T2T and M2T Association with Combined Hypotheses

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This paper presents a procedure to combine the top association hypotheses generated in a track-to-track (T2TA) association problem. The standard procedure for such problems consists of keeping only the most likely hypothesis, but the extra information carried by other hypotheses remains unused. The proposed combination method allows for the extraction of this information in an efficient way, improving over a similar method [5], providing system tracks that account for the correlation ambiguity. This method will prove useful when there is track contention (correlation ambiguity), and the information carried by the best hypothesis alone renders optimistic estimates. As a result of using this method, both better estimates (fused system tracks) are obtained and an estimate of the difficulty of the association problem is obtained based on the aggregation of neighboring tracks. In this work we consider two applications, one consisting of a T2T fusion (T2TF) and a dynamic tracking problem where measurement-to-track association (M2TA) hypotheses from a multiple hypothesis tracker (MHT) are combined. The comparison of results from the proposed procedure vs. the standard approach indicate that the latter can be improved upon in scenarios with significant association ambiguities.

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1. INTRODUCTION

The types of problems in data association for tracking are (i) measurement-to-measurement association (M2MA), i.e., track initiation, (ii) measurement-to-track association (M2TA), i.e., track continuation, (iii) track-to-track association (T2TA), for track fusion. Among the M2TA algorithms, it is well known that the Multiple Hypothesis Tracker (MHT) performs, due its time window, much better than other methods, such as nearest neighbor or PDA (which have a time window of depth 1) when there is heavy clutter or track ambiguity, i.e., when tracks are very close or cross each other. The idea behind MHT is to maintain several track-to-measurement association hypotheses over its time window, some of which may have low likelihood but might later become the most likely after some frames of measurements have been added. In general, however, only the best hypothesis is retained when obtaining the results of the tracker at a particular time, thus neglecting the information contained in the subsequent hypotheses. In the T2TA problem, the use of the approach [3] yields only the most likely association, in a manner similar to the MHT.

This paper presents methods to combine the top hypotheses generated in M2TA and T2TA problems, extending the results from [5] which proposed the Coordinated Presentation (CP). The T2TA problem consists of estimating the parameters of interest for an unknown number of targets, using the track lists obtained by S observers, which are received by a fusion center (FC). The fusion center generates several association hypotheses, each of them formed by associating tracks (the list elements) into S-tuples, using an m-best multidimensional assignment (MDA) algorithm based on Lagrangean relaxation [8]. The goal is to combine those hypotheses to obtain a better estimate than the one calculated using the top hypothesis alone. The best hypothesis estimate has the disadvantage of being optimistic, especially when there is track ambiguity, i.e., tracks are close to each other relative to their covariances (small normalized distance). For example, if the second best hypothesis has a likelihood close to the best, it should be accounted for: the covariances calculated assuming the best hypothesis is guaranteed to be true are optimistic because the second best might be the true one. The use of the top m hypotheses to asses the quality of the association was proposed in [6]. There the best assignment is used to update only if all of its association S-tuples are substantially present in the subsequent hypotheses. If some of them do not appear in subsequent hypothesis with high probability, an extended window is used to hopefully clear up the problem. Our approach is to combine the hypotheses to avoid incurring any delay.

The M2TA problem considered requires the assignment of noisy measurements from a single radar arising from N targets. At time k window containing S-1 frames of data (lists of measurements) and the list of accepted tracks from time $k - S + 1$, i.e, a total of S lists is used to generate the m-best association hypotheses to be combined. After the new track estimates are obtained, the accepted tracks are extended to the next frame ($k - S + 2$), and a new frame (from time $k + 1$) is incorporated, and the process repeated with a total of S lists, shifted one step forward.[1]

The paper is organized as follows: Section 2 discusses the procedure to combine the hypotheses in a T2TA problem, and compares it to the method in [5]. Section 3 presents a track-to-track association scenario and shows the results of applying the algorithms discussed previously. M2TA is considered in Section 4. Finally, in Section 5 conclusions are drawn based on the results obtained.

2. COMBINATION OF THE m-BEST HYPOTHESES IN T2TA

Each of the m hypotheses obtained by the MDA algorithm is formed by N_i, $i = 1,\ldots,m$ S-tuple associations, which we will simply call 'associations.' Our goal is to combine these top hypotheses in a combined hypothesis (discussed in detail in Sec. 2.2, from which the combined (system) track estimates are better than the best hypothesis alone.

The hypothesis combination consists of two subproblems:

- Finding similar associations (deemed to represent the same target) from different hypotheses to form *combinable association sets* (called $\mathcal{C}$-sets for brevity), which is a data association/combination problem.
- Combination of these sets into a unique estimate, to provide both an estimate of the number of targets present, as well as estimates of the parameters of interest and their covariances.

