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Delayed Merging Gaussian Mixture PHD Tracker with Embedded MHT for Close Target Tracking

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Abstract: For multi-target tracking it is difficult to obtain target trajectories from measurements of close targets and clutter. The Gaussian Mixture Probability Hypothesis Density (GMPHD) as a closed form solution for the Probability Hypothesis Density (PHD) filter can easily provide track labels of targets in clutter. But when targets are too close to each other, such as crossing and occluded conditions, the GMPHD tracker can't resolve identities of the targets which affects and even interferes with the decision of the commander. Based on the separation distance we proposed, delayed merging GMPHD tracker is proposed to correctly track close targets in clutter. Simulation results show that our proposed approach significantly improves the tracking performance of the GMPHD filter for correctly identifying targets in close proximity.

Key words: Target tracking, probability hypothesis density (PHD), Gaussian mixture PHD tracker

INTRODUCTION

It's more and more attractive to use Random Finite Set (RFS) theory (Goodman *et al.*, 1997) to solve the Multi-Target Tracking (MTT) problem. In the traditional MTT algorithms, such as Joint Probabilistic Data Association (JPDA) filter (Chang *et al.*, 1986) and Multiple Hypotheses Tracking (MHT) (Blackman, 2004), the data association problem makes up the bulk of the computational load. However, the methods based on the RFS theory all treat observations as a whole as well as targets and map the tracking of multiple targets into a single target tracking problem. So they avoid the explicit associations between observations and targets.

Among all the methods based on RFS theory the PHD filter (Mahler, 2003) is still rather effective and computationally tractable approach. There are two major implementations of the PHD filter known as particle-PHD filter or SMC-PHD filter (Vo *et al.*, 2005) and GMPHD filter (Vo and Ma, 2006) for linear Gaussian models. The GMPHD tracker can easily determine the target trajectories directly from the evolution of the Gaussian mixture (Panta *et al.*, 2006).

However, when targets are too close to each other, such as small angle crossing or occlusion condition, the performance of the GMPHD tracker degrades significantly. Perhaps the identities of the targets in close proximity can't be resolved by the original GMPHD tracker. In (Panta *et al.*, 2009) the theoretical constraints of the GMPHD tracker are discussed and an 'estimation-to-track' scheme is applied to distinguish between the two

targets. However, the separation distance in the article is not reasonable in multi-dimensional state space. A recent paper (Yazdian-Dehkordi *et al.*, 2012) proposed a novel method called competitive GMPHD (CGMPHD) filter employing a renormalization scheme to re-manage the weights assigned to each target while it's a pity to find the CGMPHD tracker is still not effective for some crossing scenes by simulation experiments.

In short, the problem of tracking targets in close proximity hasn't been well solved. In this paper based on the separation distance between close targets an improved GMPHD tracker for close target tracking and identifying called delayed merging GMPHD (DM-GMPHD) tracker with embedded MHT is proposed. When the distance between the predicted states of two target estimates is lower than some threshold, we associate the updated state hypotheses with the distinguishable past trajectories. Then the identity of each state hypothesis is determined by "hypothesis-to-track" delayed decision and the track hypotheses with highest scores are selected as estimates of target states. Simulation results are presented to demonstrate the capability of the proposed approach.

PROBLEM FORMULATION

GMPHD filter and labeling: For linear Gaussian multi-target models there is a closed-form solution for PHD filter, called GMPHD filter. The GMPHD tracker records the evolution of each Gaussian component and assigns the same identity or label to individual Gaussian terms

over all the branches of one tree. Assuming J_{k-1} is the number of Gaussian components at time step $k-1$, in the prediction process the same labels with the existing J_{k-1} Gaussian components are assigned to the corresponding predicted J_{k-1} components. Then, each measurement $z \in Z_k$ is used to update all of the J_{k-1} -predicted Gaussian components. Each predicted component gives rise to $1+|Z_k|$ Gaussian components with the same identity label, where $|Z_k|$ is the number of measurements. As a result, the updated Gaussian components for every predicted Gaussian component constitute a part of the tree structure. All branches of a tree have the same identity label and each branch is a possible trajectory of a target. In order to reduce the computation load, merging the Gaussian terms within a certain distance are very necessary. When the means and covariance satisfy:

$$(m_k^{(i)} - m_k^{(j)})^T (P_k)^{-1} (m_k^{(i)} - m_k^{(j)}) \leq U \quad (1)$$

the two Gaussian terms are merged.

