



Online Adapting the Magnitude of Target Birth Intensity in the PHD Filter

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ABSTRACT

Capturing new targets that spontaneously appear in the multi-target tracking (MTT) scene requires a formation of TBI (target birth intensity) item in the PHD (probability hypothesis density) equations. That is, in the particle implementation of the PHD filter, a number of new particles with a certain weight mass are added to the underlying particle set during the propagation of the PHD. In general, TBI is assumed to hold for the same magnitude at all scans. This ad-hoc option is simple but is not always desirable. In this paper, a measurement-driven adaptive mechanism is proposed that determines the magnitude of TBI in real time based on the estimated number of new-born targets, which is calculated by employing the newest measurements. Simulation demonstration of the particle PHD filter has been provided.

1 Introduction

The multi-target tracking (MTT) has a long history of research over a half of century, with many applications in both military and commercial realms, including, air traffic control, intelligence, surveillance, and reconnaissance (ISR), space applications, oceanography, autonomous vehicles and robotics, remote sensing, computer vision, and biomedical research [1]. MTT involves the joint estimation of the number and states of multiple targets in the presence of spontaneous birth of new targets, detection uncertainty, noise and false alarms, etc. which is far more complex than clutter-free single target tracking. Apart from handling the respective process and measurement noises in the dynamic and measurement models, one has to contend with many more challenges, such as the following: 1) The number of targets is unknown and time varying with regards to the spontaneous birth, spawn and death of targets; 2) False alarms (clutter) exist and can be significant; 3) The sensor probability of detection is less than unity; and 4) Most challengingly, data association

between measurements and targets in the presence of clutter is required to apply the traditional filtering.

The states and observations of target are mathematically a finite-set-valued random variable that is random in both the number of elements and the values of the elements themselves, i.e. random finite sets (RFS). The idea of modelling states and observations as RFS is natural and does not need to consider the data order. With the incorporation of RFS and point process theory in the MTT problem, the probability hypothesis density (PHD) filter affords a concise yet adequate formation of the challenging MTT problem [2] which has attracted increasing attention in terms of algorithm design (see a review given in [3]) and parallel processing [4]. Despite the data association difficulty, the PHD filter still need to deal with target birth, false alarms and detection of low probability. A key step before filtering is the system modelling that includes setting up as much as possible the close-to-truth model for new birth targets (such as the birth intensity function [5]), target moving dynamics (such as model uncertainty [6]), measurement



model (such as detection uncertainty [7]) and background identification (such as clutter estimation [7, 8]). In particular, a target birth intensity (TBI) item is required in the PHD equation due to the spontaneous appearance of new targets. The goal of TBI is to capture the newly appearing targets online, integrating them into the underlying PHD which is arguably the prerequisite of the consequent ‘tracking’. Nevertheless, information about the birth of new targets is very limited in passive target tracking e.g. the average number of new targets in each scan is unknown due to the spontaneity of the target birth, rendering the modeling of TBI very challenging.

Basically, two critical issues are involved with the modeling of TBI. One is the birth function (area and birth model) of new targets, which is the main part of TBI. The other is the probability of new target birthing or the expected number of new targets, namely the magnitude of TBI. For the birth area of new targets, a typical case is that it is known a priori. For example, targets appear around the fixed area such as airports [9] or most likely from the edges of the field of view [10]. In this case, the appearance area of new-birth targets can be built efficiently. In more common cases, where the targets can appear anywhere, it has to cover the entire state space. To overcome this computational inefficiency, various measurement-driven target birth models have been proposed for the particle implementation in [5] and [11], which position new particles around measurements to represent newborn targets. In the closed-form implementation, measurements are classified into two parts, namely, the measurements for the newborn targets and those for the survival targets in [12, 13] and a detector based on the continuity of measurements were used to generate intensities of new targets. Further on, Doppler information might be used to initialize a more realistic target/track velocity [14].

In contrast, less work is devoted to adapting the magnitude of TBI. For example, the previous work [5] has proposed an adaptive TBI function to model the target birth intensity function, yet

offered no clue about how to determine the TBI magnitude, which still need to be manually assumed. In current works, the TBI was simply assigned with a constant magnitude, i.e. a certain number of new targets or a new target with a certain probability was assumed. This simple selection of the magnitude of TBI is in fact an ‘ad-hoc’ approach and is not always desirable. Especially in industrial applications, this ad-hoc specification can cause many unexceptional problems. In this paper, a data-driven adaptive mechanism is proposed to determine the magnitude of the TBI by using the newest measurements. This paper primarily investigates the case of the particle implementation of PHD filters.

