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Article

Uncertainty-Aware δ -GLMB Filtering for Multi-Target Tracking

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Abstract: The δ -GLMB filter is an analytic solution to the multi-target Bayes recursion using in multi-target tracking. Theoretically, the δ -GLMB filter handles uncertainties in measurements in its filtering procedure. However, in practice, degeneration of the measurement quality affects the performance of this filter. In this paper, we will discuss the effects of increasing measurement uncertainty on δ -GLMB filter and also will propose two heuristic methods to improve the performance of the filter in such conditions. The base idea of proposed methods is to utilize the information stored in the history of the filtering procedure, which can be used to decrease the measurements uncertainty effects on the filter. Since the GLMB filters have shown good results in the field of multi-target tracking, an uncertain immune δ -GLMB can play as a strong tool for this area. In this study, the results indicate that the proposed heuristic ideas can improve the performance of the filtering in presence of uncertain observations.

Keywords: multi target tracking; N-Scan δ -GLMB; refined δ -GLMB; measurement uncertainty effect reduction

1. Introduction

Multi-Target tracking (MTT) is the procedure of estimating a time-varying number of targets and their states from a sequence of observations. The number of targets are usually unknown and the observations are noisy due to uncertainty of detection and presence of spurious targets (clutter) [1–5]. The trajectory of a target is another important outcome of MTT, [6] proposes a Bayesian multi-target tracking solution that also provides estimates of target trajectories. MTT suffers from main challenges including detection uncertainty and clutter that mislead the tracker and cause efficiency reduction in estimating number of targets, their states and trajectories. However there are many approaches to MTT, three paradigms are discussed as the main solutions. These are, Multiple Hypotheses Tracking (MHT) [7–9], Joint Probabilistic Data Association (JPDA) [10–12], and Random Finite Set (RFS) [13–16]. Using RFS approach in MTT, provides a sophisticated Bayesian formulation for this problem in which a group of target states (multi-target states) are considered as a finite set [17,18]. This framework is a very popular method in estimating multi-target with applications in computer vision [19,20], robotics [21–23], sonar [24–26], monitoring and surveillance systems [27,28], sensor networks [29–31], cell biology [32,33], augmented reality [34,35], and etc. In RFS approach the density of multi-target states is propagated recursively forward in time using the Bayes multi-target filter [36]. The Bayes filter is a multi-target tracker, where target specifications are incorporated into individual state (as what occurs in RFS method, states of multi-target in a unit of time are incorporated in a single set). Since Bayes multi-target filter is intractable due to intense numerical complexity, the Probability Hypothesis Density (PHD) [37], Cardinalized PHD (CPHD) [38] and multi-Bernoulli filters [39] have been developed as approximations to the Bayes filter. In this work, we concentrate on an analytic solution to the Bayes MTT, known as the δ -Generalized Labeled Multi-Bernoulli (δ -GLMB), which uses RFS notion to behave targets as distinguishable and unique entities. This filter is applicable of keeping trajectories and it includes conjugate priors, which are closed under Chapman-Kolmogorov

equation. However, results in [40–42] show promising performance in this filter, the performance of the filter decreases in situations that observation quality drops. The aim of this paper is to reduce effect of low detection rate and existence of clutter on the δ -GLMB filtering procedure. Consequent to the mentioned weakness, in particular we propose two methods, N-scan δ -GLMB and Refined δ -GLMB to alleviate the uncertainties in the observations using the information that are extracted from history of filtering during the time, which we believe to contain useful information in order to decrease uncertainties. The key innovation is to detect the components which are considered for truncation in the filtering procedure, however their truncation may cause targets get lost in a low detection rate. Detecting such situation is verified from the aspect of considering filtering history during the running time. The keyword *N-scan* is adopted from [43] which is utilised in order to induce the concept of using history of information in a certain window with size N.

This paper is organized as follows. A brief overview of RFS, Bayesian multi-target filtering and GLMB filter is provided in section 2. In section 3, N-scan δ -GLMB and refined δ -GLMB are introduced and discussed. Results of numerical examples are discussed in section 4 and concluding remarks and extensions are discussed in section 5.

2. Background

This section explains summary of the labeled RFS formulation of the MTT and the δ -GLMB filter proposed in [41] with implementation details in [40].

In this paper, the standard inner product notation is shown as $\langle f, g \rangle \triangleq \int f(x)g(x)dx$. Considering h as a real valued function then the notation of multi-object exponential is shown as $h^X \triangleq \prod_{x \in X} h(x)$ where $h^\emptyset = 1$ by convention. For a given set X , the cardinality (element numbers of that set) is denoted by $|X|$. The generalisation of the Kroneker delta is denoted by

$$\delta_Y(X) \triangleq \begin{cases} 1, & \text{if } X = Y \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

where the the input argument may be in any arbitrary form such as vectors, sets, etc. A generalisation of the indicator function, by

$$1_Y(X) \triangleq \begin{cases} 1, & \text{if } X \subseteq Y \\ 0, & \text{otherwise} \end{cases} \quad (2)$$

In this paper single target states are represented by lowercase letter e.g. x , Multi-target states are represented by uppercase letter e.g. X , Spaces are represented by blackboard bold e.g. $\mathbb{X}$.

