An efficient approach to decompose the multidimensional assignment problem

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Abstract - ***The primary contribution of this paper is the introduction of a new method to reduce significantly the computation time necessary to solve the multidimensional assignment (MDA) problem. In the first part of the track oriented method clusters are formed to reduce the amount of computation time necessary for correlation. For each formed target tree a mean track is formed. The different mean tracks are used to determine independent components. Each independent component corresponds with a cluster. In the second part of the method the original MDA problem is decomposed in smaller, independent MDA problems, using a root track label for each target tree.***

Keywords: Multiple target tracking, data-association, MDA, estimation , sensor data fusion.

1 Introduction

The data-association problem has been shown to be NP-hard for a number of sensors ≥ 3 ([6]). In [2] a formulation of the multitarget (multisensor) tracking problem as a multidimensional assignment (MDA) problem is given. Poore ([9], [11]) introduced a window technique to consider only the last W data sets. The sliding window in Fig. 1 contains only three data sets ($W = 3$) . The problem is to find solutions for the optimization problem using the measurements contained within the window and the track hypotheses falling outside the window. In Fig. 1 those track hypotheses are related with the data sets with a number $\leq N$. Given W data sets, the objective is to find the assignment of measurements to track hypotheses which maximizes the formulated linear object sum [2]. Before the actual MDA problem can be solved it is necessary to determine the decision variables and the track formation costs (Fig. 2).

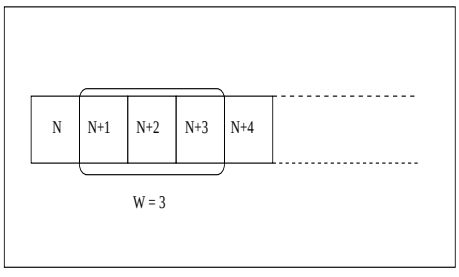

Fig. 1: The sliding window contains only three data sets.

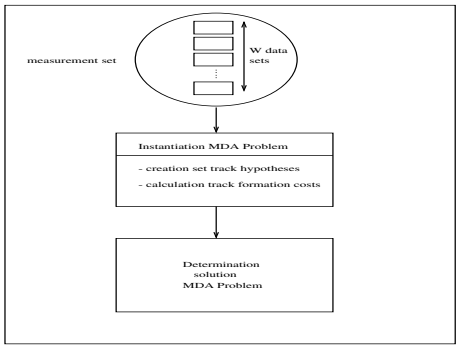

Fig. 2: The MDA problem instantiation and solution process.

In the MDA approach a track oriented approach is assumed to generate the set of track hypotheses. In this approach target trees are constructed where the branches contain the possible track hypotheses which have the root node as common ancestor (Fig. 3). The branches are extended by assigning correlating measurements. The root of each tree is assumed to represent the appearance of a new target or a target from the best solution produced by the Semi-Greedy Track Selection algorithm proposed in [2]. Every path from the root to a node v in the tree represents the track hypothesis formed by extending the root with the measurements along the path to the node v. A measurement i from the dataset j is denoted by i_j. In fig.3 the track $\{1_1, 2_2\}$ represents the track hypothesis consisting of the measurement $1_1, 2_2$ and $W - 2$ missed detections, where W denotes the number of data sets contributing to the tree at time T.

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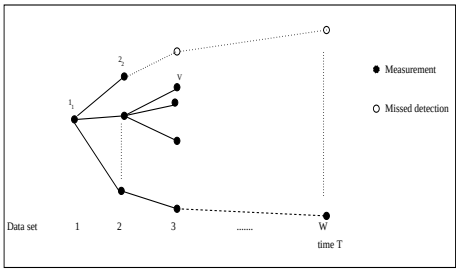

Fig. 3: The number of track hypotheses is determined by the number of nodes K_1.

A new decomposition algorithm for the multidimensional assignment problem is proposed in the paper. The goal of the algorithm is twofold:

- Reduce the number of correlation tests between existing track hypotheses and received measurements, using clustering;
- Partition the MDA problem into a number of smaller subproblems which can be solved independently.

A cluster is defined as a set of track hypotheses which are competing for the same measurements. This competition of measurements can be determined in two different ways, by application of independent components (a priori, section 2) or by decomposition of the cost matrix in a number of independent submatrices [3] (a posteriori). In Fig. 4 it is shown that a cluster can continuously merge with other clusters and split in smaller clusters during the time interval Δt corresponding with the size of the window W. The same

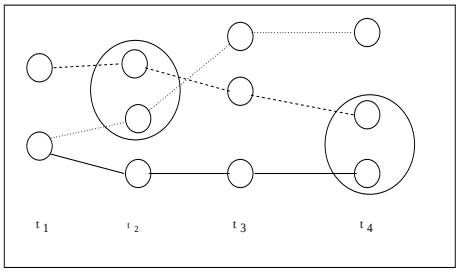

Fig. 4: Clusters can split and merge with other clusters.

measurement can be used to extend branches of different trees. This means that the trees must be a member of the same cluster.