To be able to weight the contribution of each hypothesis to the final estimate, the probability of a hypothesis needs to be computed. This probability is obtained from the costs of the hypotheses. The cost of hypothesis i is the sum of the costs of the N_i associations that comprise it. These association costs are based on the negative log likelihood ratio (NLLR), that is, the negative of the logarithm of the likelihood function of the set of tracks from an association having common origin divided by the likelihood function of not having a common origin, given by

$$\ell_i \stackrel{\Delta}{=} -\ln \mathcal{L}(H_i) = -\sum_{j=1}^{N_i} \ln(\Lambda_{ij}/\Lambda_{0j}), \qquad i = 1,\ldots,m \tag{1}$$

where $\mathcal{L}(H_i)$ is the LR of H_i, Λ_{ij} is the likelihood function of the association tuple j from hypothesis i having common origin, and Λ_{0j} is the likelihood function of this tuple not having common origin. The probability of hypothesis i is obtained by normalization of these costs as

$$P\{H_i\} = \frac{e^{-\ell_i}}{\sum_{j=1}^{m} e^{-\ell_j}}, \qquad i = 1,\ldots,m. \tag{2}$$

For this to be meaningful, the probability of the mth hypothesis should be much smaller than the highest one, so the hypotheses left out can be deemed to have negligible probability.

Thus, for purposes of association combination, each association j in hypothesis i is assigned two numbers:

1. A value corresponding to the association weight equal to $P\{H_i\}$, to be used to quantify the number of tracks in each $\mathcal{C}$-set.
2. A value corresponding to the probability of an association, called combination weight. This value is defined in a similar way to the probability of a hypothesis (2) within a $\mathcal{C}$-set, but using the NLLR of the association A_{ij} instead of the likelihood of the complete hypothesis, as detailed below in (4). This probability is needed at the fusion center for weighting the contribution of each association in a $\mathcal{C}$-set to the overall estimate from such a set.

The association weights are used to define the total probability of a $\mathcal{C}$-set. For each $\mathcal{C}$-set an indicator function is defined, which is one when association A_{ij} is included in $\mathcal{C}_k$, namely,

$$\chi_{ij}(\mathcal{C}_k) = \begin{cases} 1 & A_{ij} \in \mathcal{C}_k \\ 0 & \text{otherwise} \end{cases}. \tag{3}$$

Using this indicator function, the total probability of a $\mathcal{C}$-set is defined in terms of the association weights as

$$P\{\mathcal{C}_k\} = \sum_{i,j} \chi_{ij}(\mathcal{C}_k) P\{H_i\}. \tag{4}$$

2.1. $\mathcal{C}$-set Generation

The criterion for combining associations in a $\mathcal{C}$-set is based on the number of common reports (tracks in the T2TA case, measurements in the M2TA case) shared by associations in the set of all associations

$$\mathcal{A} = \{A_{ij},\ i = 1,\ldots,m,\ j = 1,\ldots,N_i\}. \tag{5}$$

This follows the reasoning from the Coordinated Presentation (CP) approach [5]. In that work a *minimal similarity criterion* is used, i.e., if two associations share one or more elements (tracks or measurements), they are deemed as coming from the same origin and thus are included in the same $\mathcal{C}$-set. This approach will be shown to be prone to incorrect combinations.

[1]In T2TA, S is the number of observers, while in M2TA S is the time depth of the window. In both cases one has S lists and the dimension of the assignment is S.

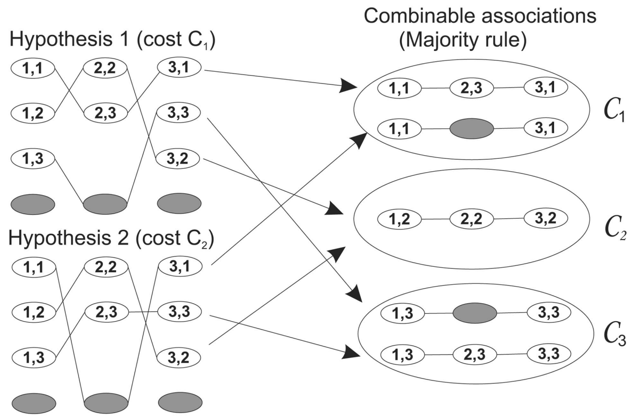

Fig. 1. Associations from 2 hypotheses in a 3 target and 3 sensor case (solid elements correspond to dummies—missing elements in an association). List elements are indexed by number pairs corresponding to (sensor, element). $\mathcal{C}$-set formation criterion is majority rule.

In the present work, the rules used for defining $\mathcal{C}$-sets are:

- Each of the associations in the best hypothesis initializes a $\mathcal{C}$-set.
- Associations are added to these $\mathcal{C}$-sets using a *K-similarity criterion*, that is, if they share at least K common elements with an association already in the $\mathcal{C}$-set. In general K will be taken as $\lfloor S/2 \rfloor + 1$, where S is the number of lists, thus the criterion reduces to a *majority rule criterion*.
- If an association passes the K-similarity criterion for more than one $\mathcal{C}$-set, these are merged into a single one including all the associations in the overlapping $\mathcal{C}$-sets.

Other rules for inclusion to a $\mathcal{C}$-set can be used, as normalized distance between tracks, or normalized distance with respect to a centroid, but are not considered in the sequel.

Fig. 1 shows a simple case with 2 hypotheses, where 3 targets are present and 3 sensors provide tracks. If the $\mathcal{C}$-sets are formed based on associations that satisfy the majority rule, then there will be 3 such sets. Only one of them, $\mathcal{C}_2$ is formed by the same association in each hypothesis, the other are composed of hypotheses that share 2 elements with common origin.

