Efficient Implementation Scheme of K Best Algorithm for Target Tracking in a cluttered Environment

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***Abstract*—In a cluttered target tracking environment multiple hypotheses tracking (MHT) based algorithms improves the data association by considering a batch of measurements. To reduce the computational complexity generated by the exponential growth of hypotheses the number of hypotheses is limited to k in the k best MHT algorithm. The decision of which target belongs to which measurement is taken in K-best MHT algorithm using N scans of measurements.**

The value of k and the number of scans N are fixed in general for simple and complex scenario as well. This paper proposes a method to keep the value of k and N dynamic depending on the scenario complexity and also depending on the likelihood of the valid hypotheses. If the maximum value of the likelihood of the hypotheses is lower than a threshold it indicates that the association decisions embedded in the hypotheses is not appropriate. The likelihood threshold is a pre computed value based on a statistical measure proposed in this paper depending on scenario.

The proposed algorithm adaptively increases the number of k best hypotheses or the number of scans N to improve the maximum value of the likelihood of the hypotheses. Using this adaptive mechanism the computational complexity of the k best algorithm based MHT implementation is kept at low for less ambiguous data association scenarios. The decision on the adaptive value of N and k are obtained using the proposed method in this paper.

The Monte Carlo simulation results carried out in this paper justifies the advantage of the proposed method compared to the fixed k-best MHT algorithm.

Key words: MHT, target tracking, K-best, N-scan

I. Introduction

Tracking multiple targets, especially closely-spaced targets inevitably introduces the possibility of miscorrelation where a sensor plot may be incorrectly used to update a track that is following a different object. Multiple hypothesis tracking (MHT) is a deferred decision logic in which alternative track hypotheses are formed whenever there are potential track-to-plot assignment conflicts. That is in the event that a sensor measurement passes the gates of more than one track, all of those hypotheses are maintained until later sensor measurements arrive to resolve the situation. This approach is clearly very attractive in multi-target scenarios, in that a near optimal solution is possible. The full MHT approach however requires the maintenance of numerous such track branches and in dense target environment the number of such branches will grow exponentially. This in turn requires very rigorous pruning of redundant or incorrect branches to maintain the load within the manageable limits. So MHT is only practical to use for a fairly small number of targets, even when pruning is employed. It is largely in the view of these computational considerations that practical tracking systems have, tends to implement cheaper alternatives such as GNN and JPDA approach.

Pruning is essential to any practical implementation of MHT algorithm. For pruning we use k-best and N-scan back pruning. The N-scan algorithm assumes that any ambiguity at scan S is resolved by scan S + N. The probabilities of the leaf nodes are calculated for each branch of hypotheses tree. Whichever branch has the greatest probability is retained. A larger N implies a larger window hence the solution can be more accurate, but makes the running time longer. Another disadvantage of the MHT method is that the data association decision is often deferred which can likely be overcome by using the most probable best current hypothesis up to the current time.

One advantage of MHT method is that it provides a systematic track initiation procedure. Another advantage of the MHT method is that it is most likely to have the correct association solution as one of its hypothesis with best cost.

The assignment problem can be generalized to enumerate the first k-best assignments. Listing solutions by order of cost is used in the generation of alternative solutions. The efficiency of ranking algorithm is extremely important as several solutions have to be ranked. Recent work in MHT proves that with optimized implementation of Murtys algorithm real time multi-target tracking is feasible with MHT in some circumstances.

II. RELATED RESEARCH

In[1], an algorithm that efficiently generates the k-best solutions in assignment problems, called the Murty's algorithm, was proposed. Murty's algorithm has been widely used to generate the k-best assignments in multi target tracking, making the MHT feasible in practice. In[6], three optimized implementations of Murty's algorithm in which the input cost matrix for Murty's algorithm is formed by appending dummy values to the standard target-to-measurement cost matrix are discussed. The proposed algorithm substantially reduced its complexity from $O(mn^4)$ to $O(mn^3)$. The types of problems in data association for tracking are track initiation, track continuation and track fusion. Among many track continuation algorithms, it is well known that MHT performs much better than other methods like nearest neighbor or PDA(which have a time window of depth 1), due to its time window 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[18]. Fig.1 outlines the basic