2 Independent components

A logical way to determine clusters is to use the available correlation ellipses or ellipsoids. Targets with overlapping ellipses or intersecting ellipsoids are assumed to be a member of the same cluster. The disadvantage of such an approach are the necessary intersection calculations which in terms of processing power become prohibitively expensive for a large number of track hypotheses and/or for higher ellipsoid dimensions.

The objective is to determine a relatively cheap approximation method to calculate if two correlation or measurement ellipses/ellipsoids possibly intersect. Assuming a normal probability density function for the measurements, the measurement ellipsoid is defined by

$$[\vec{z}_k - h(\bar{s}(t_k))]^T B^{-1} [\vec{z}_k - h(\bar{s}(t_k))] \leq r^2 \qquad (1)$$

where $\bar{s}(t_k)$ is the estimated track state vector predicted to the measurement time t_k, $\vec{z}_k$ is the measurement vector, $h(\cdot)$ is the transformation from cartesian to polar coordinates and B is the covariance matrix $B = H_k \bar{P}_k (H_k)^T + R_k$. R_k is the measurement noise covariance matrix, H_k is the Jacobian of $h(\cdot)$ taken at the predicted state vector $\bar{s}(t_k)$ and $\bar{P}_k$ is the track error covariance matrix predicted to the measurement time t_k. Using the dimension n of the measurement vector and accepting a certain risk to make an erroneous correlation decision, the factor r^2 can be read from the χ^2-distribution table. A measurement falling within the gate is assumed to be a likely association candidate for the track hypothesis under consideration. In this paper it is assumed that a measurement $\vec{z}_k$ contains $(R_k, \beta_k, \varepsilon_k)$ information, but the approach can be easily extended to higher dimension measurement vectors. At measurement time t_k, R_k represents the range, β_k the bearing angle and ε_k the elevation angle of the measurement.

The approximation approach contains two steps. First a check is made if the two ellipsoids are close enough along the ε-axis that an intersection is possible by determination of the maximum and minimum ε-values for both ellipsoids, using the method described in app. B . Intersection is possible if the two ε-intervals overlap. If intersection is possible, the next step is carried out which is based on theorem 7.4.3 from Wilks [13] which states

If $(x_1, \cdots, x_k)$ *is a vector random variable having the k-variate normal distribution* $N(\{\mu_i\}, \| \sigma_{ij} \|), i, j = 1, \cdots, k$, *the marginal distribution of* $(x_1, \cdots, x_{k_1})$, $(k_1 < k)$, *is the* k_1*-variate normal distribution* $N(\{\mu_i\}, \| \sigma_{ij} \|), i, j = 1, \cdots, k_1$.

In this theorem $\| \sigma_{ij} \|$ represents the covariance matrix of the normal distribution . If it is assumed that the probability density function for the measurement vectors (R, β, ε) is normal and centered in $h(\bar{s}(t_k))$, this means that the probability density function of the measurement vectors containing (R, β) information is also normal and can be directly derived from the distribution for (R, β, ε). For (R, β) measurements eq. 1 defines an ellips in the $\{R, \beta\}$-plane in measurement space, using an appropriate value for r^2. If those ellipses intersect, the two corresponding track hypotheses possibly compete for the same measurements. To determine if two ellipses intersect the

algorithm developed by Eberly [7] is used. Using this approach each ellipsoid is approximated by an *hatbox* as shown in Fig. 5. Two targets with intersecting hatboxes are now assumed to be a member of the same cluster.

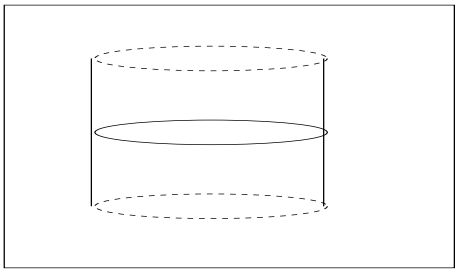

Fig. 5: The correlation ellipsoid is approximated by a *hatbox*.