2.2. Combination in a $\mathcal{C}$-set

2.2.1. Estimation of the number of targets in a $\mathcal{C}$-set

Once the $\mathcal{C}$-sets are generated, the combination of the associations in each of them needs to be done. Also, the estimation of the number of true target(s) from which the tracks in each $\mathcal{C}$-set originated is performed, using the total probability of the hypotheses in the $\mathcal{C}$-set. Possible situations are

1. Exactly the same association is present in all hypotheses. In this case a set will contain only this association, and the total probability of such set will be $P\{\mathcal{C}_k\} = \sum_{i=1}^{m} P\{H_i\} = 1$, indicating that all the associations correspond to a unique target. Such a case indicates the high quality of the association, and hence it can be trusted and presented as is.
2. At least one different association satisfying the common set inclusion condition is present in each hypothesis. In this case, the $\mathcal{C}$-set will contain different associations, and the total probability $P\{\mathcal{C}_k\}$ of such a set can be greater than 1, indicating that the combined estimate represents closely spaced tracks.[2]
3. Not all the hypotheses contribute to a $\mathcal{C}$-set. In this case, the total probability of the $\mathcal{C}$-set will be smaller than 1. This can happen when there are associations containing false tracks, or few tracks, thus having not enough in common with established sets.

In the second case, some associations will K-overlap some other associations, and two or more associations from the same hypothesis may be included in the set. If the total probability of the set is higher than 1, this indicates that there is more than one true track in such a set, which now represents a *cluster of targets*. This cluster is considered to contain as many targets as the (rounded up) total probability $P\{\mathcal{C}_k\}$. A unique estimate that plays the role of a centroid can be obtained from such a cluster by combining the estimates arising from each association in it. If the total probability is close to 1, the combination of the associations in the cluster should provide a better estimate of the target it represents, compared to the one provided by the best hypothesis alone. This is discussed in more detail later.

2.2.2. Combination of associations in a $\mathcal{C}$-set

The combination of the associations in a $\mathcal{C}$-set can be done using the CP method from [5], which we call the Coordinated Presentation (CP) Mixture Approach. This combines the estimates of these association using the association weighting to define the combination probability. Our approach, called Direct Mixture (DM), will use a different—likelihood ratio based—weighting, defined before as combination weighting.

CP Mixture (CP) Approach

For each association in a $\mathcal{C}$-set the following events are defined:

$$A_i = \{\text{set } X_i \text{ of } n_i \text{ tracks are associated}\} \tag{6}$$

where $X_i = \{\hat{x}^{i_j}, P^{i_j}\}_{j=1}^{n_i}$ is the set of estimates and covariances contained in association i. Suppose that the set of all the N associations in a $\mathcal{C}$-set A is

$$A = \{A_i,\ i = 1,\ldots,N\}. \tag{7}$$

[2]Suppose two hypotheses such that $P\{H_i\} = .5$, with two associations each. H_1 contains $\{M_1^1–M_2^2\}$ and $\{M_2^1–M_1^2\}$, while H_2 contains $\{M_1^1–M_1^2\}$ and $\{M_2^1–M_2^2\}$, where M_i^j corresponds to element i of list j. If the set inclusion condition is to have at least 1 common element, then the $\mathcal{C}$-set will be $\{\{M_1^1–M_2^2\},\{M_2^1–M_1^2\},\{M_1^1–M_1^2\},\{M_2^1–M_2^2\}\}$, which has $P\{\mathcal{C}\} = 2$.

The mixing probability p_i for association event A_i is taken as the probability of the hypothesis k_i it comes from, $P\{H_{k_i}\}$, as defined before.

For each association event A_i, the combined "system" state estimate and covariance are $\hat{x}^i$ and P^i. The combination of these estimates is done using the mixture pdf

$$p(x \mid A) = \frac{1}{\sum_{j=1}^{N} p_j} \sum_{i=1}^{N} p(x \mid A_i) p_i. \quad (8)$$

The mean and covariance of this mixture are

$$\hat{x} = \frac{1}{\sum_{j=1}^{N} p_j} \sum_{i=1}^{N} \hat{x}^i p_i \quad (9)$$

$$P_{\hat{x}} = \frac{1}{\sum_{j=1}^{N} p_j} \sum_{i=1}^{N} (P^i + \hat{x}^i (\hat{x}^i)') p_i - \hat{x}\hat{x}'. \quad (10)$$

Direct Mixture (DM) Approach

Using the previous definition of event A_i, the likelihood ratio (LR) of event A_i can be written as

$$\mathcal{L}(A_i) = \frac{\Lambda(A_i)}{\mu^{n_i - 1}} \quad (11)$$

where $\Lambda(A_i)$ is the likelihood function (LF) of association event A_i—that X_i have common origin—and μ^{n_i-1} is the LF of not having common origin [3]. The term μ is the density of extraneous measurements, defined as n_{ex}/V, where n_{ex} is the number of extraneous tracks, and V is the volume of the state space corresponding to the surveillance region.

The mixing probability of association i within its $\mathcal{C}$-set can be taken as

$$\tilde{p}_i = \frac{1}{c} \mathcal{L}(A_i) \quad (12)$$

where

$$c = \sum_{i=1}^{n} \mathcal{L}(A_i). \quad (13)$$

Using (dimensionless) likelihood ratios makes it possible to have associations with different n_i in a $\mathcal{C}$-set.