The merging process perhaps evolves Gaussian terms with different labels and the label of the Gaussian term with the maximum weight is assigned for the term after merging. If true target estimate owns a smaller weight when targets are in close proximity, the merged term maybe is wrongly identified.

Drawback of the PHD Filter for tracking close targets:

For the PHD recursion derived from RFS multi-target Bayesian filter, an important assumption that the predicted multi-target RFS is Poisson holds (Panta *et al.*, 2006).

However, when two targets are close and there are large observation noise and process noise which result in great estimation covariance, interactions amongst targets are non-ignorable and the Poisson assumption becomes unreasonable.

So, when close targets are within a certain distance of each other, the PHD filter can't be effectively approximate to RFS multi-target Bayesian filter and can't distinguish between them.

The next section will demonstrate the separation condition between close targets for PHD filter in detail, as well as the improved GMPHD tracking scheme.

DELAYED MERGING GMPHD TRACKER

Separation distance: Consider a situation where two targets are in the surveillance region. Ideally the intensity function $D_k(x)$ would be represented by a sum of two weighted Gaussians with Gaussian means m_k^1 and m_k^2 :

$$D_k(x) = w_k^1 N(x; m_k^1, P_k) + w_k^2 N(x; m_k^2, P_k) \quad (2)$$

For simplicity, the covariance matrices P_k for both Gaussians are considered to be the same.

If the weights for both Gaussians are also the same.

Proposition 1: The intensity function D_k in (2) is unimodal with the mean $(m_k^1 + m_k^2)/2$ if and only if:

$$(m_k^1 - m_k^2)^T P_k^{-1} (m_k^1 - m_k^2) \leq 4 \quad (3)$$

We can prove Proposition 1 partly by reference to the statement for the condition that the multi-target posterior is unimodal in one-dimensional space (Goodman *et al.*, 1997).

In addition, we consider the conclusion on the condition that two Gaussian mixtures $D_k(x)$ have different weights.

Proposition 2: The intensity function $D_k(x)$ with different weights w_k^1 and w_k^2 in (2) is unimodal when:

$$\begin{cases} w \exp(-2zD)(z+1) + (z-1) = 0 \\ (1-z^2)D \leq 1 \end{cases} \quad (4)$$

Where:

$$w = w_k^1/w_k^2, D = (m_k^1 - m_k^2)^T P_k^{-1} (m_k^1 - m_k^2)/4$$

From the first equation of (4) z is the function of w and D . Then according to the second inequality of (4) we can determine the scope of the variable D .

For the scope S of D in (4) has no analytical solution with respect to the parameter w , we analyze the scope by polynomial fitting the numerical solutions with respect to w . In order to keep the fitting output not less than the real solution S , we enlarge S a little, such as to $S+0.04$.

Finally we get the conclusion:

$$(m_k^1 - m_k^2)^T P_k^{-1} (m_k^1 - m_k^2)/4 \leq f(w) \quad (4)$$

where $f(w)$ is 4-order polynomial function of w and the polynomial coefficients are as follows:

$$a = [-0.0107 \quad 0.1528 \quad -0.8294 \quad 2.0062 \quad -0.4132]$$

In order to make $w \geq 1$, if $w_k^1 > w_k^2$, $w = w_k^1/w_k^2$, else we get $w = w_k^2/w_k^1$. Furthermore $f(w)|_{w=1} = 1$.

From the separation condition as (2) and (4) we know for the PHD filter the separation distance demonstrating

whether two targets are too close is the Mahalanobis distance of two state estimates weighted by the inverse of the covariance matrix. If estimates of two targets satisfy (5), the PHD filter can't distinguish between them.

