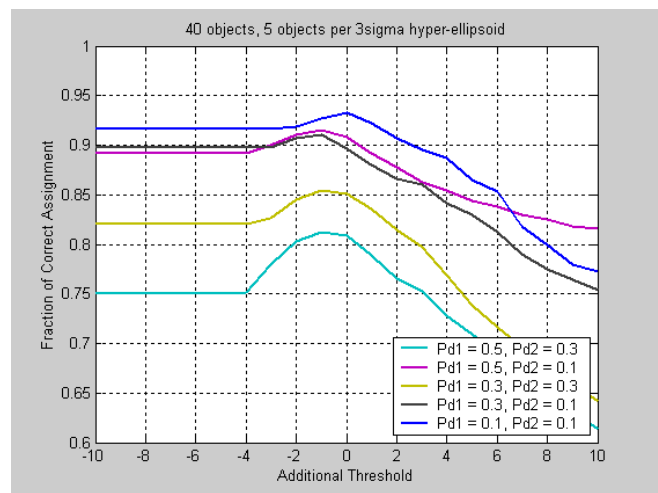


Figure 9. Adjusted Threshold Performance when  $P_d^1 \neq P_d^2$

## 5 Conclusions

In this paper we have compared the performance of the MAP association algorithm to the classical fixed threshold algorithm and to adjusted adaptive threshold algorithms in terms of fraction of correct associations. These comparisons were made when the target state distributions are Gaussian. In this case the MAP algorithm can be thought of as a version of the fixed threshold algorithm with an adaptive threshold. Simulation results were presented in section 3 that show the MAP algorithm performs as well as or better than any fixed threshold algorithm. In section 4 simulation results were presented that show the MAP algorithm performs (almost) as well or better than adjusted adaptive threshold algorithms except in high target density situations.

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