For each association we can obtain the combined (system) state estimate and covariance

$$\hat{x}^i = \varphi(X_i \mid A_i) \quad (14)$$

$$P^i = \Phi(X_i \mid A_i) \quad (15)$$

according to [3].

The combination of these estimates is also done using a mixture, with different weights $\tilde{p}_i$ based on their individual likelihood ratios (12), rather than based on the hypotheses probabilities. The mixture pdf is

$$p(x \mid A) = \sum_{i=1}^{N} p(x \mid A_i) \tilde{p}_i \quad (16)$$

with mean and covariance

$$\hat{x} = \sum_{i=1}^{N} \hat{x}^i \tilde{p}_i \quad (17)$$

$$P_{\hat{x}} = \sum_{i=1}^{N} (P^i + \hat{x}^i (\hat{x}^i)') \tilde{p}_i - \hat{x}\hat{x}' \quad (18)$$

where the estimates coming from the combination of X_i in (14),(15) are given by[3]

$$P^i = \left(\sum_{j=1}^{N} (P^{i_j})^{-1} \right)^{-1} \quad (19)$$

$$\hat{x}^i = P^i \left(\sum_{j=1}^{N} (P^{i_j})^{-1} \hat{x}^{i_j} \right). \quad (20)$$

3. SIMULATION RESULTS

The results presented in this section correspond to the track-to-track association problem from [1], where missile launch event parameters are estimated at a fusion center collecting track reports from several observers. The scenario consists of a set of N_s observers which transmit track/event reports to a fusion center through a particular (real-world based) communication network among one of N_n networks. The network discards the observer's track identity (ID), replacing it by a network-generated ID and the observer ID, thus losing the information on the origin of the tracks sent by each observer. The FC has to associate the common origin (same event) tracks from each observer, then associate and fuse the most recent common origin tracks across the observers. For more details, see [1].

3.1. Problem Description

The parameters to be estimated are positions in x, y, heading and launch time. The surveillance area is $[0, 10000]$ distance units both in x and y, $[0, 30]$ degrees for the heading, and $[0, 10]$ units of time for the launch time. We assume that the sensors used have enough spatial resolution to detect the events as unique, and also that the time difference between launches is enough to recognize them as different events. Track/event reports are produced by 4 observers, and are transmitted to a fusion center for processing. These reports are based on observations corrupted by Gaussian noise with a standard deviation of 800 in both x and y coordinates, 10 degrees for the heading and 3 units of time for the launch time. Fusion is performed every 20 units of time, over a time span of 200 time units. The initial frames of data (reports) have larger variance (because they are based on fewer measurements) than the latter ones, which are about 5 times more accurate due to the processing of

[3]Assuming as in [1] that the track errors are uncorrelated.

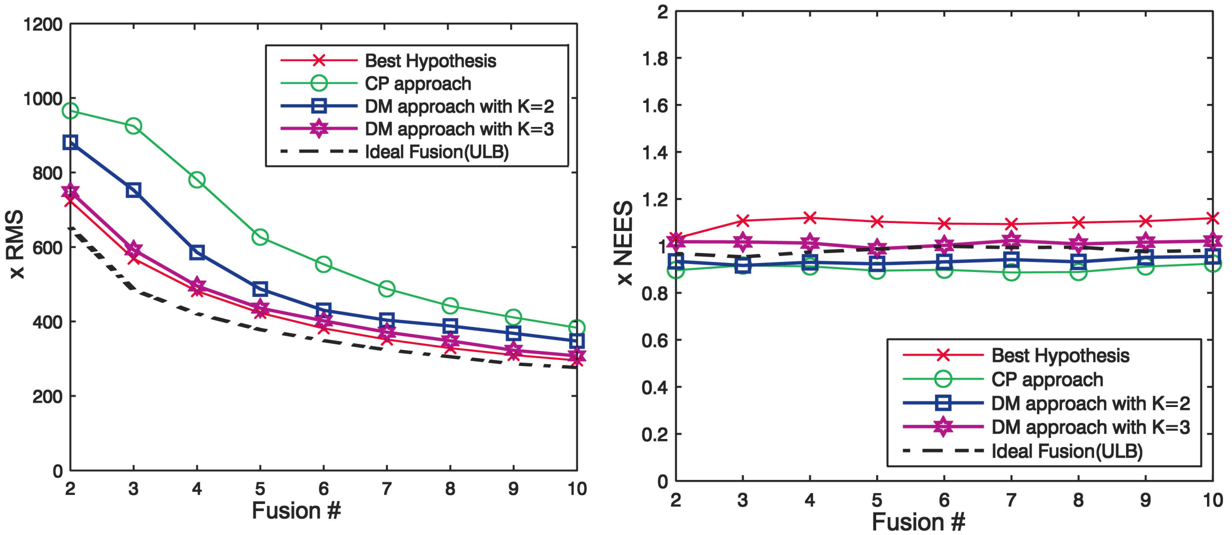

Fig. 2. RMS and NEES in the x coordinate. The normalization is done w.r.t the obtained covariance from the fuser for each estimate.