In Fig. 6 an example of a cluster containing 6 track hypotheses is shown at a certain time t. The time t is determined by a measurement which has to be assigned to a cluster. All track hypotheses are contained in the cluster track hypotheses list. In this example the correlation gates are ellipses in polar coordinates. The cluster in the figure clearly contains three independent components. The hatbox method provides an exact solution for the cluster given in Fig. 6. Track

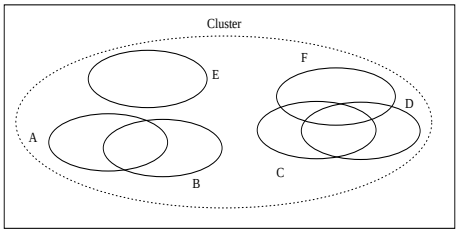

Fig. 6: At measurement time t the example cluster contains several independent components

hypotheses with intersecting ellipses are a member of the same independent component. Three independent components containing the track hypotheses $\{A, B\}$, $\{C, D, F\}$ and $\{E\}$ have been found.

If an independent component has been found, a new cluster can be initiated immediately. For each of the track hypotheses in the track hypotheses list of the cluster the n-dimensional correlation gate is approximated by a cube (or rectangle) in measurement space. In Fig. 7 an example of a rectangle-approximation is given. The cube-approximation for the ellipsoids can be used to determine the cluster size as shown in (Fig. 8), using the mean tracks which are discussed in section 3. Each mean track represents the track hypotheses contained in a complete target tree. The cluster size is used to find the possibly association candidates for each measurement, which significantly reduces the amount of expensive correlations which have to be made (Fig. 9).

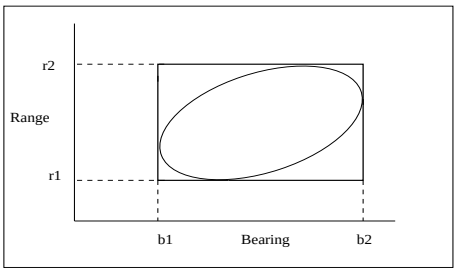

Fig. 7: The correlation ellips is approximated by a rectangle.

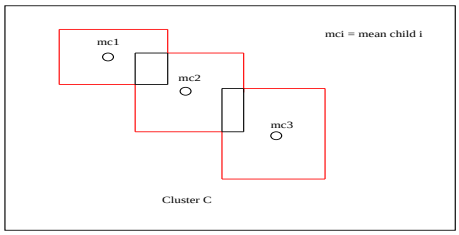

Fig. 8: The cluster size is defined using the cube-approximation for the correlation ellipsoids of the mean tracks.

Algorithms to determine independent components in the single sensor situation and the multiple sensor situation can be found in [5].

3 Tree reduction

Assume that the W data sets contain N measurements. The track hypotheses contained in the different trees form a set of track hypotheses. This set contains M track hypotheses ($M \gg N-1$), which are predicted to the measurement time T_N. At the begin of the window the set of root track hypotheses contains r track hypotheses ($r < N$) which are obtained from the hypothesis with the highest object sum before processing the last data set. Within the window a maximum of $N-1$ new trees can have been created. A total number of $r+N-1$ trees is possible. The number of tree nodes K_i determines the number of track hypotheses in the i^{th} tree.

The objective for the application of clusters is to reduce the amount of computation time necessary for correlation. It is assumed that the different clusters are determined if $T - t_l > \Delta t$ (e.g. $\Delta t = 1.5$ sec.), where t_l is the last time the clusters have been determined. Differences within the time interval are neglected. Due to the multisensor environment, the size and the orientation of the measurement ellipsoid for a track hypothesis varies with the sensor which produces the measurement. To account for this variability the following approach is used. Assume that there are k sensors, each with their own measurement noise covariance matrix. Each of the k covariance matrices is transformed from polar space to cartesian space and expressed in absolute cartesian coordinates. This produces the covariance matrices $R_1^1, R_2^1, \ldots, R_k^1$. The

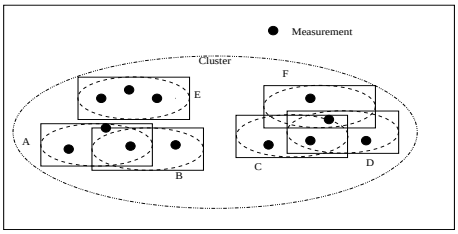

Fig. 9: Each measurement is only correlated with the track hypotheses in the relevant newly initiated cluster.

next step is to compute the average covariance matrix $R_m = \frac{R_1^1 + R_2^1, \cdots + R_k^1}{k}$. In figure 10 the two-dimensional measurement ellipses for two sensors are illustrated and approximated by the dotted ellips representing the mean measurement ellips corresponding with the mean measurement noise covariance matrix R_m which has been transformed to polar space.

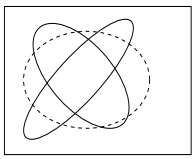

Fig. 10: Mean correlation ellips.