The basic content of the particle PHD filter and the modeling of the TBI are reviewed in section II. Our approach is presented in section III. Simulation is given in section IV before we conclude in section V.

2 Problem stamen

2.1 Assumptions and definitions

In the standard setup of MTT, indistinguishable targets move continuously in a given region, typically independently according to a known Markov process. Targets birth at random in space and time (spontaneously), can persist for a random length of time, and then cease to exist. The partial states of moving targets are measured, either at random intervals or more typically in periodic scans that measure the positions of all targets simultaneously. The position measurements are noisy and occur with detection probability less than one, and there are spurious position reports as referred to false alarms [15].

Furthermore, the following assumptions are required in the PHD filter. (A.1) Each target is assumed to evolve and generate measurements independently of others; (A.2) The clutter distribution is assumed to be Poisson and independent of the measurements; (A.3) One target can generate no more than one observation; (A.4) the surviving-target process is Bernoulli and the appearing-target process is



Poisson [16]. The first three assumptions are common in general Bayesian multi-target trackers while the fourth is specific for the PHD recursion.

For a formal statement, the state space of targets is denoted as $\chi \subseteq \mathbb{R}^{nx}$ and the Markov transition density is modeled as $f_{k|k-1}(\cdot|\cdot)$, i.e. given a state x_{k-1} at time $k-1$, the probability density of a transition to the state x_k at time k is $f_{k|k-1}(x_k|x_{k-1})$. The observation space is denoted as $\mathbb{Z} \subseteq \mathbb{R}^{nz}$ and the likelihood function is modeled as $g_k(\cdot|\cdot)$, i.e. given a state x_k at time k , the probability density of receiving the observation $z_k \in \mathbb{Z}$ is $g_k(z_k|x_k)$. At time k , the collections of states and measurements can be represented as finite sets $X_k = \{x_{k,1}, \dots, x_{k,N(k)}\} \in F(\chi)$ and $Z_k = \{z_{k,1}, \dots, z_{k,M(k)}\} \in F(\mathbb{Z})$ respectively, where $N(k)$ and $M(k)$ are the number of targets and measurements and $F(\chi)$ and $F(\mathbb{Z})$ are the collections of all finite subsets of targets and measurements, respectively. We have

$$X_k = \left(\bigcup_{x \in X_{k-1}} S_{k|k-1}(x) \right) \left(\bigcup_{x \in \mathbb{I}} B_{k|k-1}(x) \right) \cup R_k$$

where $S_{k|k-1}(x)$ and $B_{k|k-1}(x)$ are the RFS of targets that survive and spawn at scan k from target states X_{k-1} , and R_k is the RFS of targets that appear spontaneously at scan k .

$$Z_k = \left(\bigcup_{x \in X_k} G_k(x) \right) \cup \Gamma_k$$

where $G_k(x)$ is the random set of measurements coming from target $x \in X_k$ and Γ_k is the set of measurements coming from clutter at scan k .

A. The PHD filter and its particle implementation

Let $D_{k|k}$ and $D_{k|k-1}$ be the intensity functions (i.e. PHD) associated to the multi-target posterior point process and the multi-target prior point process, namely $D_{k|k} = D_{k|k}(x_k|Z_{1:k})$, $D_{k|k-1} = D_{k|k-1}(x_k|Z_{1:k-1})$, the PHD filter has the following recursions

$$\dots \rightarrow D_{k-1|k-1} \rightarrow D_{k|k-1} \rightarrow D_{k|k} \rightarrow \dots$$

which evolves via two types of updating steps:

1) time-update step (PHD predictor)

$$D_{k|k-1} = \int_{\chi} \phi_{k|k-1}(x|u) D_{k-1|k-1}(u) du + \gamma_k(x) \quad (3)$$

where the following abbreviation is used

$$\phi_{k|k-1}(x|u) = p_S(u) f_{k|k-1}(x|u) + b_k(x|u)$$

where $b_k(x|u)$ denotes the intensity function of the RFS of targets spawned from the previous state u , $p_S(x)$ is the survival probability of a target and $\gamma_k(x)$ is the birth intensity function of new targets at scan k . The TBI may be integrated into the PHD updater [17] rather than the predictor as above.