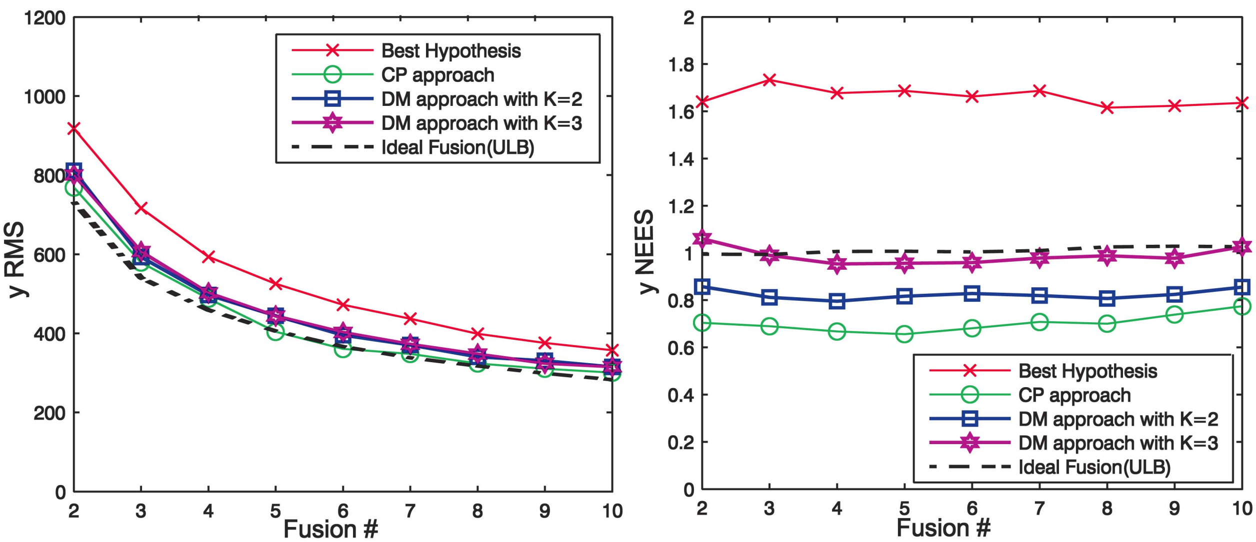

Fig. 3. RMS and NEES in y coordinate. The normalization is done w.r.t the obtained covariance from each estimate.

more measurements. Thus, we expect more tracks contending at the beginning and this contention should be resolved for most cases by the final time.

Results shown are based on 500 Monte Carlo runs. In each run, the RMS error is calculated for the CP and DM association algorithms using the combined m-best hypotheses, for the single best hypothesis, as well as for the true association (known only in simulations) to be used as a reference. Also the normalized estimation error squared (NEES) [3] is obtained for each. The total number of $\mathcal{C}$-sets and the number of $\mathcal{C}$-sets with total probability 1 will be used to quantify the degree of aggregation of the track estimates.

3.2. Scenario

We consider a scenario with 8 launches uniformly distributed in a line parallel to the x axis. The distance between neighboring launches is 800 meters. For this case, missasociation and clustering is expected to happen often for the initial time, while towards the end time this effect should decrease. Results for the CP approach as well as our DM approach with $K = 2,3$ are shown in Figs. 2 and 3 for the x and y coordinates, respectively. These figures contain five curves, one corresponding to the best hypothesis, a second one that corresponds to doing the ideal association, i.e., using the true association indexes,[4] and other three corresponding to the m-best hypotheses combination methods.

From the NEES values it can be seen that for this problem the best hypothesis estimate is optimistic for both coordinate estimates.

The geometry of the problem results in different behavior for the estimates in x and y coordinates. For the y coordinate estimation, the aggregation of tracks does improve the estimate, as these tracks have varia-

[4] This curve corresponds to the unattainable lower bound (ULB).

TABLE I
Average Number of $\mathcal{C}$-sets and Average Total Number of Targets Reported by Each Method

# of single target $\mathcal{C}$-sets/# of cluster $\mathcal{C}$-sets/# of targets									
Fusion	2	3	4	5	6	7	8	9	10
Ideal	NA/NA 6.64	NA/NA 7.68	NA/NA 7.76	NA/NA 7.84	NA/NA 7.84	NA/NA 7.92	NA/NA 7.92	NA/NA 8.00	NA/NA 8.00
CP	0.82/1.02 6.29	0.91/1.04 7.84	1.22/1.08 7.94	1.30/.98 7.96	1.38/1.10 7.97	1.32/1.05 8.0	1.44/1.12 8.0	1.75/1.12 8.0	1.87/1.13 8.0
DM with $K = 2$	1.12/1.23 6.24	1.28/1.21 7.76	1.04/1.12 7.92	1.34/1.07 7.92	1.77/1.23 7.92	1.98/1.17 8.0	2.15/1.51 8.0	2.84/1.27 8.0	3.11/1.37 8.0
DM with $K = 3$	2.42/1.18 6.56	2.54/1.73 7.84	3.21/1.45 7.84	3.56/1.41 7.92	3.63/1.85 8.0	3.88/1.15 8.0	4.01/1.42 8.0	4.23/1.27 8.0	4.40/1.36 8.0