2.1. Labelled Random Finite Sets

The RFS is a random variable finite set which includes random number of unordered points [14]. Since the number of points is random it is possible to consider a cardinality distribution for the RFS. The collection of target states is treated as a RFS with a certain cardinality distribution which enables MTT process without knowing the number of targets in the system. Labelled RFS is an extension to RFS notion which tries to keep the track of each target identity. For this purpose each target state $x \in \mathbb{X}$ is augmented with a unique unobserved label drawn from a discrete countable space $\ell \in \mathbb{L} = \{\alpha_i; i \in \mathbb{N}\}$, where α_i 's are distinct and $\mathbb{N}$ denotes a positive integer set.

2.1.1. Bernoulli RFS

The probability density of a Bernoulli RFS X on $\mathbb{X}$ is denoted by [44]

$$\pi(X) = \begin{cases} 1 - r, & X = \emptyset \\ r \cdot p(x), & X = \{x\}. \end{cases} \quad (3)$$

where r is the probability that the RFS have only one element and $1 - r$ is the probability that the RFS is empty. The element inside the RFS (in case of existence) is distributed according to probability density $p(\cdot)$. It is also remarkable that a Bernoulli RFS cardinality distribution is a Bernoulli distribution with parameter r .

2.1.2. Multi-Bernoulli RFS

A Multi-Bernoulli RFS X consists of union of multiple independent Bernoulli RFS $X^{(i)}$ with existence probability $r^{(i)} \in (0, 1)$, which $i = 1, \dots, M$, i.e., $X = \cup_{i=1}^M X^{(i)}$. $p(\cdot)$ is a probability density defined on $\mathbb{X}$. In [41] Multi-Bernoulli RFS is denoted by following alternative form which is abbreviated $\pi = \left\{ (r^{(i)}, p^{(i)}) \right\}_{i=1}^M$.

2.1.3. Labelled Multi-Bernoulli RFS

In [41] there is a derivation shows that the following formulation is alternative form of the LMB mentioned in [Appendix A](#)

$$\pi(X) = \Delta(X) 1_{\alpha(\Psi)}(\mathcal{L}(X)) [\Phi(X; \cdot)]^\Psi \quad (4)$$

where $\Delta(X)$ denotes the distinct label indicator $\delta_{|X|}(|\mathcal{L}(X)|)$ and $\mathcal{L}$ is a function defined on $\mathcal{L} : \mathbb{X} \times \mathbb{L} \rightarrow \mathbb{L}$ and a projection $\mathcal{L}((x, \ell)) = \ell$, hence $\mathcal{L}(X) = \{\mathcal{L}(x) : x \in X\}$ is the X labels set. The parameter $\Phi(X; \cdot)$ is defined as following [41]

$$\Phi(X; \zeta) = \sum_{(x, \ell) \in X} \delta_{\alpha(\zeta)}(\ell) r^{(\zeta)} p^{(\zeta)}(x) + (1 - 1_{\mathcal{L}(X)}(\alpha(\zeta))) \left(1 - r^{(\zeta)}\right) \quad (5)$$

It is remarkable that a labelled RFS and its unlabelled version have the same cardinality distribution [41], proposition 2.

2.2. Generalised Labelled Multi-Bernoulli RFS

Generalised Labelled Multi-Bernoulli (GLMB) RFS is a family of labelled RFS distributions. GLMB is closed under the multi-object Chapman-Kolmogorov equation with respect to the multi-object transition kernel [41]. The probability density of a GLMB RFS X on $\mathbb{X}$ is denoted by

$$\pi(X) = \Delta(X) \sum_{\xi \in \Xi} w^{(\xi)}(\mathcal{L}(X)) [p^{(\xi)}]^X \quad (6)$$

where Ξ is a discrete index set, the weight term $w^{(\xi)}(L)$ (Non-negative weights) and the exponential term $p^{(\xi)}$ satisfy the following conditions

$$\sum_{L \in \mathbb{L}} \sum_{\xi \in \Xi} w^{(\xi)}(L) = 1, \int p^{(\xi)}(x, \ell) dx = 1. \quad (7)$$

A GLMB family can be explicated as a mixture of multi-target exponentials which its points are not statistically independent. The GLMB cardinality distribution is also given by

$$\rho(n) = \sum_{L \in \mathcal{F}_n(\mathbb{L})} \sum_{\xi \in \Xi} w^{(\xi)}(L) \quad (8)$$

where $\mathcal{F}_n(\mathbb{L})$ presents the collection of finite subsets of $\mathbb{L}$ with exactly n elements (if no subscript n exists in the definition then there is no restriction on number of elements).