However, in simulation the merging threshold $U = 4$ makes the merging condition as (1) precisely the same to the separation condition as (3). So perhaps the estimates of two close targets have been merged into one Gaussian with one tag and the same identity is assigned to the subsequent tracks. In order to make sure that the state estimates of two close targets wouldn't be merged and obtain target trajectories with the right identities, we propose our DM-GMPHD tracker.

DM-GMPHD tracker: We assume to have recorded all the estimates of the absolutely distinguishable targets including the states estimates $\hat{X}_{k-1}^i$ and firstly propose to construct a root node set $\hat{X}_{k-1}^i$ where for every estimate $m_{k-1}^i \in \hat{X}_{k-1}^i$ there at least one other $m_{k-1}^j (i \neq j)$ for which the predictions of m_{k-1}^i and m_{k-1}^j satisfy (5), so do the updated terms. Then keep all kinds of relatively high hypothesis generated from new observations and the estimates from $\hat{X}_{k-1}^i$ and associate these hypotheses with the recorded estimates forming 'hypothesis-to-track' trees.

The scheme includes three steps:

Step 1: Association launch condition: In PHD filter, we get all the predicted term $m_{k/k-1}^i$ and updated terms $m_{k/k}^i(z)$ of the state estimate $m_{k-1}^i \in X_{k-1}$ with the tag τ_i . Calculate:

$$D_{pre} = (m_{k/k-1}^i - m_{k/k-1}^j)^T P_{k/k-1}^{-1} (m_{k/k-1}^i - m_{k/k-1}^j)$$

for the arbitrary i -th and j -th estimates from the set of target state estimates $\hat{X}_{k-1}$, the weight ratio $w = w_{k/k-1}^i / w_{k/k-1}^j$ and just analyze the predicted terms when $D_{pre} \leq U_s$ where U_s is a given threshold used to select relatively close targets. Then we judge whether the predicted terms ($m_{k/k-1}^i$ and $m_{k/k-1}^j$) or updated terms ($m_{k/k}^i(z)$ and $m_{k/k}^j(z)$) satisfy (5) and make marks in the state estimates m_{k-1}^i and m_{k-1}^j . If different measurements are too close which results in that updated terms of m_{k-1}^i and m_{k-1}^j both satisfy (5) and, we also make marks in the state estimates m_{k-1}^i and m_{k-1}^j . The selecting threshold U makes the improved GMPHD tracker not to start the association scheme when two targets can be distinguished. Subsequently keep the updated terms of the marked estimates not merged and all the relatively high hypotheses are outputted.

Then stop executing the merging process for all the updated terms of the marked state estimates $\hat{X}_{k-1}^i$ and record the corresponding output. The marked state estimates from $\hat{X}_{k-1}^i$ become the root nodes of track hypothesis trees.

Step 2: 'Hypothesis-to-track' association: The identity of a track hypothesis is given by the label of the state estimate in $\hat{X}_{k-1}^i$ as the initializing track. The score of each track is represented by its LLR that is initialized with $\log(w_{k-1}^i)$. We propagate the mean and covariance of each track hypothesis as $\tilde{m}_{k/k-1}^i = F_{k-1} m_{k-1}^i$ and $\tilde{P}_{k/k-1}^i$. For each hypothesis branch $\tilde{m}_k^j (j \in T_k)$ of the initializing track its LLR is incremented as:

$$LLR_{k,i}^j = LLR_{k-1,i}^j + \log(N(\tilde{m}_k^j, \tilde{P}_{k/k-1}^j, P_k^j + \tilde{P}_{k/k-1}^j)) \quad (6)$$