tion around the same value. On the other hand, for the estimates in the x coordinate, the aggregation decreases the quality of the estimate, as the different tracks combined possess different x coordinate values. In Fig. 2 the error in x is shown for all the methods considered. It can be seen that the CP approach does provide very inaccurate x estimates as a result of its loose set inclusion condition, which forces the combination of insufficiently similar tracks in the same $\mathcal{C}$-set. The proposed DM combination scheme using $K = 2$ does improve over the CP case, but only marginally. The more stringent condition $K = 3$ provides enough discrimination so as to reduce the RMS error to the level of the top hypothesis alone (but with consistency as good as the ideal). Overall, the methods provide consistent (or nearly so) covariance calculations, as can be seen from the normalized error plots. Fig. 3 shows the error in estimation of the y coordinate values. As opposed to the x estimates, all the methods using the top m hypotheses provide good estimates, as explained before, although the CP method does report a slightly pessimistic variance estimate. On the other hand, the top hypothesis alone does not only provide a more inaccurate estimate, it also lacks consistency, reporting very optimistic results, up to 80% off from its correct value.

It can be concluded that the proposed DM combination method with $K = 3$ is able to combine similar hypotheses effectively and keep enough unique track sets. As a result, the estimates in the x coordinates are as good as the ones provided by the top hypothesis alone, and much better than the estimates obtained by the other two combination schemes. For the y coordinate estimates both the estimation accuracy as well as consistency are improved over the top hypothesis alone, while the results for the other two schemes are comparable.

Table I shows the number of $\mathcal{C}$-sets with unity total probability,[5] i.e, single target, and the number of cluster $\mathcal{C}$-sets (with multiple targets), as well as the total number of targets declared by each method.

[5]These are the $\mathcal{C}$-sets with total probability between 0.5 and 1.5.

4. COMBINATION OF THE m-BEST HYPOTHESES IN MHT

The M2TA combination problem is very similar to the T2TA combination problem, differing mainly in the way the association costs are calculated. In this problem, the first list in the sliding window MHT implementation consists, at the current time k, of the track estimates at time $k - S - 1$ and the following S-1 lists of measurements from frames $k - S + 2, \ldots, k$. Thus, each of the S-tuple associations is formed by a track and S-1 measurements. The incremental cost of such an association is obtained based on the innovation and innovation pdf of the last measurement. The likelihood ratio for continuation of track t with measurement z_j is [2]

$$L_{tj} = \frac{f_t(z_j(k))}{\lambda_\theta} P_{D_t}(k) \tag{21}$$

where $f_t(z_j(k))$ is the pdf of the predicted measurement for track t and λ_θ represents the density of extraneous measurements.

The likelihood ratio in case a measurement is not associated to track t is

$$L_{t0} = 1 - P_{D_t}(k). \tag{22}$$

Thus, considering independent measurement errors, the cost of an association is obtained by summing up the negative of the logarithm of the likelihood ratios involved, calculated sequentially by updating the track from frame 1.

After the m-best hypotheses have been calculated, the $\mathcal{C}$-set generation is done following the same procedure outlined in Subsection 2.1. Associations from different hypotheses sharing K elements are to be combined, and an estimate of the number of tracks in the obtained centroid can be calculated based on the hypothesis probability.

4.1. Track Combination

The combination of track estimates, which will be used in the following cycle of the algorithm, requires careful analysis. The concept is that out of the S-tuple associations to combine, only the estimates corresponding to the first measurement to track association should be taken into account. These combined tracks, originating from elements in the first and second frame, form the new (combined) track estimate, with combination weights based on the cost of the complete association. A better understanding of the combination is obtained by looking first at the way information is processed in the conventional MHT, and then looking at the proposed approach.

4.1.1. Conventional Implementation

From the initial time, the tree of associations is expanded until time S (except for applying steps to reduce the number of branches of the tree). At time S one has the most probable hypothesis, designated by the index $l^*(S)$, as

$$\Theta^{S,l^*(S)} \stackrel{\Delta}{=} \Theta^{[1,S],l^*(S)} = \{\theta(1)^{l^*(S)}, \Theta^{[2,S],l^*(S)}\} \tag{23}$$

written decomposed into its initial part $\theta(1)^{l^*(S)}$ from time 1, and its part $\Theta^{[2,S],l^*(S)}$ from the interval $[2,S]$.

At $k = S+1$ the hypotheses to be considered are

$$\Theta^{S+1,l} = \{\theta(1)^{l^*(S)}, \Theta^{[2,S+1],l}\} \tag{24}$$

i.e., all the hypotheses have a frozen common root behind the window $[2,S+1]$, of length S.

In general, at time $k > S$, the hypotheses to be considered are

$$\Theta^{k,l} = \{\Theta^{[1,k-S],l^*(k-1)}, \Theta^{[k-S+1,k],l}\} \tag{25}$$

i.e., behind the window $[k-S+1,k]$, all the associations are frozen.

4.1.2. Implementation with Combined Hypotheses

The new alternative is to use a *combination* of the hypotheses behind the window, rather than only the most likely one.

This is accomplished as follows. Let the combined hypothesis at time 1 based on the data at time S be

$$\bar{\theta}(1) \stackrel{\Delta}{=} \bar{\theta}[\theta(1)^{i,S},\ i = 1,\ldots,n_1] \tag{26}$$

where $\theta(1)^{i,S}$ is hypothesis i based on the data at time S, and n_1 is the number of hypotheses at time 1 used in the combination.