2.3. Bayesian multi-target filtering

MTT system is used to jointly estimate the number of targets and their states from the measured observations. Due to dynamic nature of the MTT problem, births, spawn and death of targets, the number of targets is a changing variable over time. In MTT the targets and observations are considered

as random finite sets which is defined respectively as $X_k = \{x_{k,1}, \dots, x_{k,N(k)}\}$, $Z_k = \{z_{k,1}, \dots, z_{k,M(k)}\}$, where k is the indicator of time, $N(k)$ is the number of targets in multi-target RFS at time k and $M(k)$ is the number of observations at time k . Some observations in Z_k may be a clutter and some may be missed according to a underlying probability density function. $g_k(\cdot|\cdot)$ is the multi-target likelihood function at time k which encapsulates the underlying models for clutter and detection. $f_{k|k-1}(\cdot|\cdot)$ is the multi-target transition density at time k which encapsulates the underlying models of births, spawns, deaths and target motions. The multi-target Bayes filter propagates π_k in time [44] according to the following update and prediction

$$\pi_k(X_k|Z_k) = \frac{g_k(Z_k|X_k)\pi_{k|k-1}(X_k)}{\int g_k(Z_k|X)\pi_{k|k-1}(X)\delta X'} \quad (9)$$

$$\pi_{k+1|k}(X_{k+1}) = \int f_{k+1|k}(X_{k+1}|X_k)\pi_k(X_k|Z_k)\delta X_k \quad (10)$$

where the integral is a set integral and $\pi_k(\cdot|Z_k)$ presents the multi-target filtering density at time k .

2.4. Measurement Likelihood Function

The multi-object observation set $Z = \{z_1, \dots, z_{|Z|}\}$ is a union of detected states and clutters. Each state $(x, \ell) \in X$ is either detected with probability $P_D(x, \ell)$ or missed with $1 - P_D(x, \ell)$. If the state is detected, it generates an observation point z with likelihood function $g(z|x, \ell)$. Considering independent detection conditioned on X and independent clutter from detection points with a Poisson distribution with intensity function κ the multi-object likelihood function is denoted by

$$g(Z|X) = e^{-\langle \kappa, 1 \rangle} \sum_{\theta \in \Theta(\mathcal{L}(X))} [\psi_Z(\cdot; \theta)]^X \quad (11)$$

where

$$\psi_Z(x, \ell; \theta) = \begin{cases} \frac{p_D(x, \ell)g(z_{\theta(\ell)}|x, \ell)}{\kappa(z_{\theta(\ell)})}, & \text{if } \theta_{(\ell)} > 0 \\ 1 - p_D(x, \ell), & \text{if } \theta_{(\ell)} = 0 \end{cases} \quad (12)$$

2.5. Delta-Generalized Labeled Multi-Bernoulli

Delta-Generalized Labeled Multi-Bernoulli (δ -GLMB) is an analytic solution to the Bayes multi-target filter which is a member of GLMB family. Despite the closeness of this family under Chapman-Kolmogorov equation (hence, closed under the Bayes recursion), the numerical implementation of such family is ambiguous. In order to solve this problem, there is an alternative form for GLMB known as δ -GLMB which is denoted by

$$\pi(X) = \Delta(X) \sum_{(I, \xi) \in \mathcal{F}(\mathbb{L}) \times \Xi} w^{(I, \xi)} \delta_I(\mathcal{L}(X)) [p^{(\xi)}]^X \quad (13)$$

Substitution the term $w^{(\xi)}(I)$ with $w^{(I, \xi)}$ in Equation 6 is a new presentation that simplifies the numerical implementation [40].

The δ -GLMB filter and specially the prediction operation, is conditioned on measurements observed up to time k . The discrete space Ξ contains the association map histories from the initial point of filtering history up to present time of filtering [40]. Let Θ_t shows the association map space at time t , then Ξ can be defined as $\Theta_{0:k} \triangleq \Theta_0 \times \dots \times \Theta_k$. Hence the update and prediction densities of a δ -GLMB is denoted as following, respectively

$$\pi_k(X|Z_k) = \Delta(X) \sum_{(I, \xi) \in \mathcal{F}(\mathbb{L}_{0:k}) \times \Theta_{0:k}} w_k^{(I, \xi)} \delta_I(\mathcal{L}(X)) [p_k^{(\xi)}(\cdot|Z_k)]^X \quad (14)$$

$$\pi_{k+1|k}(X) = \Delta(X) \sum_{(I, \xi) \in \mathcal{F}(\mathbb{L}_{0:k+1}) \times \Theta_{0:k}} w_{k+1|k}^{(I, \xi)} \delta_I(\mathcal{L}(X)) [p_{k+1|k}^{(\xi)}]^X \quad (15)$$

where $\xi = (\theta_0, \dots, \theta_k)$, $\theta_k \in \Theta_{0:k}$ is a association history map up to time k . It is noticeable that the history association map contains every target label during the time, births, deaths and spawned targets. considering $I \in \mathcal{F}(\mathbb{L}_{0:k})$ as a representation of a track label at time k , the pair $(I, \xi) \in \mathcal{F}(\mathbb{L}_{0:k}) \times \Theta_{0:k}$ is known as *hypothesis*. The weight of a hypothesis $w_k^{(I, \xi)}$ is the probability of the corresponding weight. $p^{(\xi)}$ is the density of the kinematic state of track ℓ for each ξ .