Step 3: End condition: Supposing at time step k $\tilde{m}_k^i$ and $\tilde{m}_k^j$ as the track hypotheses of the highest LLRs are selected, we need to judge whether the two targets are already enough far from each other. In order to make sure that not only the two targets can be distinguished at current time step but also the next step, we propose to consider the separation distance of $\tilde{m}_k^i$ and $\tilde{m}_k^j$ as well as the predicted terms and the imaginary updated terms. Only when three end conditions become true we stop the association scheme and output the hypothesis tree of the highest LLRs. The first and second conditions are, respectively:

$$(\tilde{m}_k^i - \tilde{m}_k^j)^T \tilde{P}_k^{-1} (\tilde{m}_k^i - \tilde{m}_k^j) > 4 \quad (7)$$

$$(\tilde{m}_{k+1/k}^i - \tilde{m}_{k+1/k}^j)^T \tilde{P}_{k+1/k}^{-1} (\tilde{m}_{k+1/k}^i - \tilde{m}_{k+1/k}^j) > 4 \quad (8)$$

Now we review the update process. For an imaginary observation z_i , from:

$$(\tilde{m}_{k+1}^i(z_i) - \tilde{m}_{k+1}^j(z_i))^T \tilde{P}_{k+1}^{-1} (\tilde{m}_{k+1}^i(z_i) - \tilde{m}_{k+1}^j(z_i)) > 4$$

we get:

$$(\tilde{m}_{k+1/k}^i - \tilde{m}_{k+1/k}^j)^T (I - K_{k+1} H_{k+1})^T \tilde{P}_{k+1}^{-1} (I - K_{k+1} H_{k+1}) (\tilde{m}_{k+1/k}^i - \tilde{m}_{k+1/k}^j) > 4 \quad (9)$$

where K_{k+1} is gain matrix.

Making the problem simplified, for the updated terms generated by two imaginary observations z_i and z_t to one predicted Gaussian, suppose:

$$z_i = H\tilde{m}_{k+1/k}^{(i)} + \sigma_{z_i} R_{k+1}^{1/2} I_{nd}, z_t = H\tilde{m}_{k+1/k}^{(t)} + \sigma_{z_t} R_{k+1}^{1/2} I_{nd}$$

where, H is measurement matrix, R_{k+1} is covariance of measurement noise and $I_{n \times 1}$ is an n -row vector of which each element is one, we get the third end condition including (9) and:

$$\Delta z = \max(\text{abs}(H(m_{k+1/k}^i - m_{k+1/k}^j)) - \sigma_{pre} R_{k+1}^{1/2} I_{nd}), 0) \quad (10)$$

$$\Delta z^T K_{k+1}^T \tilde{P}_{k+1}^{-1} K_{k+1} \Delta z > 4$$

where σ_{pre} is a small threshold describing the deviation of imaginary observations and predicted observations.

Once we end the association scheme, we need to re-manage the weights of selected hypotheses to make GMPHD filter work regularly at subsequent time steps, even to delete the non-selected branches.

SIMULATION RESULTS

For illustration purpose, we consider a two-dimensional scenario. The moving model and the measurement model are the same as that in (Panta *et al.*, 2006) and (Yazdian-Dehkordi *et al.*, 2012).

The general parameters using the GMPHD filter include the pruning threshold $T_{th} = 10^{-5}$ merging threshold $U = 4$, weight threshold $w_{Th} = 0.5$ and maximum number of Gaussian terms $J_{max} = 200$. In addition, the selecting threshold $U_c = 50$, $U_s = 16$ and $\sigma_{pre} = 0.15$.

Scenario 1: There are two targets moving in straight paths with the same velocity in x axis. We set the standard deviation of the process noise $\sigma_v = 0.5$ (m/Sec²) and the standard deviation of the observation noise $\sigma_v = 1$ m.

Figure 1 shows an example of two crossing targets with speed deviation $\Delta v = 1.2$ m sec⁻¹. Results presented in Fig. 2 show that the original GMPHD tracker fails to correctly keep separate identities of the two targets while by our association scheme DM-GMPHD tracker can correctly keep the identities of the two targets as shown in Fig. 3.

We also respectively apply the GMPHD tracker with ‘estimate-to-Track’ association in (Panta *et al.*, 2006) and the CGMPHD filter in (Yazdian-Dehkordi *et al.*, 2012) to track the two targets in scenario 1. The results of both schemes are absolutely the same as the results of the original GMPHD tracker as shown in Fig. 2.