This leads to the set of track estimates at time 1

$$X(1 \mid 1) \stackrel{\Delta}{=} \{\hat{x}^t[1 \mid 1,\bar{\theta}(1)]\}_{t=1}^{n_t(1)} = \kappa[\hat{x}[1 \mid 1,\theta(1)^{i,S}],\ i = 1,\ldots,n_1] \tag{27}$$

where t is the target index and κ is the combination function. This will become the sufficient statistic (initial condition) to be used in forming the new hypotheses in the next window $[2,S+1]$.

At time $S+1$, the hypotheses can therefore be written as

$$\Theta^{S+1,l} = \{X(1 \mid 1), \Theta^{[2,S+1],l}\} \tag{28}$$

which replaces (24). Similarly, for general $k > S$, (25) is replaced by

$$\Theta^{k,l} = \{X(k-S \mid k-S), \Theta^{[k-S+1,k],l}\}. \tag{29}$$

The resulting algorithm is designated as Top m Hypotheses Tracker (TmHT).

4.2. Simulations

The results presented in this section correspond to a simple M2TA problem where $N = 2$ targets move in formation, following parallel straight line trajectories. The purpose of the simulations is to compare the performance when the targets are close to each other, such that the measurements from one of them are likely to be confused as originated from the target of interest.

A nearly constant velocity (NCV) motion model based on a discretized continuous time white noise acceleration (CWNA) model is used to characterize the dynamics of the target [4], namely,

$$x(k+1) = Fx(k) + v(k) \tag{30}$$

where

$$F = \begin{bmatrix} 1 & 0 & T & 0 \\ 0 & 1 & 0 & T \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}. \tag{31}$$

The discrete time noise $v(k)$ has covariance matrix

$$Q = \begin{bmatrix} T^3/3 & 0 & T^2/2 & 0 \\ 0 & T^3/3 & 0 & T^2/2 \\ T^2/2 & 0 & T & 0 \\ 0 & T^2/2 & 0 & T \end{bmatrix} \tilde{q} \tag{32}$$

where $\tilde{q}$ is the power spectral density (psd) of the continuous time zero-mean white process noise that models possible target maneuvers.

The measurement vector z consists of x and y elements,

$$z(k) = Hx(k) + w(k) \tag{33}$$

where

$$H = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{bmatrix} \tag{34}$$

with measurement noise covariance matrix R. The targets are considered to travel in parallel trajectories with velocity $v_x = 0$ in the x direction and $v_y = 5$ in the y direction. The separation between the targets is parameterized by c, the distance in the x direction, while the distance in y is taken to be 0. The sampling time is $T = 1$, and the measurement noise is zero mean i.i.d. Gaussian with standard deviations $\sigma_x = 4$, $\sigma_y = 2$. The value of the density of extraneous measurements used

TABLE II
RMS Error for x and y Coordinates for the 3 Association Methods, as a Function of Different Separations c (in the x direction), using a Window of $S = 3$ Frames

	x			y		
c	TmHT-CP	TmHT-DM	MHT	TmHT-CP	TmHT-DM	MHT
14	6.36	3.45	3.70	1.19	1.50	1.31
12	5.77	3.34	4.16	1.14	1.48	1.48
10	5.33	2.78	4.53	1.06	1.45	1.48
8	4.43	2.81	5.32	1.02	1.28	1.51

TABLE III
RMS Error for x and y Coordinates for the 3 Association Methods, as a Function of Different Separations c (in the x direction), using a Window of $S = 4$ Frames

	x			y		
c	TmHT-CP	TmHT-DM	MHT	TmHT-CP	TmHT-DM	MHT
14	6.07	2.48	2.50	1.18	1.47	1.46
12	5.59	3.03	3.41	1.14	1.47	1.45
10	5.26	3.19	4.91	1.05	1.46	1.46
8	4.49	3.16	5.29	1.02	1.30	1.51

is proportional to the inverse of the square root of the volume of the measurement noise covariance matrix, $\lambda_\theta = c_1 \left(\pi\sqrt{\det(R)}\right)^{-1}$. The value of c_1 used is 0.05. For simplicity it is assumed that the target detection probability is unity. The approach is applicable to detection probability less than unity using the likelihood ratio as in (21).

The three aforementioned algorithms are used to track the targets for each of the possible separations. The first two pertain to the family of Top m MHT (TmHT) algorithms, namely the CP approach (TmHT-CP) and the DM approach using the majority rule (TmHT-DM), while the third is the conventional MHT, which retains only the most likely hypothesis at the rear end of the sliding window. RMS errors are obtained from 100 Monte Carlo runs for each of the methods, and for two different number of frames in the sliding window (the time depth), $S = 3,4$.

Tables II and III present the RMS errors in x and y coordinates for the cases of using windows of $S = 3$ and $S = 4$ lists, respectively. The more important results correspond to the x coordinate, as it is the resolvable one, and the one for which the separation is varied. For the case $S = 3$ it can be seen that CP is a simplistic approach, and that coalescence is too prone to happen, thus loosing track accuracy. The MHT gives good results when track separation is larger, but its performance degrades as the targets get close to each other, due to track switching. The DM approach performs better than both of them, at the expense (when compared to MHT) of losing the track ID whenever tracks coalesce. This indeed may be an advantage, as it is preferable to know that a region of potential confusion arised, making the tracker lose the target IDs, rather than keeping the potentially wrong IDs.