For propagating the densities forward in time Bayesian recursion is used. As shown in [40] the results are closed form solutions for updating and prediction. The update formula of a δ -GLMB is denoted by

$$\pi(X|Z) = \Delta(X) \sum_{(I, \xi) \in \mathcal{F}(\mathbb{L}) \times \Xi} \sum_{\theta \in \Theta(I)} w^{(I, \xi, \theta)}(Z) \delta_I(\mathcal{L}(X)) [p^{(\xi, \theta)}(\cdot|Z)]^X \quad (16)$$

where $\Theta(I)$ denotes association maps which are related to components with identity domain I ,

$$w^{(I, \xi, \theta)}(Z) \propto w^{(I, \xi)} [\eta_Z^{(\xi, \theta)}]^I, \quad (17)$$

$$\eta_Z^{(\xi, \theta)}(\ell) = \langle p^{(\xi)}(\cdot, \ell), \psi_Z(\cdot, \ell; \theta) \rangle, \quad (18)$$

$$p^{(\xi, \theta)}(x, \ell|Z) = \frac{p^{(\xi)}(x, \ell) \psi(x, \ell; \theta)}{\eta_Z^{(\xi, \theta)}(\ell)}, \quad (19)$$

And the prediction formula is denoted by

$$\pi_+(X_+) = \Delta(X_+) \sum_{(I_+, \xi) \in \mathcal{F}(\mathbb{L}_+) \times \Xi} w_+^{(I_+, \xi)} \delta_{I_+}(\mathcal{L}(X_+)) [p_+^{(\xi)}]^{X_+} \quad (20)$$

where (considering S as a survival component indicator and B as newly born ones, $\supseteq$ is sign for super set concept and subscript $+$ is used for time $k + 1$)

$$\begin{aligned} w_+^{(I_+, \xi)} &= w_S^{(\xi)}(I_+ \cap \mathbb{L}) w_B(I_+ \cap \mathbb{B}) \\ w_S^{(\xi)}(L) &= [\eta_S^{(\xi)}]^L \sum_{I \supseteq L} [1 - \eta_S^{(\xi)}]^{I-L} w^{(I, \xi)} \\ \eta_S^{(\xi)}(\ell) &= \langle p_S(\cdot, \ell), p^{(\xi)}(\cdot, \ell) \rangle \\ p_+^{(\xi)}(x, \ell) &= 1_{\mathbb{L}}(\ell) p_S^{(\xi)}(x, \ell) + 1_{\mathbb{B}}(\ell) p_B(x, \ell) \\ p_S^{(\xi)}(x, \ell) &= \frac{\langle p_S(\cdot, \ell) f(x|\cdot, \ell), p^{(\xi)}(\cdot, \ell) \rangle}{\eta_S^{(\xi)}(\ell)} \end{aligned} \quad (21)$$

δ -GLMB performs filtering via a recursion which propagates the multi-target filtering density π_k forward in time [40] each iteration consist of a prediction, update and state extraction which estimates the target states from the filtering density.

2.6. N-Scan GM-PHD filter

GM-PHD filter has been proposed by [45] as a closed-form solution to the PHD filter [37]. The GM-PHD filter models each target with a Gaussian component with an associated weight (w_k^i), mean (m_k^i) and covariance (S_k^i). After performing predict and update phase, this filter extracts the Gaussian components whose weights are greater than a predefined threshold to estimate the multi-target states at each step and discard those components recon as non-informative, due to the value of their weights [45]. This pruning method is not always effective, suppose that the measurement of the target is uncertain hence, the weight of the target is significantly decreased and the estimation of the target is lost. [43] proposes a N-scan approach which improves the performance of the GM-PHD filter. This method benefits from the N last history of the targets to prevent missing the estimation of the targets in different

uncertainties. N-Scan GM-PHD defines each Gaussian component with extra parameters including θ_k^i and WH_k^i in order to improve the tracking performance of the GM-PHD method, where θ^i is a binary confidence indicator showing a component is extracted before or not and WH^i is a weight history for component i containing the N last weights of the component, $WH_k^i = [w_{k-N+1}^i, \dots, w_{k-1}^i, w_k^i]$. N-Scan GM-PHD filter propagates parameter set $x_k^i = \langle w_k^i, m_k^i, S_k^i, \theta_k^i, WH_k^i \rangle$ in time and utilise these parameters in state extraction section in order to propose a new method for pruning, instead of discarding components compared with a predefined threshold. It calculates the number of weights WH_k^i which exceed the predefined threshold and treat them with a new pruning policy which considers the whole N sized history window of weights (More details are available in [43]). Experiment results in [43] shows that considering the history of weights instead of a single weight at a moment k , improves immunity of the filtering procedure to the uncertainties occurring in the measurement.

3. Proposed Methods

Each iteration of δ -GLMB filter involves a prediction operation followed by an update operation. These operations generate multi-target exponential weighted sums [40] which the terms number are intractable due to super-exponential growth of the terms in time. It is not rational to exhaustively consider all the terms in computations, hence it is obligatory to prune some terms. Multi-object densities are truncated by keeping the most informative terms respect to their weights and discarding those reckon non-informative respect to their insignificant weights (the components with a weight lower than a predefined threshold are truncated). This section analyses truncation in uncertain conditions and shows that pruning phase of δ -GLMB causes some terms to be truncated from the filtering procedure which are informative during a time window, however their weights have decreased at the moment due to an uncertainty conditions like miss-detection.

As a sequel to [46] which proposed concept of N-scan δ -GLMB, this section details the N-scan δ -GLMB implementation and presents enhanced update and prediction phase regarding N-Scan concept.