Using the track hypotheses set directly to determine the clusters at measurement time T_N, the maximum number of operations is given by $c \times M \times M$, where $c \leq \frac{T}{\Delta t}$. If clustering is not applied, the maximum number of correlations is given by $(N-1) \times M \approx N \times M$. Normally $c \times M^2 \gg N \times M$ which means that the number of operations to form clusters has to be reduced to apply clustering usefully.

At time T_N each target tree contains track hypotheses that have been predicted to the time stamp T_N. In this section a track hypothesis is characterized by a track number, an update (prediction) time, an estimated (predicted) state vector and an estimated (predicted) error covariance matrix. This means that track hypothesis i (root track or descendent) is given by track i $= \{i, T_N, \bar{s}_i, \bar{P}_i\}$ where $\bar{s}_i$ is the predicted state vector and $\bar{P}_i$ is the predicted error covariance matrix.

Assume a priori that one of the track hypothesis in the tree labelled by root track hypothesis j forms an explanation for the related measurements. At time T_N the tree contains K_j hypotheses, where $\sum_{i=1}^{r+N-1} K_i = M$. It is clear that the different track hypotheses in the tree can only take certain values for $\bar{s}$ and $\bar{P}$, which means that the corresponding conditional probability density function $p_j^i = p(\text{track i} \mid \text{root track j})$ is a conditional probability function. This conditional probability is defined as

$$p_j^i = \frac{e^{c_j^i}}{\sum_{j=1}^{K_i} e^{c_j^i}} \tag{2}$$

where c_j^i are the costs to create track hypothesis i from root track hypothesis j [12]. The conditional probability density function $p(\vec{s} \mid \text{track i}, \text{root track j})$ is estimated by the extended Kalman filtering process and is given by the normal density function $N(\bar{s}_i, \bar{P}_i)$.

It is possible to write

$$\begin{aligned} \vec{s} &= \vec{s} - \bar{s}_i + \bar{s}_i \\ &= \vec{\Delta}_2 + \vec{\Delta}_1 \end{aligned} \tag{3}$$

where $\bar{s}_i$ is the predicted state vector for track hypothesis i and $\vec{\Delta}_1 = \bar{s}_i$. The corresponding conditional probability density function is defined by

$$\begin{aligned} &p(\vec{\Delta}_1, \vec{\Delta}_2 \mid \text{root track j}) = \\ &p(\vec{\Delta}_2 \mid \vec{\Delta}_1, \text{root track j}) \times p(\vec{\Delta}_1 \mid \text{root track j}) \end{aligned} \tag{4}$$

The objective is to find an approximation for eq. 4 where the variables $\vec{\Delta}_1$ and $\vec{\Delta}_2$ are independent random variables. The concept is illustrated in Fig. 11.

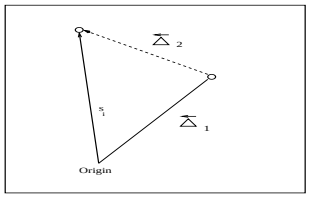

Fig. 11: The state vector $\vec{s}$ is approximated by the independent random variables ($\vec{\Delta}_1$, $\vec{\Delta}_2$).

It is reasonable to assume that the different track hypotheses with high cost values (or probability values) in the tree whose root track hypothesis is j have approximately the same dynamical behaviour, due to the fact that they originate from the same root track hypothesis and the fact that the W data sets cover a very limited time interval. The validity of this assumption is also supported by an experiment described in section 5. The conditional probability density function $p(\vec{\Delta}_2 \mid \vec{\Delta}_1, \text{root track j})$ is now approximated by

$$\begin{aligned} &p(\vec{\Delta}_2 \mid \vec{\Delta}_1, \text{root track j}) \approx \\ &p(\vec{\Delta}_2 \mid \text{root track j}) = N(0, \bar{P}^j) \end{aligned} \tag{5}$$

where the covariance matrix is estimated by averaging over all predicted track hypothesis covariance matrices and is given by

$$\bar{P}^j = \sum_{i=1}^{K_j} p_j^i \times \bar{P}_i \tag{6}$$

How higher the probability of the track hypothesis is, how more important its contribution to $\bar{P}^j$ is. Due to the approximation of $p(\vec{\Delta}_2 \mid \vec{\Delta}_1, \text{root track j})$ (eq 5) it is possible to approximate the conditional probability density function $p(\Delta_1, \Delta_2 \mid \text{root track j})$ by

$$\begin{aligned} &p(\Delta_1, \Delta_2 \mid \text{root track j}) \\ &\approx p(\vec{\Delta}_2 \mid \text{root track j}) \times p(\vec{\Delta}_1 \mid \text{root track j}) \end{aligned} \tag{7}$$

which is a product of two independent conditional probability density functions. Using this approximation, $\vec{\Delta}_1$ and $\vec{\Delta}_2$ can be considered independent random variables. The probability (density) function $p(\vec{\Delta}_1 \mid \text{root track j}) = p(\text{track i} \mid \text{root track j})$. The average state vector $\bar{s} = \bar{S}_s^j$ (eq. 14) can be used to define a mean track (child). The situation in the state space at time T_N is shown in Fig. 12, where the mean track is indicated by the thick line. The error