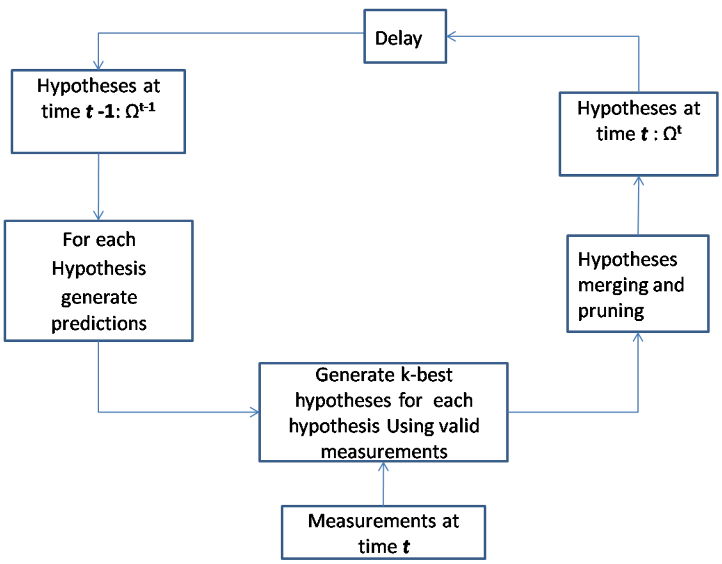

Fig. 1: MHT k-best Algorithm flow chart

operation of the MHT k-best algorithm. An iteration begins with the set of current hypotheses from iteration $(t-1)$. Each hypothesis represents a different set of assignments of measurements to features[11]. K-best assignments are generated from the given ambiguity matrix, which concisely models the ambiguities present in assigning measurements to tracks[11]. Pruning is based on a combination of an N-scan-back algorithm. The N-scan-back algorithm assumes that any ambiguity at time k is resolved by time $k+N$. Thus if hypothesis Ω_k at time k has q children, the sum of the probabilities of the lead nodes is calculated for each of the q branches and whichever branch has the greatest probability is retained[20]. In order to evaluate the hypotheses Reid recursively defines a posterior probability of a hypothesis Ω_i at time k given a set of new measurements as [1]

$$P_{\Omega_i}^{k} = \frac{1}{c} P_D^{N_{DT}} (1-P_D)^{(N_{TGT}-N_{DT})} \beta_{FT}^{N_{FT}} \beta_{NT}^{N_{NT}} \times \left[\prod_{m=1}^{N_{DT}} N(Z_m - H_{x_j}, P_j) \right] P_{p(\Omega_i)}{}^{k-1} \quad (1)$$

Where $P_{\Omega_i}^{k}$ is the hypothesis probability, $P_{p(\Omega_i)})^{k-1}$ is probability of parent hypothesis at time $(k-1)$, P_D is the detection rate, β_{NT} and β_{FT} are the new target and false target density, N_{TGT}, N_{DT}, N_{FT} and N_{NT} represent current hypothesis configuration parameters and c is normalization constant. The likelihood to assign a measurement *m* to track *j* is modelled by the normal distribution *N* of its kalman filter with its state x_j and P_j. Thus the measurements are assumed to be indistinguishable and the likelihood of assignment to a track only depends on their position. In order to prevent the set of hypotheses from growing exponentially over time, the unlikely ones are pruned at every time-step to a fixed maximal cardinality k_{max}. Many schemes have been developed to control the computational burden of MHT type methods by limiting the selection of assignment sequences to the most likely. Such pruning methods, however inevitably sacrifice any optimality property of the full algorithm. A generalization of Murtys algorithm for ranking k-best bipartite assignment problems and its application to track-oriented MHT systems was discussed in [19]

III. MODIFIED MHT ALGORITHM WITH ADAPTIVE SELECTION OF K-VALUE

The focus of this work is on track continuation or track maintenance. Our main aim is to reduce the track deviation and track loss in real-time multi-target tracking by dynamically changing the k value without incurring much additional computational cost. We initially form clusters of tracks which are spatially separated and which do not share any measurements in common. Clustering helps for doing parallel processing and reduces the amount of required memory and computation time significantly.

Keeping k-value big increases the execution time and increases the complexity of the data association algorithm.

Low value of k may not be sufficient to resolve ambiguities arising during the data association process which lead to track deviation and track loss. Fixed value of k for the entire scenario is not a suitable option in multi target tracking.

So choosing k-value is crucial decision in track continuation for multi target tracking. Fixed number of k may not suit for every scenario of tracking. In this paper we propose a new algorithm with dynamic k-value for Multi target tracking. Initial decision of k-value depends on the number of tracks and valid measurements in the tracking region. That is we generate almost all feasible hypotheses in order to get the threshold value for the first few scans. Usually during tracking the confusion arises at few places. Otherwise with a modest number of k-best hypotheses are good enough for smooth target tracking. Because of the wrong data associations at few places lead to track deviation or track loss.

First we need to identify places where the given data association may lead to track deviation. Once we identify the area, we can go back n scans and recalculate the of hypothesis tree with increased k value which may resolve the ambiguity and then avoids track deviation. By recalculating the hypothesis tree with increased k-value may help to recover the hypothesis with best cost which was not covered with modest k value. This may result in reduced cost of best global hypothesis. The increment of k can be done in small steps.