3.1. Uncertainty Effects on δ -GLMB

In δ -GLMB filtering procedure, the pruning phase might cause a weak performance in scenarios with high uncertainty level (e.g. low detection probability, high clutter ratio, etc.). Suppose that one or more targets are not detected, due to miss-detection of these targets, their associated hypotheses weight ($w^{(I,\xi)}$) diminish hence the associated hypotheses of true tracks are removed from the filtering procedure and cause the filtering performance drops. Furthermore, from a mathematical point of view as it is obvious in Equation 12 the low detection rate cause the parameter ψ to decrease and as the result, the multi-state target density decreases. In such conditions losing true tracks produces a less informative approximation to the posterior distribution in Equation 14 which is clearly obvious inferred from Equation 18, Equation 17 and Equation 16.

3.2. N-Scan δ -GLMB

In δ -GLMB filtering procedure there is a pruning operation that discards the hypotheses (I, ξ) whose weights are lower than an empirical predefined threshold W_{Th} .

$$\Omega_k = \{\forall (I, \xi) \in \mathcal{F}(\mathbb{L}_k) \times \Theta_k \mid w_k^{(I,\xi)} \geq W_{Th}\} \quad (22)$$

where Ω_k is defined as the pool of containing all hypotheses after pruning. All the hypotheses which exist in this pool continue in the filtering procedure and those which do not exist any more, are discarded. As mentioned before this operation takes occur in order to prevent increasing hypotheses numbers exponentially during the time and eventually make the filtering procedure intractable. This pruning and its sequel state extraction is not always effective as pointed out in subsection 3.1. Whenever the weight of a hypothesis degenerates below the threshold W_{Th} the hypothesis is discarded however, weight devaluation of a hypothesis may be a sequence of miss detection or another uncertainty.

In this paper, a simple and effective N-scan approach [43,46] is used for truncating the hypotheses instead of discarding those with weight lower than an empirical predefined threshold W_{Th} . Using N-scan approach improves the performance of the previous methods specially in scenarios with lower SNR ratio which reckon as uncertain conditions. The suggested method benefits from the N last history of the weights of hypotheses to struggle with possible uncertainties. A δ -GLMB is completely characterised by the set of parameters $\{(w^{(I,\xi)}, p^{(\xi)}) : (I, \xi) \in \mathcal{F}(\mathbb{L}) \times \Xi\}$. This paper follows [40] which considers parameters set of δ -GLMB as an enumeration of all hypotheses together with their weights and track densities. This assumption aims ease of the implementation procedure. Considering the mentioned assumption the δ -GLMB parameters set are shown as $\{I_k^{(h)}, \xi_k^{(h)}, w_k^{(h)}, p_k^{(h)}\}_{h=1}^H$ where $w^{(h)} \triangleq w^{(I^{(h)}, \xi^{(h)})}$ and $p^{(h)} \triangleq p^{(\xi^{(h)})}$. With respect to this presentation of parameters set the N-scan method adds two additional parameters $\gamma^{(h)}$ and $WH^{(h)}$, therefore new parameters set is shown as following

$$\{I_k^{(h)}, \xi_k^{(h)}, w_k^{(h)}, p_k^{(h)}, \gamma_k^{(h)}, WH_k^{(h)}\}_{h=1}^H \quad (23)$$

where $\gamma^{(h)}$ is the binary confidence indicator for all hypothesis in $\mathbb{H}$. It determines whether a hypothesis h is discarded in previous iterations or not. The value of γ for each hypothesis is initialised to zero at initiation of the hypotheses, whenever a hypothesis satisfies the extraction conditions, the value of $\gamma^{(h)}$ is changed to one. $WH^{(h)}$ is the weight history of each hypothesis $h \in \mathbb{H}$ which keeps the last N weights of a hypothesis h , i.e.

$$WH_k^{(h)} = [w_{k-N+1}^{(h)}, \dots, w_{k-1}^{(h)}, w_k^{(h)}] \quad (24)$$

These extended version of parameters set is propagated during the filtering procedure. The additional parameters are utilised to improve the tracking performance of the δ -GLMB filter in more uncertain conditions. The overall steps of proposed N-scan δ -GLMB algorithm is summarised as follows.

3.2.1. Initialization

In the δ -GLMB filter, each hypothesis is initialised by a proper setting. Additional to that setting w.r.t new parameter set it is needed that $\gamma_0^{(h)}$ and $WH_0^{(h)}$ be initialised too. Since the newly born hypothesis has not been extracted before, the initial value for $\gamma_0^{(h)}$ is zero. All first $N - 1$ elements of $WH_0^{(h)}$ is set to zero (no history is available before initialisation) and the N^{th} element is set to the ordinary initialisation value of a hypothesis

$$\gamma_0^{(h)} = 1, \quad (25)$$

$$WH_0^{(h)} = [0, 0, 0, \dots, 0, 0, w_0^{(h)}] \quad (26)$$

where $|WH_k^{(h)}| = N$.

Note that the initialisation of a hypothesis may occur in the middle of filtering time due to new born targets or spawned targets. In this situation initialisation of γ and WH is the same as mentioned above.