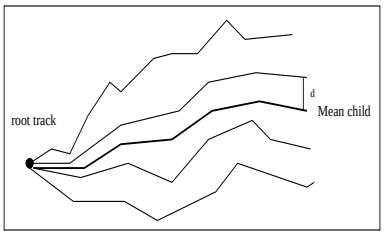

Fig. 12: The mean child is the mean of the predicted track hypothesis distribution.

covariance matrix corresponding with the mean track is defined by

$$\begin{aligned} \bar{P}_m^j &= E(\vec{s} - \bar{S}_s^j) \times E(\vec{s} - \bar{S}_s^j)^T \\ &= eq.15 \; from \; appendix \; A \\ &= \bar{P}^j + \bar{P}_s^j \end{aligned} \tag{8}$$

The covariance matrix which represents the spread of the predicted state vectors in the tree is defined by

$$\bar{P}_s^j = E((\bar{s}_i - \bar{S}_s^j) \times (\bar{s}_i - \bar{S}_s^j)^T) \tag{9}$$

and can be estimated by

$$\bar{P}_s^j = \sum_{i=1}^{K_j} p_j^i \times (\bar{s}_i - \bar{S}_s^j) \times (\bar{s}_i - \bar{S}_s^j)^T \tag{10}$$

A track hypothesis with deviating dynamical behaviour has a very low cost value, which means that it will never be included in the optimal solution. If it is not accounted for by the mean track, the only effect is that the number of unlikely correlations is reduced.

Formally, the mean child or mean track corresponding with the tree labelled by root track hypothesis j is now defined by mean track $= \{j, T_N, \bar{S}_s^j, \bar{P}_m^j\}$. If the set of mean tracks is used to form clusters, the maximum number of necessary operations is given by $c \times (r+N-1) \times (r+N-2) \approx c \times (r+N)^2$. Due to the fact that $c \times (r+N)^2 \ll c \times M^2$, a significant reduction in the number of maximally necessary operations is resulting.

4 Independent MDA problems

In Fig. 4 it has been shown that clusters can continuously merge and split. Clusters can not be used to decompose the original MDA problem in smaller, independent problems. Another approach is necessary.

Each tree is a member of a certain independent MDA problem. It is assumed that each track hypothesis i in a certain tree points directly back to the root track hypothesis of the tree. Each root track hypothesis has a label which designates the MDA membership. If a measurement correlates with track hypotheses in different trees, each correlating track hypothesis is extended with this measurement. At the same time, the root track labels are determined by the label of the oldest tree a measurement is shared with. If a tree is initiated and the responsible measurement is not shared with another tree, the root track label is determined by the measurement number.

After the last measurement within the frame of received measurements has been assigned to one or more trees, the different independent MDA problems are determined by comparing the different root track labels with each other. Trees are a member of the same MDA problem if the root track labels are equal. If a maximum number of $r + N - 1$ trees is assumed (section 3), the maximum number of comparison operations is given by $(r + N - 1) \times (r + N - 2) \approx (r + N)^2$. After determination of the independent MDA problems, each MDA problem is solved independently.

5 Experiments

The predicted state vector $\bar{s}_i$ for track hypothesis i is given by the column vector $\bar{s}_i = (x, y, z, v_x, v_y, v_z, a_x, a_y, a_z)^T$ which expresses the predicted position, velocity and acceleration for the track hypothesis. The predicted covariance matrix $\bar{P}$ of the track hypothesis is expressed in cartesian coordinates. T_1 is a track hypothesis with predicted state vector $\bar{s}_1$ and with predicted error covariance matrix $\bar{P}_1$. Furthermore, t_2 is a track hypothesis with predicted state vector $\bar{s}_2$ and predicted error covariance matrix $\bar{P}_2$. Both two track hypotheses are in the same target tree. The mahalanobis distance between the predicted state vectors of two track hypotheses t_1 and t_2 is defined by

$$d = \sqrt{(\bar{s}_1 - \bar{s}_2)^T R^{-1} (\bar{s}_1 - \bar{s}_2)} \tag{11}$$

where $R = \bar{P}_1 + \bar{P}_2$ is the sum of the predicted covariance matrices of both track hypotheses. Define $B = R^{-1}$. If B is a symmetrical square positive definite matrix, then there exists a unique symmetrical positive definite matrix D such that $B = D^T \times D$ [8]. This allows us to rewrite eq. 11 as:

$$\begin{aligned} d &= \sqrt{(\bar{s}_1 - \bar{s}_2)^T (D^T D) (\bar{s}_1 - \bar{s}_2)} \\ &= \sqrt{(D\bar{s}_1 - D\bar{s}_2)^T (D\bar{s}_1 - D\bar{s}_2)} \end{aligned} \tag{12}$$