2) data-update step (PHD updater)

$$D_{k|k}(x) = \left[(1 - p_D(x)) + \sum_{z \in Z_k} \frac{p_D(x) g_k(z|x)}{\kappa_k(z) + C_k(z)} \right] D_{k|k-1}(x) \quad (4)$$

where the following abbreviation is used

$$C_k(z) = \int p_D(u) g_k(z|u) D_{k|k-1}(u) du \quad (5)$$

Where $g_k(z|x)$ is the single-target single-sensor likelihood, $p_D(x)$ is the probability of detection and $\kappa_k(z)$ is the clutter intensity at time k , respectively. The clutter intensity function can be slimmed based on gating technology [23].

The PHD recursions can be implemented approximately via particles [9] or finite GM (Gaussian mixture) [18]. The particle filter is a powerful approximation method that is free of linearity and Gaussian assumptions [19, 20] and thereby can meet requirements of general MTT scenes. The particle implementation uses a set of samples to approximate the PHD predictor and updater. Given the importance densities $p_k(\cdot|Z_k)$, $q_k(\cdot|x_{k-1}, Z_k)$ and supposing that there are L_{k-1} original particles in time step $k-1$ and J_k new particles are allocated for possible new-born targets, according to (3), the particle approximation of the predictor can be written as

$$D_{k|k-1}(x_k) = \sum_{i=1}^{L_{k-1} + J_k} w_{k|k-1}^{(i)} \delta_{x_k^{(i)}}(x_k) \quad (6)$$

where

$$x_k^{(i)} \sim \begin{cases} q_k(\cdot|x_{k-1}^{(i)}, Z_k), i = 1, \dots, L_{k-1} \\ p_k(\cdot|Z_k), i = L_{k-1} + 1, \dots, L_{k-1} + J_k \end{cases} \quad (7)$$

$$w_{k|k-1}^{(i)} = \frac{\phi_{k|k-1}(x_k^{(i)}|x_{k-1}^{(i)}) w_{k-1}^{(i)}}{q_k(x_k^{(i)}|x_{k-1}^{(i)}, Z_k)}, i = 1, \dots, L_{k-1} \quad (8a)$$

$$w_{k|k-1}^{(i)} = \frac{\gamma_k(x_k^{(i)})}{J_k p_k(x_k^{(i)}|Z_k)}, i = L_{k-1} + 1, \dots, L_{k-1} + J_k \quad (8b)$$

The particle approximation of the PHD updater is



$$D_{k|k}(x_k) = \sum_{i=1}^{L_{k-1}+J_k} w_{k|k}^{(i)} \delta_{x_k^{(i)}}(x_k) \quad (9)$$

where

$$w_{k|k}^{(i)} = \left[1 - p_D(x_k^{(i)}) + \sum_{z \in Z_k} \frac{p_D(x_k^{(i)}) g_k(z|x_k^{(i)})}{\kappa_k(z) + C_k(z)} \right] w_{k|k-1}^{(i)} \quad (10)$$

$$C_k(z) = \sum_{j=1}^{L_{k-1}+J_k} p_D(x_k^{(j)}) g_k(z|x_k^{(j)}) w_{k|k-1}^{(j)} \quad (11)$$

2.2 Modeling of TBI

The birth intensity can be written as $\gamma_k(x) = r_k \times p_k(x)$ where r_k is the magnitude and $p_k(x)$ models the birth function. r_k and $p_k(x)$ correspond to two critical issues that need to be considered by the user separately. r_k reflects the average number of new targets and $p_k(x)$ provides the area and birth function of new target. The birth model $p_k(x)$ is addressed in a way that is more realistic such as measurement-driven target birth function [5, 11-13], uniform birth function [21] or entropy distribution [22], etc. whereas the magnitude of TBI has yet to attract enough attention. Furthermore, it is pointed out that in contrast to the sole use of position (including bearing) measurements, amplitude information and Doppler information (that depends on the hardware ability and additional information fusion) can be further considered provide initial target velocities [18].