Suppose at the current scan we have calculated m best hypotheses but the $(m+1)$ hypothesis may be the best one in future scans. It may happen because all the first m hypotheses which are formed are from mismatched associations. For the rest of the scenario k value remains some average value.

A global hypothesis is formed from a parent hypothesis and a current association. This joint event is made cumulative, conditioned upon the sequence of measurements up to the current time t. The posterior probability of this cumulative joint event is given by Blackman and popoli.

Cost of global hypothesis = cost of an assignment + parent hypothesis cost

$$c(\Omega_i^t) = c(a_i) + c(\Omega_{p_i}^{t-1})$$

We define delta as
Δ = c(Ω_i)-c(Ω_{i-1}), where c(Ω_i) is cost of best global hypothesis at scan *i*.

The best global hypotheses have the lowest total costs. Our objective is to minimize the function $c(a_i) + c(\Omega_{p_i}^{t-1})$. The problem is a synonymous to travelling salesman problem which is standard NP hard problem. So we adopt sub-optimal method to solve the problem.

We define threshold as a permissible value increase of cost of best global hypothesis from scan to scan. The global hypotheses are typically compared using a cost function based on the negative log likelihoods of each assignment. Determining the single best assignment is then a matter of determining the assignment that minimizes this sum.

To calculate the threshold value initial few scans we generate all the possible hypotheses in each scan. If *M* is the valid number of measurements and *T* is number of targets then the size of the feasible solution space *A* is i.e., The number of data association assignments as derived in [10,17] is

$$|A| = \sum_{j=1}^{min(T,M)} \frac{M!T!}{j!(M-j)!(T-j)!}$$

Threshold is obtained by averaging the increase in best global hypothesis cost in each scan. If the given scenario is going for recalculation frequently then we increase the threshold value based on the average delta value. Cost of an assignment denoted by $c(a_i)$, can be determined by summing the individual costs corresponding to the *S*-tuples occurring in the assignment.i.e.,

$$c(a_i) = \sum_{i_1,i_2,i_3,\ldots,i_s} c_{i_1} \ldots c_{i_s}$$

IV. PSEUDO CODE

Step 1. For the first *s*-scans *k* value is equal to the size of feasible solution space *A* or some big value.
Step 2. Calculate Delta (Δ) of each scan as Δ = cost of the best global hypothesis at the time t $-$ cost of the best global hypothesis at the time *(t-1)*
Step 3. Threshold(δ) = Average value of Δ for the first s -scans.
Step 4. Let *K* be some modest value
Step 5. Let Ω^{t-1} are the global Hypotheses at time *t -1*
Step 6. For each hypothesis generate predictions. Generate *K*-best hypotheses for each Hypothesis at time *t-1* by using valid measurements at time *t*.
Step 7. Calculate the Cost of the global hypotheses. Calculate Delta value of the best global hypothesis at time *t*
Step 8. If ($\Delta > \delta$) and not recalculated then go back *n* scans and each scan generate all possible hypotheses from each hypothesis for back *n* scans.
Step 9. Do hypotheses pruning and merging, we keep top m hypotheses, where m is determined by the size of problem and the characteristics of application. Go to step 5.

V. EXPERIMENTAL RESULTS

The results presented in this section correspond to a simple problem where $T = 4$ targets, three targets are moving in straight line formation and another target is crossing over these three targets. The targets are considered to travel with constant velocity. The sampling time is $t = 1sec$. In our simulations the normalizing constant is dropped and comparisons are made between the association likelihoods. As a simple scenario we have created four closely moving targets, with $P_D = 0.9$ and with some clutter. We have compared the number of deviations and time of computation for $k = 1, k = 2, k = 3$ and $k = 4$ in Table 1.We run the scenario for 100 scans. We have generated random data using some measurement noise. For calculating threshold value we kept K value as feasible hypotheses size which depends on the number targets and number of valid measurements in the current scan, for first 10 scans. For some runs we fixed this value to 5. For the rest of the 90 scans $k = 2$. Whenever the delta exceeds threshold value we go back by 5 scans and recalculate the hypothesis tree. We have incremented k in steps of 2. As a simple pruning method we have kept top 5 hypotheses and ignore the rest. We run a scenario with some simulated data with fixed $k = 2$ and the results are shown in fig.2. The run time is 6.04 seconds. We have run the scenario with same data using dynamic value of k value and the results are shown in fig.3. For the given scenario fixed value of $k = 2$ could not handle the scenario. By using our new approach of Dynamic value of k could resolve the ambiguities by dynamically changing the k value when ever deviation starts and run time is 10.508 seconds.