The transformed state vector for track hypothesis t_i is given by $\bar{s}_i^* = D \times \bar{s}_i$. The length of state vector $\bar{s}_i^*$ is defined as $d_i = \sqrt{\bar{s}_i^T D^T \times D\bar{s}_i}$. The average length of $\bar{s}_1^*$ and $\bar{s}_2^*$ is $d_M = \frac{d_1 + d_2}{2}$. The track hypotheses t_1 and t_2 are said to have a similar dynamical behaviour

if the following test is verified:

$$\frac{d}{d_M} \leq \nu \tag{13}$$

where ν is a small pre-defined constant.

In section 3 it was assumed that all track hypotheses with a reasonably high likelihood (probability) have a similar dynamical behaviour. An experiment has carried out to verify this assumption. The layout of the experiment is as follows. There are two similar surveillance sensors scanning a certain surveillance area. In this area five aircraft appear at the same time instant and they all converge to the same final position following a straight trajectory (Figure 13). The process noise of the target is set to $50\frac{m}{s^2}$. The simulated sensors have a minimum detection range of 0.2 km and a maximum detection range of 100 km. The measurement noise in range is 0.03 km and in bearing and elevation 0.3 degrees. Targets move with a constant velocity of $500\frac{m}{s}$.

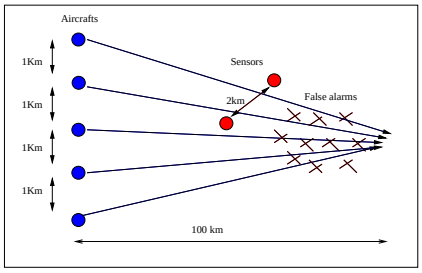

Fig. 13: Simulation scenario

The cluster decomposition process is carried out forty times. Every time a tree is randomly selected from all available trees. If p is the highest conditional probability of a track hypothesis in the tree, the similarity test is carried out only for track hypotheses which fulfil the condition $\frac{p(t)}{p} \geq 0.2$. Here $p(t)$ denotes the conditional probability of the track hypothesis t in the tree.

Fig. 14 shows for every selected tree the number of times that the similarity test has been performed and the number of times that condition 13 has been fulfilled. The value of ν was to 0.15.

Other experiments are planned with the objective to test:

- If using the hatbox approximation to determine clusters produces approximately the same results as using the original ellipsoids;
- If the determined cluster structure using the mean children of the trees is approximately the same as the one which would be obtained using all track hypotheses in the trees;
- Once the measurement has been assigned to a cluster, the correlation test is normally carried out for all track hypotheses within the cluster. An alternative approach is to use only the mean children of the different trees in the cluster to correlate the measurements. If a measurement correlates with the mean child of a tree, it is assumed to correlate with each track hypothesis in the tree. If this alternative approach produces approximately the same results, a further reduction in computation time can be achieved;
- As it has been discussed in section 3, a mean measurement noise covariance matrix is used instead of the measurement noise covariance matrices of the different sensors . However, it has still to be verified if the resulting tracking performance is satisfactory.

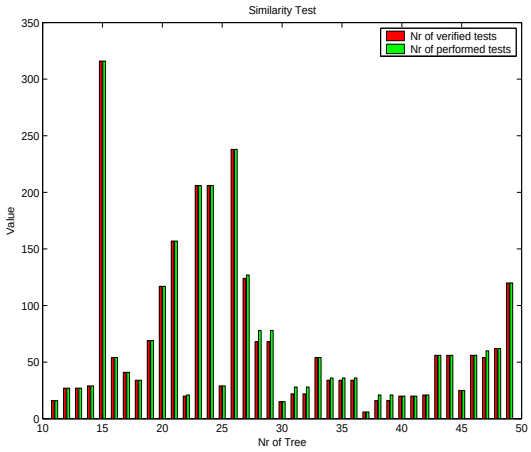

Fig. 14: Similarity Test.

Results and analysis of the planned experiments will be presented in [4].