On the other hand, $\gamma_k(x)$ is commonly applied with a constant magnitude i.e. r_k is fixed. For example, it is assumed as 20% [9, 23], 20% (10% each in two regions) [18], 5% [24], 25% [5], or 10% and 1% [17] (separately in two regions). That is, in the particle implementation, the same amount of new particles are generated at each step. This ad-hoc selection is simple but is not always desirable and can be problematic. If it can be “known” simply that targets birth are more likely to occur at special steps, the magnitude of TBI should be large. Otherwise, it should be small or even naught. To employ an optimal magnitude that matches the background is the same necessity for robust system modelling as employing a suitable TBI function, although the latter may appear more mathematical. Based on this, we propose a data-driven adaptive method that calculates the magnitude of the TBI by using the information

of newest measurements, as called measurement-driven magnitude-adaptive TBI. Note that the proposed approach is not specified to any particular $p_k(x)$.

3 Magnitude-Adaptive TBI

3.1 Measurement-driven magnitude-adaptive mechanism

Since the appearance of new targets is often deemed as spontaneous event, the assumption that new targets are possible to appear at any step must still be applied. In our approach, a tentative TBI $\hat{\gamma}_k$ is assumed with magnitude \hat{r}_k e.g. $\hat{r}_k = 0.2$ for each step. As common, a fixed number N_p of particles per target are used in the particle PHD filter. That is to assign $\hat{J}_k = \hat{r}_k \times N_p$ new particles $\{x_k^{(i)}, w_k^{(i)}\}_{i=1, \dots, \hat{J}_k}$, where the state is determined according to a specified birth model $p_k(x)$ according to (8b) while the weight can be determined as

$$w_{k|k-1}^{(i)} = \frac{r_k}{J_k} = \frac{1}{N_p} \quad (12)$$

The next step is to calculate the required TBI magnitude r_k based on the assumed \hat{r}_k and the underlying measurement Z_k . Using the PHD updater (10), the weight of each ‘tentative’ particle is updated as

$$w_{k|k}^{(i)} = \left[1 - p_D(x_k^{(i)}) + \sum_{z \in Z_k} \frac{p_D(x_k^{(i)}) g_k(z|x_k^{(i)})}{\kappa_k(z) + C_k(z)} \right] w_{k|k-1}^{(i)} \quad (13)$$

To note, $C_k(z)$ used in (13) is the same with (11) that needs to sum up all particles, although here updating is only for new particles.

Then, the updated weight mass of these new particles is

$$r_k = \sum_{i=1}^{\hat{J}_k} w_{k|k}^{(i)} \quad (14)$$

which can be interpreted as an estimate of the average number of new targets in the assigned TBI region according to the physical meaning of the PHD.

It is necessary to note that dense clutter can cause an overestimation of the magnitude of the



TBI as clutter can fall into the target birth area to pull up the estimation of (14). In this case, even the original PHD filter may also be ‘cheated’ to obtain an overestimation of the number of targets. Inevitably, not much can be done to avoid this as long as the measurement of clutter is indistinguishable with that from targets. For conservative reasons, in our approach, the magnitude can be further hard-limited to be not bigger than an upper threshold r_{upper} , e.g. $r_{\text{upper}}=0.8$ since a large value r_k can be obtained from (14) due to heavy clutter. It is only sensible to add just sufficient particles to capture new targets. In summary, the modified magnitude r_k for the TBI is given as follows

$$r_k = \min \left(\sum_{i=1}^{\hat{J}_k} w_{k|k}^{(i)}, r_{\text{upper}} \right)$$

That is, $J_k=r_k \times N_p$ ‘definitive’ new particles with uniform weight $\frac{1}{N_p}$ will be introduced into the prediction model (6) to approximate the TBI in the PHD updating.

3.2 Implementation with multiple TBI model

In cases that new targets have multiple birth forms e.g. new targets appearing at different areas; they need to be modelled as separate functions with individual magnitudes. In this case, the magnitude of each TBI function can be modelled as described in the single TBI model, which is independent of each other. That is, in each TBI model, an assumed number of tentative particles are used to process the tentative PHD updating and then, their weight sum are interpreted as the estimated number of targets in that area and further hard-limited as (15) to serve as the required magnitude of TBI for the underlying TBI function. We call this the independency of the magnitude of the TBI. This will be demonstrated in our simulation. Although our approach is not specified to particular target birth function, it is unable to assign magnitude for different TBI functions which assumes target birth in the same area since their PHDs could be overlapped in close proximity and thus are indistinguishable.