Table 1 demonstrates the rate that targets are correctly identified over 200 simulations for two targets with different speed deviations and shows that we have achieved the goal to obtain enough high accurate rate.

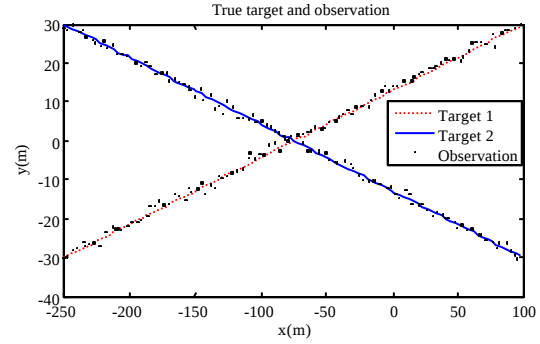


Fig. 1: Crossing target trajectories with target ‘1’ (dashed line) and target ‘2’ (solid line).

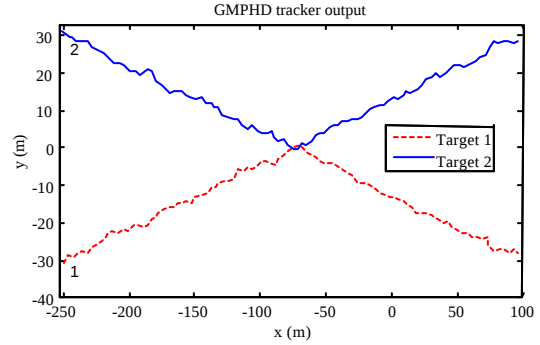


Fig. 2: Trajectories (wrongly identified) given by the original GMPHD tracker.

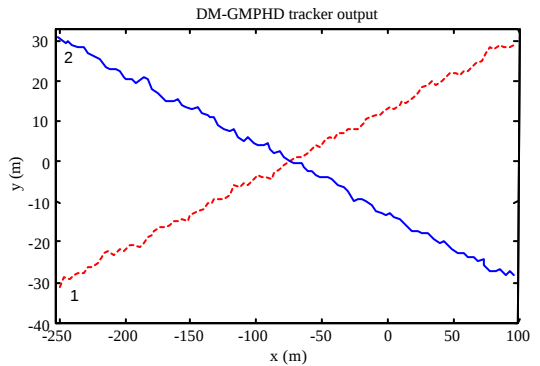


Fig. 3: Trajectories given by DM-GMPHD tracker

Table 1: Accurate rate of the original GMPHD tracker and the improved scheme for different speed deviation

Speed deviation (m sec ⁻¹)	The original GM-PHD tracker	CGMPHD	DM-GMPHD tracker
$\Delta v = 1$	0.03	0.435	0.915
$\Delta v = 1.2$	0.075	0.54	0.945
$\Delta v = 1.4$	0.165	0.725	0.96
$\Delta v = 1.6$	0.3	0.8	0.96
$\Delta v = 1.8$	0.4	0.87	0.97
$\Delta v = 2$	0.58	0.925	0.97

Scenario 2: There are three targets moving in straight paths. We set the process noise $\sigma_c = 7\text{m}$ and the observation noise $p_{s,k} = 0.99$. Each target has a survival probability of $\sigma_c = 7\text{m}$ at each time step.

Figure 4 shows the observations of three crossing targets and clutter at each time step. The detection probability and the mean of clutter are set to 0.99 and $2 \times 10^{-6} \text{m}^{-2}$.

As shown in Fig. 5 target 2 and target 3 are assigned the same tag after crossing by the original GMPHD tracker. If we just keep the label of the estimate with the strongest weight when multiple estimates have the same label, the result is shown in Fig. 6. The CGMPHD tracker also fails to correctly keep the identities of target 2 and target 3 as shown in Fig. 7 while by our association scheme DM-GMPHD tracker can correctly keep the identities of the three targets as shown in Fig. 8.