6 Complexity

The process to solve a MDA problem is divided in an problem instantiation phase and the actual solution phase (Fig. 2). The tree reduction approach, introduced in section 3, is applied during the problem instantion phase. The complexity analysis of the proposed approach is divided in the following stages:

- Computation of the mean child for each tree;
- Determination of the clusters using the hatbox approximation for the correlation gate of each mean child for the different trees and computation of the cluster sizes;
- Selection of the cluster to which a measurement is assigned and correlation of the measurement with the track hypotheses within the trees inside a cluster;
- Formation of independent MDA subproblems and the solution of each subproblem using the Semi-Greedy Track Selection algorithm [2].

A complexity analysis is given for each stage. Three parameters are used for the analysis: the number M of existing track hypotheses, the number N given by the sum of the number of measurements within the window plus earlier established track hypotheses, and the cardinality F of the batch of the measurements received since the last time that clusters have been determined.

The first stage starts with the prediction of the state vector and covariance matrix for each existing track hypothesis. Next, for each tree a mean child is determined. This means that the number of operations is $O(M)$.

In the second stage the first step is to determine the hatbox approximation (section 2) for the correlation gate of each mean child, which results in $O(N)$ operations. Using the mean children, the number of intersection calculations necessary to form the different cluster is given by $O(N^2)$. The size of the different clusters is determined by approximating the correlation ellipsoid of each mean child by a cube in R, β and ε, using the calculation in app. B. For this last step the amount of operations is in the order of $O(N)$. The means that the complexity of the second stage is $O(N^2)$.

To decide whether a measurement can be assigned to a cluster, it is sufficient to check if the measurement falls within the calculated cluster size. This requires $O(N)$ operations. Once the measurement has been assigned it must be correlated with all the track hypotheses in the cluster. Assuming that the track hypotheses are uniformly distributed over l clusters, $\frac{M}{l}$ correlation tests must be performed for each cluster. Repeating this for every measurement in the batch of F measurements, the total number of operations needed in the third stage is $O(F \times \frac{M}{l})$.

The final stage starts with the determination of the independent MDA subproblems (section 4), which requires $O(N^2)$ operations. Finally, the complexity of the complete approach, determined by the highest complexity term, is given by $\max\{O(M), O(F \times \frac{M}{l})\}$. This compares favorably with the number of operations $O(N \times M)$, which is necessary when clustering is not applied.

In section 5 an alternative approach has been introduced to correlate a measurement with the mean track of each tree, and not with all the track hypotheses in a tree. If this approach produces approximately the same results, a reduction in complexity is achieved. In that case for a measurement at most N correlation tests are performed in a cluster, which means that the complexity of the third stage reduces to $O(F \times N)$. Normally $F \times N < M$, which means that the complexity of the complete approach reduces to $O(M)$.

The MDA decomposition method, introduced in section 4, reduces the computation time necessary to solve the actual MDA problem. Here a discussion of the complexity of the computation time necessary to solve the different MDA problems is given. Each of the independent MDA problems is solved with the SGTS algorithm [1]. It is assumed that there are L independent MDA problems. If T_i is the number of track hypotheses in MDA problem P_i ($i \in [1, L]$), the number of operations required to solve P_i is $O(T_i \times \log(T_i))$. In the worst case there is only one MDA problem which means that the complexity is given by $O(M \times \log(M)$, where M is the total number of track hypotheses. Assuming that the track hypotheses are uniformly distributed over the L independent MDA problems, the total computation time complexity to solve the total MDA problem is given by $L \times O(\frac{M}{L} \times \log(\frac{M}{L}) = O(M \times \log(\frac{M}{L})$.

This section is concluded with a complexity comparison between the proposed approach to determine the independent MDA problems (section 4) and the method proposed by Poore [10]. Poore creates a graph to determine the independent MDA subproblems. The nodes of the graph are measurements. Two measurements are connected by an edge if there is at least one track hypothesis containing both measurements. The connected components of the graph correspond to subproblems that can be solved independently. In order to construct the graph, for any pair of measurements a check is carried out if there exists a track hypothesis containing both measurements. In that case, an edge is inserted between the two measurements. It is straighforward to determine the complexity of the Poore approach [10], which is given by $O(M \times N^2)$. Using the root track labels approach, given in section 4, the independent MDA subproblems can be determined in $O(N^2)$.

7 Conclusions

In this paper a new method has been proposed to reduce the computation time necessary to solve the MDA problem by the application of clusters and decomposition of the MDA problem in a number of smaller, independent MDA problems. A track oriented approach is taken, where the different track hypotheses are contained in target trees. The first part of the method is dedicated to determine for each tree a mean track or child. This mean track is characterized by an average state vector and an average error covariance matrix. The mean tracks are used to determine clusters which are used to significantly reduce the amount of computation time. The method has the additional advantage that there are no correlations created for unlikely track hypotheses.