3.3 Discussion

The proposed approach can be viewed as a

look-ahead step where newest measurements are employed to shape the desired magnitude of TBI in a rehearsal trial. This is similar to the auxiliary variable idea [25] that employs knowledge about the next observation before resampling to ensure that particles which are more likely to have high likelihood have a good chance of surviving while here we employ the information of the next observations to determine our parameter (the magnitude of the TBI). Although the assumption of a tentative magnitude \hat{r}_k remains necessary, it will not affect much the result. For the computational requirement, we have

Remark 1. Since the prediction steps of all particles are independent of each other, the prediction (8a) and likelihood calculation $g_k(z|x_k)$ of the original L_{k-1} particles for all $z \in Z_k$, which are the main computation of the PHD updating, do not need to process twice but instead, the results calculated within (13) can be directly used in the definitive PHD updating step (10). Therefore, the likelihoods of the original L_{k-1} particles are stored after the calculation of (13).

Remark 2. As a matter of fact, if the birth intensity function is adapted in accordance with the measurements, the PHD equations must be applied in a different form, see [5]. Here in our approach, due to the independence of the TBI magnitude to the target birth function as well as to the PHD derivations, our magnitude-adaptive mechanism will not inflict any modification of the original PHD equations.

Serving in the core as an environment modelling technique, the proposed approach is suitable to work together with the adaptive target-birth function e.g. [5, 11] for complete adaptive TBI. The extension of our approach is feasible to advanced extensions of the PHD filter of higher order. In what follows, we only demonstrate the efficiency of our approach in the context of the particle implementation of the general PHD filter.

4 Simulations

4.1 Single target-birth model

A two-dimensional MTT scene is considered, in which eight targets will appear individually over the region $[-100,100] \times [-100,100]$. Here, we consider the TBI case with a single target birth area i.e. all targets appear around $\bar{x} = [0, 3, 0, -3]^T$ with Gaussian distribution covariance $Q = \text{diag}([10, 1, 10, 1])^T$, i.e. the TBI function is defined as $\gamma_k = r_k N(\cdot; \bar{x}, Q)$. Each target moves according to the following Markov transition dynamics

$$x^k = \begin{bmatrix} 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & \nabla \\ 0 & 1 & 0 & 0 \\ 1 & \nabla & 0 & 0 \end{bmatrix} x^{k-1} + \begin{bmatrix} 0 & \nabla \\ 0 & \nabla_5 \setminus \nabla \\ \nabla & 0 \\ \nabla_5 \setminus \nabla & 0 \end{bmatrix} \begin{bmatrix} N_1^{x^k} \\ N_2^{x^k} \end{bmatrix} \quad (16)$$

where the sampling time $\Delta=1$, $x_k = [x_{1,k}, x_{2,k}, x_{3,k}, x_{4,k}]^T$, $[x_{1,k}, x_{3,k}]^T$ is the position while $[x_{2,k}, x_{4,k}]^T$ is the velocity at time k . The process noise $\{w_{1,k}\}$, $\{w_{2,k}\}$ are mutually independent zero-mean Gaussian white noise with the standard deviation of 1 and 0.1, respectively.

The target-originated range measurements are given by

$$y_k = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{bmatrix} x_k + \begin{bmatrix} v_{1,k} \\ v_{2,k} \end{bmatrix} \quad (17)$$

where $\{v_{1,k}\}$ and $\{v_{2,k}\}$ are independent zero-mean Gaussian noise with the same standard deviation 2.5. Clutter is uniformly distributed over the region with an average rate of p points per scan, i.e. $\kappa = p/200^2$. The simulation uses $p=10$, the survival probability of a target $p_s=0.98$, the detection probability of a target $p_D=0.95$.

For the particle implementation, 500 particles per expected target are used and the total number of particles is hard-limited to be not less than 300. To capture the average performance, we run 100 trials. The trajectory of targets and observations are plotted in x and y dimension respectively in Fig.1. The scenario covers cases that new targets birth by single or multiple at positions being far or close to existing targets and then exists for a period of short or long. To extract the estimates, the Multi-EAP (Expect a Posterior) estimator [26] is employed which is proven to be computational faster, more accurate and reliable than clustering methods. The optimal sub-pattern assignment (OSPA) metric is used to evaluate the estimation

accuracy. A big OSPA distance indicates low estimation quality. The cut-off parameter used is 100, order parameter is 1, for an explanation see [27].