To study the performance of our proposed method with higher uncertainties, we provide the results of the three trackers in scenario 2 with various clutter rates and probabilities of detection. The mean Number of Target Estimation Error (NTE) (Yazdian-Dehkordi *et al.*, 2012) and

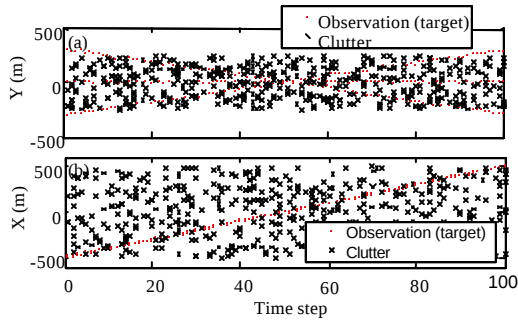


Fig. 4: Observations of three crossing targets and clutter at each time step

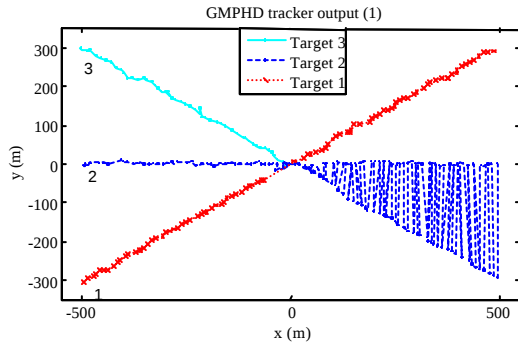


Fig. 5: Trajectories given by the original GMPHD tracker (After crossing there are two estimates with the same label)

the mean optimal subpattern assignment (OSPA) (Schuhmacher *et al.*, 2008) are computed at each time step for 500 runs and then over time.

Fig. 9-12 show the averaged NTE, OSPA and the accurate rates of tracking three targets for scenario 2 over 500 runs. For different clutter rates, the probability of detection p_D is set to 0.99 and for different probabilities of detection the clutter rate is fixed at $\lambda_c = 2 \times 10^{-6} \text{m}^{-2}$.

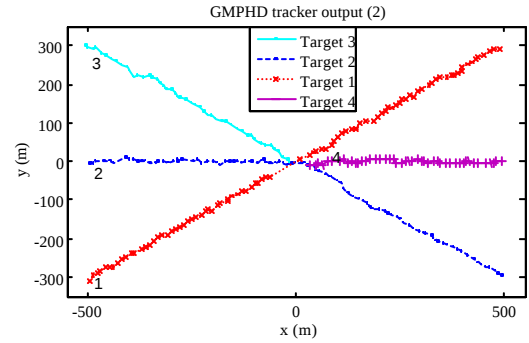


Fig. 6: Trajectories given by the original GMPHD tracker (the original identity is assigned to the branch with the strongest weight)