In the second part of the method the decomposition of the original MDA problem is based on assigning a root track label to each tree. If a measurement is shared by different trees, the root track labels are updated using the label of the oldest involved tree. Trees with the same root track label are a member of the same independent MDA problem.

The number of operations needed for the complete approach is significantly less than the number of operations needed to solve the problem without applying clustering.

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A $E(\vec{s})$ and $E(\vec{s}-\hat{s})\times(\vec{s}-\hat{s})^T$

It has been shown in section 3 that the two random variables $\vec{\Delta}_1$ and $\vec{\Delta}_2$ are independent. Using eq. 3 and 7 it is possible to write

$$\begin{aligned}&\bar{s}=E(\vec{s})=E(\vec{\Delta}_2+\vec{\Delta}_1)=\\&\sum_{i=1}^{K_i}\int_{-\infty}^{\infty}\cdots\int_{-\infty}^{\infty}\\&(\vec{\Delta}_2+\vec{\Delta}_1)f_1(\vec{\Delta}_1^i)\times f_2(\vec{\Delta}_2)d\vec{\Delta}_2=\\&E(\vec{\Delta}_2)+E(\vec{\Delta}_1)=\sum_{i=1}^{K_i}p_j^i\times\bar{s}_j=\bar{S}_s^j\end{aligned}\tag{14}$$

where the expected value $E(\vec{\Delta}_2)=0$ (eq. 5).

The error covariance matrix for the mean track (eq. 8) can be written as

$$\begin{aligned}&E(\vec{s}-\hat{s})\times E(\vec{s}-\hat{s})^T=\\&E(\vec{\Delta}_1+\vec{\Delta}_2)\times(\vec{\Delta}_1+\vec{\Delta}_2)^T=\\&\sum_{i=1}^{K_i}\int_{-\infty}^{\infty}\cdots\int_{-\infty}^{\infty}\\&(\vec{\Delta}_1^i+\vec{\Delta}_2)\times(\vec{\Delta}_1^i+\vec{\Delta}_2)^Tf_1(\vec{\Delta}_1^i)\times f_2(\vec{\Delta}_2)d\vec{\Delta}_2=\\&E(\vec{\Delta}_1\times\vec{\Delta}_1^T)+E(\vec{\Delta}_2\times\vec{\Delta}_2^T)=\bar{P}_s^j+\bar{P}^j\end{aligned}\tag{15}$$

where $\bar{P}^j$ is defined by eq. 6 and $\bar{P}_s^j$ is defined by eq. 10.

B Correlation ellipsoid approximation

The objective is to find a suitable and easy way to calculate a cube approximation for the correlation ellipsoid connected with a certain target. The mathematics used in this section is based on section 4.3.6 of the book written by Eberly [7].

An n-dimensional ellipsoid is represented by the equation

$$Q(\vec{X})=(\vec{X}-\vec{C})^t\times M\times(\vec{X}-\vec{C})=\chi^2\tag{16}$$

where $\vec{X}$ is any point on the ellipsoid, $\vec{C}$ is the centre of the ellipsoid and M is a positive definite matrix. Assume that it is necessary to determine the projection of the ellipsoid onto the line $\vec{C}+s\vec{N}$. If we designate the projection of the centre of the ellipsoid onto the line by 0, the projected interval is given by $[-r,r]$. Our objective is to determine r.

If a point $\vec{X}$ is projected to one of the end points of the interval, the normal to the ellipsoid must be parallel to $\vec{N}$. The normals for points on the ellipsoid

are determined by the gradient of $Q(\vec{X})$, which is given by

$$\nabla Q(\vec{X}) = 2M \times (\vec{X} - \vec{C}) \tag{17}$$

This means that $\vec{X}$ must be a solution of $M \times (\vec{X} - \vec{C}) = \lambda \times \vec{N}$ for some scalar λ. It follows immediately that $(\vec{X} - \vec{C}) = \lambda \times M^{-1} \times \vec{N}$. Substitution in eq. 16 produces

$$\begin{aligned} \chi^2 &= \lambda^2 \times (M^{-1} \times \vec{N})^t \times M \times (M^{-1} \times \vec{N}) \\ &= \lambda^2 \vec{N}^t M^{-1} \vec{N} \end{aligned} \tag{18}$$

The solution λ is given by

$$\lambda = \sqrt{\frac{\chi^2}{\vec{N}^t M^{-1} \vec{N}}} \tag{19}$$

Finally, r is given by

$$\begin{aligned} r &= \vec{N}^t \times (\vec{X} - \vec{C}) = \lambda \times \vec{N}^t M^{-1} \vec{N} \\ &= \sqrt{\chi^2 \times \vec{N}^t M^{-1} \vec{N}} \end{aligned} \tag{20}$$