3.2.2. Prediction

In the prediction step of the δ -GLMB filter the filtering density $\pi_+(X_+)$ is estimated as explained in subsection 2.5. However the estimation of the filtering density $\pi_+(X_+)$ in the N-scan method is not altered, the newly defined parameters which is used in further steps propagate during time. The following propagation schema is appended to the prediction step of the δ -GLMB filter

$$\gamma_{k|k-1}^{(h)} = \gamma_{k-1}^{(h)} \quad (27)$$

$$WH_{k|k-1}^{(h)} = WH_{k-1}^{(h)} \quad (28)$$

3.2.3. Update

In the update step of the δ -GLMB filter the filtering density $\pi(X|Z)$ is estimated by Equation 14. Additional to estimation of $\pi(X|Z)$ which is in presence of the observing measurements, the weight history of a hypothesis is updated too. The weight history updating procedure is denoted by

$$WH_k^{(h)} = [WH_{k|k-1}^{(h)}[2], WH_{k|k-1}^{(h)}[3], \dots, WH_{k|k-1}^{(h)}[N], w_k^{(h)}] \quad (29)$$

where $WH[\zeta]$ stands for the ζ^{th} element of vector WH . Intuitively, the update procedure of WH is equal to remove the first element of the vector WH (The oldest weight of hypothesis h) and add the current weight of the hypothesis h to the weight history. Note that the order in the weight history matters which is an indicator of how much old is a weight.

3.2.4. Pruning and Extraction

In δ -GLMB filtering recursion there is a pruning phase that intend to avoid exponential growth of system by discarding the hypothesis with insignificant weights. This paper benefits from new defined parameters WH and γ to alter the procedure of pruning. The N-scan version of δ -GLMB does not discard the hypotheses which their weights are lower than W_{Th} at iteration k because the degeneration of the hypotheses weight could be as the result of a miss-detection or another uncertainty in the observation. Similar to the idea in [43], utilising new parameters which are added to the hypothesis parameter set, this paper proposes a new discarding method which the results show outperforms the previous methods. N-scan method tends to extract the hypotheses which satisfy either one of the following conditions and prune others,

Condition 1: $\gamma_k^{(h)} = 0$ (i.e. the hypothesis h has not been extracted yet) and $N_{Tr} \geq N_{Init}$.

Condition 2: $\gamma_k^{(h)} = 1$ (i.e. the hypothesis h has been extracted already) and $N_{Tr} \geq N_{Surv}$. where N_{Tr} shows the number of weights in $WH_k^{(h)}$ which exceed W_{Th} , N_{Init} shows predefined threshold for extraction of newly born hypothesis and N_{Surv} is the threshold for surviving hypotheses.

Note that if the first condition is satisfied then the value of $\gamma_k^{(h)}$ changes to one because the hypothesis h is now extracted. algorithm 1 summarises the N-scan method.

Intuitively, this method is proposed in order to give a second chance to hypotheses that are candidate for being discarded. Dependent on value of N this chance may increase relevantly. The idea behind giving a second chance to a hypothesis is to prevent truncation of informative hypotheses which belong to true target however, at the the moment k their observation is uncertain(e.g. due to miss-detection), hence its weight have dropped. However, using N-scan method for truncation the hypotheses add a slight burden on filtering procedure, it helps to reduce missing valuable information due to uncertainties. In the following the effect of N-scan on the filtering is pointed out in more detail.

Intuitively, N-scan method treats hypotheses with a weight lower than W_{Th} , in an optimistic way, it considers the reduction of their weight as a result of an uncertainty. In a window with size N which contains the weight history of the hypotheses, if the elements exceed W_{Th} at-least ϑ times, then the hypothesis extracts. Hence, the distribution of extraction is formulated as following form which is similar to a binomial trial

$$\pi_{extraction}(x, \ell) = \sum_{i=0}^{N-\vartheta} \binom{N}{\vartheta+i} p_h^{\vartheta+i}(x, \ell) (1 - p_h(x, \ell))^{N-\vartheta-i} \quad (30)$$

where $p_h(x, \ell)$ is the probability that $w^{(x, \ell)}$ is greater than W_{Th} , this probability relates directly with $p_D(x, \ell)$ i.e. $p_h(x, \ell) \propto p_D(x, \ell)$ (generally relates with uncertainty amount) and $\vartheta = N_{Surv}$ for surviving hypotheses and $\vartheta = N_{Init}$ for newly born hypotheses.

However, with reduction of P_D the p_h falls too at the step k , the other terms which are saved inside the WH are able to increase $\pi_{extraction}$, hence the miss-detection or generally any reason that