Fig.4 is another scenario with $k = 3$. The ambiguity at one or two places caused the two tracks deviation as shown in the figure. The run time of this scenario is 6.04 seconds. Fig.5 shows that dynamic value of k successfully handle the confusion. The run time is 10.34 seconds. The simulation results for 4 tracks, 100 scans, 100 Monte Carlo trials are

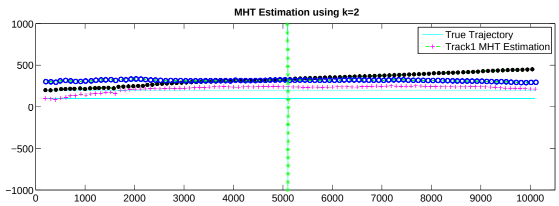

Fig. 2: MHT, With fixed k=2

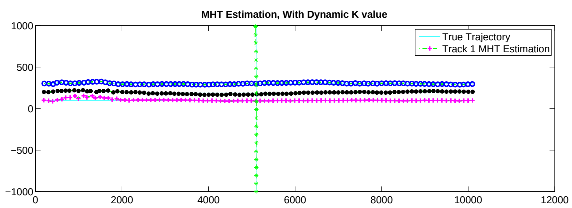

Fig. 3: MHT, with Dynamic k value

shown in the Table.1. As the Table.1. indicates as K increases the time of execution increases and the deviation were reduced. We define deviation as if one target deviate from actual path by some threshold distance. Usually once a target is deviated for some scans its deviated in the entire scenario. In the fig.6 we have shown the comparison of best hypothesis cost at each scan using fixed k value and dynamically changing k. We have compared hypotheses using negative log likelihood value. Best hypothesis is the one with minimum value. Time comparison between fixed k and dynamic k value approach is shown in the fig.7. Whenever there is confusion time is increased for recalculation of tree with increased k value in the given scan. In fig.8 we have shown how k value is variation for a given 100 scan run. For Fig.2,3,4 and 5 x-axis and y-axis are labelled as the position of targets in meters.

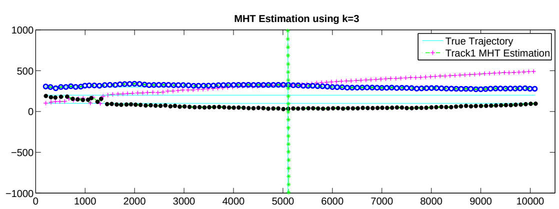

Fig. 4: MHT, With fixed k=3

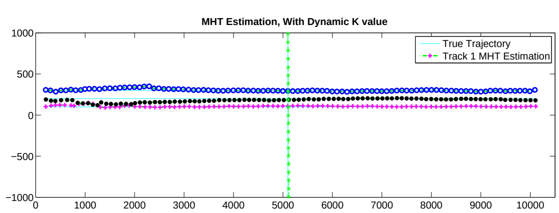

Fig. 5: MHT, with Dynamic k value

VI. Conclusion

In this paper we have presented a new approach to solve multi-target data assignment problem in clutter environment using MHT. We have showed the improved results using dynamic k number of hypothesis generation which potentially enhance the performance of MHT algorithm. We can extent this approach to generalized scenarios.

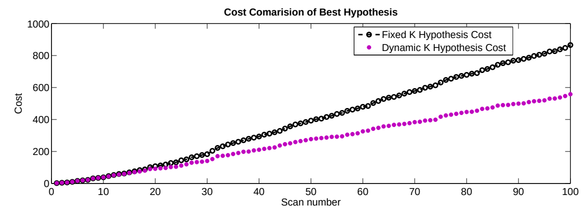

Fig. 6: Best Global Hypothesis cost comparison

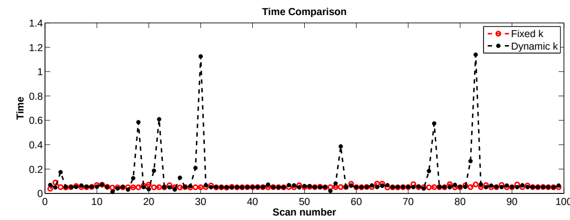

Fig. 7: Time comparison

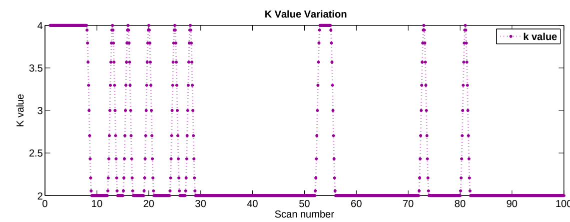

Fig. 8: K value comparison

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TABLE I: Comparison of Time and Deviations

K value	Deviations	Time(in seconds)
1	15	121.1
2	10	537.2
3	9	659.5
4	7	1083.5

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