The results for the y coordinate are very similar for all separations in this case (as well as for the case $S = 4$), and provide little information as the targets have the same y coordinate position at all times. In general the RMS error arising from the CP approach is smaller, as a result of the averaging effect of track coalescence and the fact that the y position is the same for both targets.

For the case $S = 4$ the x coordinate RMS behaves similarly as for the case $S = 3$, but including an extra list (more time depth) has a result that less tracks coalesce (due to the best hypothesis being in general stronger than the subsequent), and thus the RMS error in DM increases compared to the case of $S = 3$ due to some track switches that were not captured by the algorithm.

The inital position of the targets is such that a simple velocity gate assures correct data association. Thus the estimate for target 1 is correctly assigned the track ID T_1, and similarly track 2 (T_2) represents target 2. After a certain time, the trajectories get closer (separated c units in the x coordinate and 0 in the y coordinate) and become parallel, as stated before. For the TmHT methods, if at a certain time the track estimates are merged (the tracks coalesce, i.e., are contained in the same $\mathcal{C}$-set, and a single track estimate is kept that contains the two targets) the track IDs are lost. Thus, in case of significant contention between hypotheses, the IDs are no longer available. These IDs will be re-initiated whenever the tracks can be uniquely identified again. On the other hand, the conventional MHT will keep the IDs of the tracks when there is hypothesis contention (the algorithm has no way of discriminating this), the worst case being the occurrence of a track switch. That is, track T_i now represents target j, $j \neq i$, i.e., the IDs represent the wrong targets. The calculation of the RMS errors takes this into account, so that when a single coalesced track is present, the RMS error will be usually less than when track switch occurred as a result of the distance between the true target and the switched tracks being larger than the distance between the true targets and the merged track. In the case of no track switch, the merged estimate yields larger RMS errors.

Table IV shows measures of track switching and track coalescence for the case of a window of $S = 3$ frames (the case $S = 4$ has similar results). Two measures are used for the track coalescence, one is the percentage of tracks that have coalesced at some point during the time span of the experiment, and other is the percentage of time that this coalescence lasted. If there are track switches, the percentage of them occurring is also shown. It can be seen that the TmHT-CP does combine track estimates for all the separations presented, as a result of the weak condition for track combination, and that the tracks remain combined for most of the time span of the experiment. This prevents any track switch, but worsens the estimation RMS, as shown before. On the other hand, the TmHT-DM does combine tracks when those have relevant information in common. In

TABLE IV
Track Coalescence and Switch Measures for the 3 Association Methods, as a Function of Different Separations c (in the x direction), using a Window of $S = 3$ Frames

	TmHT-CP		TmHT-DM			MHT
c	% coalescence	% duration	% coalescence	% duration	% switches	% switches
14	100	94	0	0	1	1
12	100	93	9	4	2	9
10	100	98	42	14	3	20
8	100	99	98	30	4	56

this way tracks that are more likely to be confused, as is the case when their distance diminishes, have a larger percentage of track coalescence. Such coalescence lasts as long as there are association hypotheses that are very similar, thus not spanning the whole experiment time length. Note that some track switches still occur, but the number is significantly smaller when compared to the MHT.

5. CONCLUSIONS

A method has been presented to combine the m most significant hypotheses in a T2TA problem, which gives consistent system track estimates in the case of contention (correlation ambiguity), as opposed to using only the best hypothesis. The use of the m-best hypotheses has two main advantages. The first is the correct calculation of the variances due to mixing of related estimates, which improves the consistency of the estimator. The second is the ability to quantify the difficulty in the association by checking the total probability of the $\mathcal{C}$-sets (the combinable tracks). If this probability is close to one, the estimation for the target represented by the associations in the $\mathcal{C}$-set can be considered reliable. If the total probability is greater than one, the estimate obtained should be considered in a special manner, as it is based on wrong/mixed tracks due to missasociation.

The method proposed here, called Direct Mixture (DM) is somewhat similar to the Coordinated Presentation Mixture (CP) [5], but improves upon it in two aspects: the criterion for $\mathcal{C}$-set inclusion, and the use of likelihood based probabilities for association combination, which have been shown to improve the quality of the resulting estimates.

Overall, the proposed DM method with $K = 3$ (the overlap requirement between combinable hypotheses) yields more accurate estimates in terms of RMS error and more consistent estimates than both the top hypothesis scheme and CP.

The DM method has also been extended to a dynamic target tracking case. It has proven useful when the distance between tracks is such that there is association ambiguity (otherwise MHT, or even simpler methods as PDA suffice). The fact that estimates are merged when they have significant information in common, measured as the number of common measurements, allows for a decrease of the RMS error. This also causes the track IDs to be lost, but has the advantage of avoiding track switchings.

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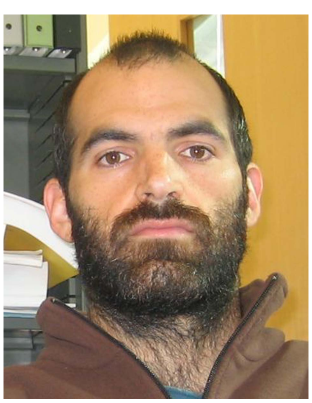

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