Input: $\{I_k^{(h)}, \xi_k^{(h)}, w_k^{(h)}, p_k^{(h)}, \gamma_k^{(h)}, WH_k^{(h)}\} \quad \forall h \in \tilde{H} = \{1, 2, \dots, H\}$
Output: $\hat{H}$
 $\hat{H} = \{\};$
while $(|(I, \xi)| \neq 0 \quad \&\& \quad \tilde{H} \neq \emptyset)$ **do**
 $h^* = \arg \max_{h \in \tilde{H}} (w_k^{(h)});$
 $L = \{h \in \tilde{H} | (I^{(h)}, \xi^{(h)}) = (I^{(h^*)}, \xi^{(h^*)})\};$
 $\gamma_k^* = \max_{h \in L} \gamma_k^{(h)};$
 $WH_k^* = [0]_{1 \times N};$
 $N_{Tr} = 0;$
 for $t = 1 : N$ **do**
 $WH_k^*[t] = \max_{j \in L} (WH_k^*[t], WH_k^j[t]);$
 if $(WH_k^*[t] > W_{Th})$ **then**
 $N_{Tr}++;$
 end
 end
 if $(\gamma_k^* = 1 \quad \&\& \quad N_{Tr} \geq N_{Surv})$ **then**
 $\tilde{H} = \tilde{H} \cup \{h^*\};$
 else
 if $(\gamma_k^* = 0 \quad \&\& \quad N_{Tr} \geq N_{Init})$ **then**
 $\tilde{H} = \tilde{H} \cup \{h^*\};$
 $\gamma_k^* = 1;$
 end
 end
 $\tilde{H} = \tilde{H} \setminus L;$
end
 $\Omega_k^{N\text{-Scan}} = \hat{H};$

Algorithm 1: Summary of N-Scan pruning algorithm.

makes p_h degenerate, can be ignored for a restricted time period (relative with size of WH). According to $\pi_{\text{extraction}}$, increasing the value of N makes the filtering procedure more immune to uncertainty in exchange for keeping more hypotheses which complicates the system computations.

From another point of view N-scan provides a super set of hypotheses as $\mathbb{H} = \mathbb{T} \cup \mathbb{C}$ where $\mathbb{H}$ is space of the all hypotheses, $\mathbb{T}$ is space of truncated hypotheses without using N-scan method and $\mathbb{C}$ is the space of hypotheses which N-scan method considers them as candidates of uncertain hypotheses. It is obvious that the space $\mathbb{C}$ is a super set of two spaces $\mathbb{C}^T$ and $\mathbb{C}^F$ where $\mathbb{C}^T$ is the space of those hypotheses which are truly under a uncertain condition and N-scan is able to detect them (e.g. uncertainty in the observations lasts at-most N iteration) hence their weights are degenerated and $\mathbb{C}^F$ is the space of those hypotheses which their degeneration in weights is not because of the uncertainty (e.g. target are dead and removed from observation permanently) or the N-scan method, due to the value of parameter N , is not able to detect them as a member of $\mathbb{C}^T$. W.r.t to definitions above, the N-scan method keeps $|C_k|$ extra hypotheses in iteration k , discards $|C_{i-(N-\emptyset)}^F|$ hypotheses and detects $|C_{i-N-\emptyset}^T|$ as uncertain hypotheses in previous iteration which is now certain. Hence, the extracted hypotheses is $\mathbb{T} \cup \mathbb{C}^T$. However, in the scenarios with certain observations the N-scan method performs exactly like the traditional discarding method and adds an irrational overhead to the filtering procedure, this method is useful in uncertain conditions despite the overhead to the filtering procedure. It is a trade off between better accuracy for MTT and a slight computation overhead. The L_1 -error distance of N-scan and traditional method of discarding is investigated in [Appendix B](#).

In the δ -GLMB filtering, computation of all the hypotheses first and then discard them is an intense-compute process. [40] introduces methods to truncate hypotheses without propagating them. [40] utilises ranked assignment and K-shortest path algorithms incorporated with update and prediction

process to reach this goal. The following sections proposes an alternative implementation of update and prediction phase based on these tricks w.r.t N-scan concept which tries to keep the hypotheses that are chosen wrongly as candidates for truncation due to high uncertainty ratio. These enhanced update and prediction phase alleviates the implementation computation complexity of δ -GLMB filter and yet try to stay immune to the uncertainties.

3.3. Enhanced Update phase

[40] proposes a tractable implementation of the δ -GLMB update which truncates the multi-target filtering density without computing all the hypotheses and their weights. This goal is achieved based on the idea which generates the association maps $\theta \in \Theta(I)$ in decreasing order of $[\eta_Z^{(\xi, \theta)}]^I$ and select the hypotheses with the highest weights. (As it is clear in Equation 14 hypothesis (I, ξ) generates a new set of hypotheses $(I, (\xi, \theta), \theta \in \Theta(I))$ with weights $w^{(I, \xi, \theta)}(Z) \propto w^{(I, \xi)}[\eta_Z^{(\xi, \theta)}]^I$). However using this idea, the highest weighted components are selected without computing all the possible hypotheses, the chance of discarding hypotheses which are afoul with uncertainty in the current moment rises. In order to solve these problems simultaneously the concept of scanning the history of the hypotheses condition in a certain N -sized windowing time is incorporated with the δ -GLMB update method proposed in [40].