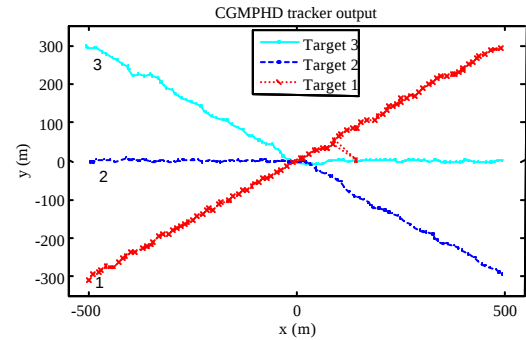


Fig. 7: Trajectories given by CGMPHD tracker

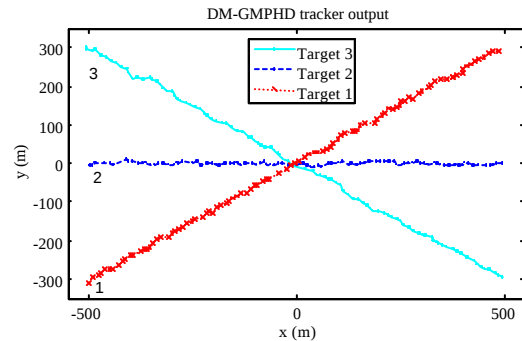


Fig. 8: Trajectories given by our proposed DM-GMPHD tracker

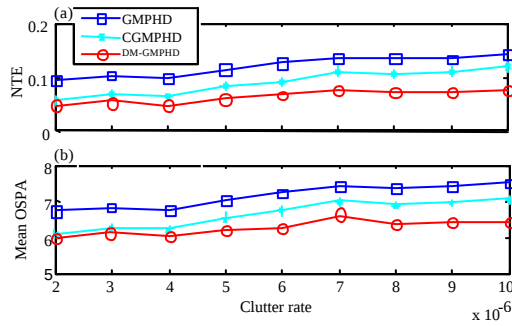


Fig. 9: Averaged NTE and OSPA of tracking three targets with different clutter rates.

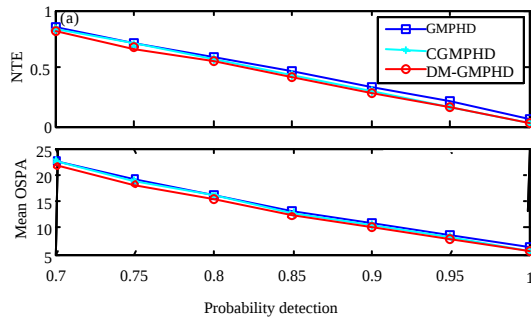


Fig. 10: Averaged NTE and OSPA of tracking three targets with different probabilities of detection.

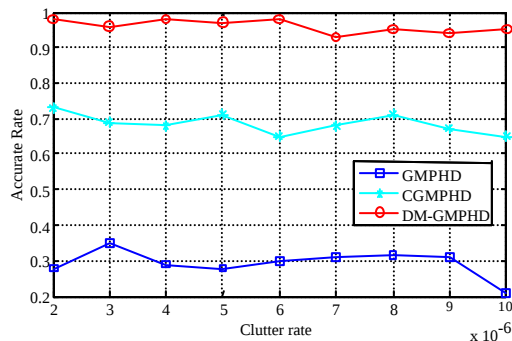


Fig. 11: Accurate rate with different clutter rates

Fig. 9 and 10 illustrate that our proposed DM-GMPHD tracker has the lowest estimation errors.

As shown in Fig. 11 and 12, the CGMPHD tracker has substantially improved the performance of the GMPHD tracker while our proposed approach has a higher accurate rate in all configurations. For different clutter rates, the accurate rates of the DM-GMPHD tracker are greater than 90%. For different probabilities of detections, the accurate rates of the DM-GMPHD tracker are greater than 80%.

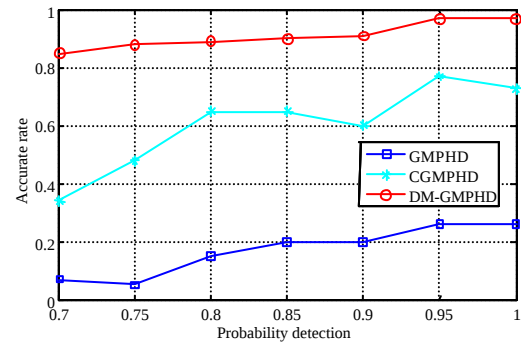


Fig. 12: Accurate rate with different probabilities of detection

CONCLUSION

This study presents an improvement on the GMPHD filter for close target tracking and identifying. We analyze the separation condition of distinguishing between close targets and propose to apply a ‘hypothesis-to-track’ association scheme when the distance between the predicted states of target estimates is within the separation distance. The simulation results show that the proposed delayed merging GMPHD tracker has a better performance in identity confirmation than the original GMPHD filter as well as the improved schemes in existing articles when tracking closely-spaced targets.

As the future work, our research plan is to apply our approach in more scenarios combining the scheme of re-managing weights in CGMPHD filter.

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