Three particle PHD filters are designed that are different from one another only in the magnitude of TBI. The basic particle PHD filter uses the constant $r_k = 0.2$ at all scans. In the exactly-known TBI model the time of target birthing is exactly known and the filter uses $r_k = 1$ at scans when new targets appear otherwise $r_k = 0$. The proposed adaptive approach applies the tentative $\hat{r}_k = 0.2$ to calculate the required magnitude that is upper-limited to be not larger than $r_{\text{upper}} = 0.8$ to avoid overshoot. The average estimated numbers of targets, magnitudes of TBI and OSPA of the three filters are given in figure 2. Compared with the TBI model with fixed magnitude, the adaptive approach and the exactly-known magnitude strategy for TBI have reduced the OPSA by 3.32% and 5.78% on average respectively. The filter using the exactly-known magnitude for TBI performs the best while the adaptive approach performs moderately and is better than the common filter that uses the fixed magnitude for TBI. In particular, obvious benefits are achieved when no new target birth. That is because integrating extra TBI into the underlying PHD recursions deflects the estimation, which may not be significant owing to the self-correction ability of the filter.

The computing time (excluding the estimate extraction step) and the number of particles used by different filters for each recursion are separately plotted in Figure 3. Compared with the TBI model with fixed magnitude, the adaptive approach has increased the computing time by 10.04% and the exactly-known magnitude strategy for TBI has reduced 0.01% on average respectively. This agrees with the analysis given in Remark 1 that the proposed magnitude-adaptive mechanism has not cost too much computation. Indeed, the simulation verifies the validity of the proposed magnitude-adaptive TBI model.



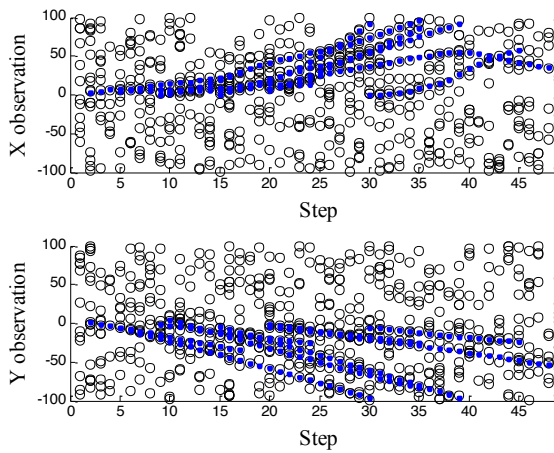


Fig. 1 Trajectories of targets (dot) and observations in one trial (circle)

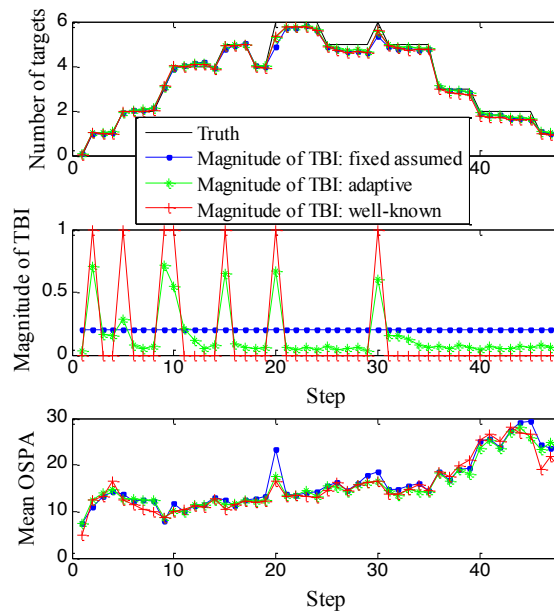


Fig.2 Estimated number of targets, magnitude of TBI used and mean OSPA of different filters

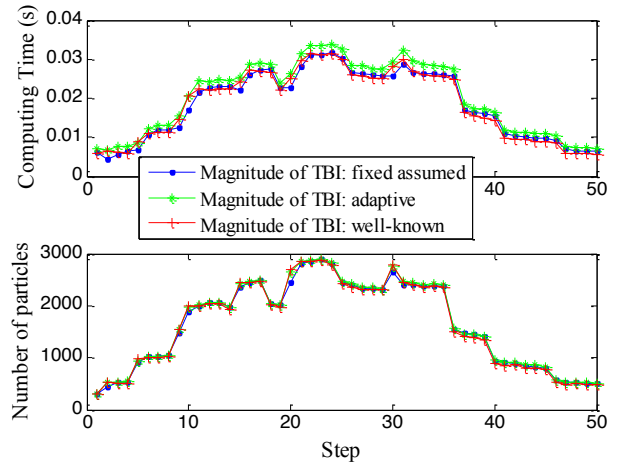


Fig.3 Computing time and number of particles used in different filters

4.2 Multiple target-birth model

In this example, we demonstrate the validity of our approach in a type of scene where new targets have different birth models based on the same state dynamic model (16) but different parameters and different observation model. The process noise $\{w_{1,k}\}, \{w_{2,k}\}$ are mutually independent zero-mean Gaussian white noise with the same standard deviation of 15. The range-and-bearing observation region is the half disc of radius 2000m. If detected the observation is a noisy range and bearing vector given by

$$y_k = \begin{bmatrix} \sqrt{x_{1,k}^2 + x_{3,k}^2} \\ \arctan(x_{1,k} / x_{3,k}) \end{bmatrix} + v_k \tag{18}$$

where $v_k \sim N(\cdot; 0, R_k)$, with $R_k = \text{diag}([\sigma_r^2, \sigma_\theta^2]^T)$, $\sigma_r = 5$ m, $\sigma_\theta = \pi / 180 \text{rad/s}$.

In this example, the birth process follows a Poisson RFS with intensity $\gamma_k = \sum_{i=1}^4 r_{k,i} N(\cdot; m_i, Q)$, where $m_1 = [-1500, 0, 250, 0]$, $m_2 = [-250, 0, 1000, 0]$, $m_3 = [250, 0, 750, 0]$, $m_4 = [1000, 0, 1500, 0]$, $Q = \text{diag}([50, 50, 50, 50]^2)$. This indicates that new targets are possible to appear from four different areas. Clutter is Poisson with intensity $\kappa = 1.6 \times 10^{-3}$ that is an average rate of $p = 10$ points per scan over the region $[0, 2000] \text{m} \times [0, \pi] \text{rad}$. The example uses $p_s = 0.98$, $p_D = 0.95$. Furthermore, 1000 particles per expected target



are used and the total number of particles is hard-limited to be not less than 600.

The trajectories of targets are plotted in the x - y position space in Fig.4. The basic particle PHD filter uses the constant $r_{k,1} = 0.02$, $r_{k,2} = 0.02, r_{k,3} = 0.03, r_{k,4} = 0.03$ at all scans. In the exactly-known TBI model the time and area of target birth is exactly known and the filter uses $r_{k,n}=1$ at scans when new targets appear in area n otherwise $r_{k,n}=0$, here n indicates the area new targets appear from. The proposed adaptive approach applies the tentative $\hat{r}_{k,1} = 0.02, \hat{r}_{k,2} = 0.02, \hat{r}_{k,3} = 0.03, \hat{r}_{k,4} = 0.03$ to calculate the required magnitude (under the upper threshold $r_{upper}=0.6$). The average magnitudes of TBI $r_{k,i}$ of the three filters, for these four different TBI functions are given in figure 5 separately. The magnitude obtained in our approach is larger than the constant assumption only at the steps when target birth incur and the following one or two steps when new targets are still around the target birth area. The results confirm that the proposed magnitude-adaptive mechanism could obtain the estimation of the magnitude of TBI that is close to the truth.

The mean OSPA, estimated number of targets and computing time of different filters on average of 100 trials with regard to each step are separately plotted in Figure 3. Compared with the TBI model with fixed magnitude, the adaptive approach and the magnitude-known strategy for TBI have increased the computing time by 16.4% and 2.92% on average respectively and have reduced the OPSA by 5.31% and 14.84% on average respectively. Again, the filter using the exactly-known magnitude for TBI performs the best while the adaptive approach performs moderately and is better than the filter that uses the constant magnitude for TBI. Particularly, the magnitude-adaptive TBI approach has spent more computational time than the single TBI models due to the complexity of the multiple TBI models.

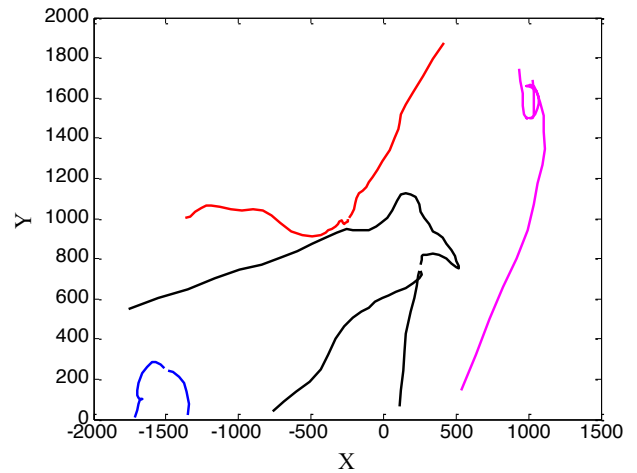


Fig. 4 Trajectories of targets birth from four areas

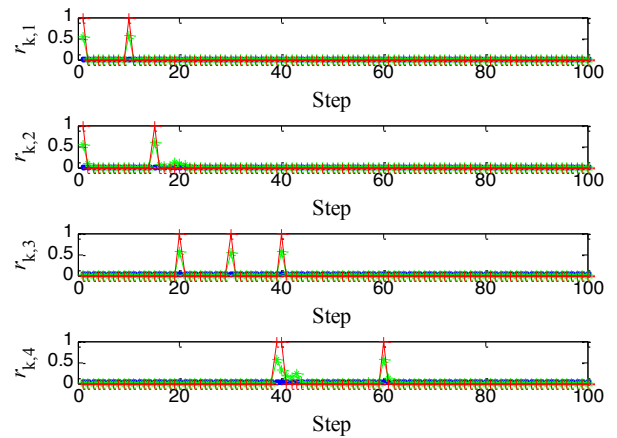


Fig. 5 Magnitudes of TBI used in each step by different filters



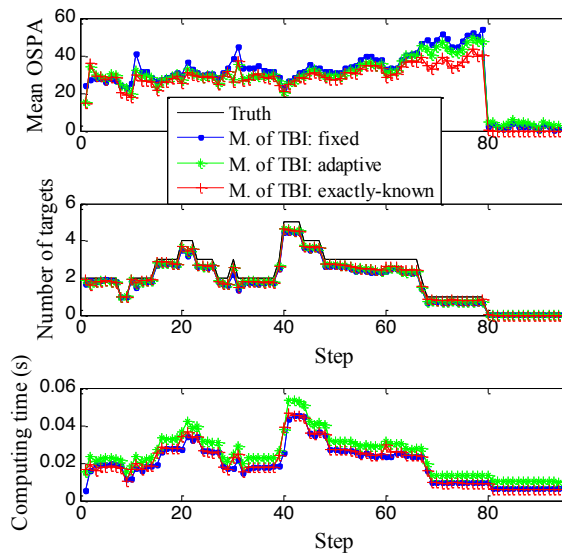


Fig.6 Mean OSPA, estimated number of targets and computing time used in different filters

Overall, the use of the magnitude-adaptive mechanism, whether for the single TBI model or for multiple TBI models, shows the advantage over the traditional ad-hoc approaches that employ constant assumptions on estimation accuracy but has disadvantage on the computing speed. The reduction of the computing speed can be compensated by reducing the number of particles used. Although the benefit due to the design of the magnitude of

TBI is not so significant, as one would expect, the proposed adaptive approach provides a reliable and adaptive solution to determine the magnitude of TBI. This avoids the blind manual specification of the magnitude of TBI in practice.

5. Conclusion

A measurement-driven magnitude-adaptive mechanism has been proposed for the target birth modeling in the PHD filter. It determines the magnitude of target birth intensity online by taking into account the information contained in the newest measurements, which requires little additional computation. The improvement on the modelling of the target birth magnitude is independent of the derivation of the PHD equations and therefore no modification needs to be made on the basic PHD equations. Simulations of the particle implementation of the PHD filter have demonstrated the validity of the proposed magnitude-adaptive approach, which provides a robust solution for industrial applications of the PHD filter.

5 References

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