Let *assignment matrix* S be a representation for each association map $\theta \in \Theta(I)$ which has the dimension $|I| \times |Z|$ where $Z = \{z_1, \dots, z_{|Z|}\}$, $I = \{\ell_1, \dots, \ell_{|I|}\}$. S consists of 0 or 1 entries where $S_{i,j} = 1$ if and only if $\theta(\ell_i) = j$ (i.e. the j^{th} measurement is assigned to track ℓ_i) otherwise $S_{i,j} = 0$. The optimal assignment *cost matrix* is denoted as a $|I| \times |Z|$ matrix [40]

$$C_Z^{(I, \xi)} = \begin{bmatrix} C_{1,1} & C_{1,2} & C_{1,3} & \dots & C_{1,|Z|} \\ C_{2,1} & C_{2,2} & C_{2,3} & \dots & C_{2,|Z|} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ C_{|I|,1} & C_{|I|,2} & C_{|I|,3} & \dots & C_{|I|,|Z|} \end{bmatrix} \quad (31)$$

where

$$C_{i,j} = -\ln \left(\frac{\langle p^{(\xi)}(\cdot, \ell_i), p_D(\cdot, \ell_i) g(z_j | \cdot, \ell_i) \rangle}{\langle p^{(\xi)}(\cdot, \ell_i), 1 - p_D(\cdot, \ell_i) \rangle \kappa(z_j)} \right) \quad (32)$$

when i, j are both natural numbers, $1 \leq i \leq |I|$ and $1 \leq j \leq |Z|$.

The cost value above can be interpreted as the cost of assignment the j^{th} measurement to track ℓ_i . Then the cost of assignment all the measurements to the tracks can be written as the Frobenius inner product of cost matrix and assignment matrix

$$\text{tr}(S^T C_Z^{(I, \xi)}) = \sum_{i=1}^{|I|} \sum_{j=1}^{|Z|} C_{i,j} S_{i,j} \quad (33)$$

In order to obtain an optimal assignment an optimal assignment matrix (S^*) is needed which minimises the cost of $\text{tr}(S^{*T} C_Z^{(I, \xi)})$. Note that each S^* has a corresponding associate map θ^* . For this purpose the concept of ranked assignment problem [47] is used. Such problem tries to find an enumeration of the least cost assignment matrices in increasing order [48]. Hence, in the case of finding the optimal assignment for measurements to tracks in δ -GLMB filter which the cost matrix is $C_Z^{(I, \xi)}$, the rank optimal assignment generates an enumeration of association maps θ in order of decreasing $[\eta_Z^{(\xi, \theta)}]^I$. Since the optimal assignment is a combinatorial problem and also enumerates the least T cost assignment, the Murty [48] algorithm is used to solve this problem. Further details are available in [40].

Despite the effectiveness of the mentioned method for ease of implementation, the uncertainty of observations affects the cost value which is the base of ranking algorithms used for truncation. As

it is obvious in Equation 37 growth of uncertainty causes $C_{i,j}$ increase. With reduction of detection rate, consequently reduction of measurement likelihood function $g(z_j|\cdot, \ell_i)$, or/and with growth of clutter rate the value inside the $-\ln(\cdot)$ drops, hence the cost value increase. Growth of the $C_{i,j}$ causes the corresponding hypothesis rank drops among the hypotheses ranks and consequently gets a higher chance to be a candidate for truncation. This behaviour may cause an informative hypothesis get truncated due to existence of the momentary uncertainties and the track of the object get lost. From a different aspect, by substituting Equation 12 in Equation 18 another form of $[\eta_Z^{(\xi, \theta)}]^I$ can be written as follow

$$[\eta_Z^{(\xi, \theta)}]^I = \exp\left(\text{tr}(S^T C_Z^{(I, \xi)})\right) \prod_{\ell \in I} \left\langle p^{(\xi)}(\cdot, \ell), 1 - p_{D(\cdot, \ell)} \right\rangle \quad (34)$$

which shows the reduction of cost matrix causes the value of $[\eta_Z^{(\xi, \theta)}]^I$ decrease and consequently, the chance of discarding corresponding hypothesis for track label I gets higher.

In order to increase immunity of the update phase to the uncertainties, we have used the N-scan idea in selection of the hypotheses according to the value of $[\eta_Z^{(\xi, \theta)}]^I$ with slight differences which is described in following.

After sorting the association maps according to $[\eta_Z^{(\xi, \theta)}]^I$ in decreasing order, the association maps with the highest value of $[\eta_Z^{(\xi, \theta)}]^I$ (which is analogous to suppose that they are hypotheses that satisfy the condition $[\eta_Z^{(\xi, \theta)}]^I \geq \eta^{Threshold}$) are considered as candidates for surviving. In contrast with the previous described update method, rest of the association maps are not truncated.

Let M , T and T' denote the set of all association maps, association maps which satisfy the condition $[\eta_Z^{(\xi, \theta)}]^I \geq \eta^{Threshold}$ and the set of rest of association maps, respectively ($M = T \cup T'$). The relevant hypotheses to the set T propagate into the next step (prediction step). Due to the uncertainty conditions it is possible that the set T' contains association maps which their $[\eta_Z^{(\xi, \theta)}]^I$ is decreased momentary. The following schema is presented in order to find such association maps which, however their $[\eta_Z^{(\xi, \theta)}]^I$ is under the $\eta^{Threshold}$, in future of the filtering time their $[\eta_Z^{(\xi, \theta)}]^I$ increase due to annihilation of the uncertainties.

Considering a δ -GLMB parameters set denoted by $\{I_k^{(h)}, \xi_k^{(h)}, w_k^{(h)}, p_k^{(h)}\}_{h=1}^H$, the parameter Y is added, in order to keep the track of the value of

$$\frac{\sum_{j=1}^{T_k^{(h)} \cup T_k'^{(h)}} [\eta_Z^{(\xi_k^{(h)}, \theta_k^{(h,j)})}]_{I_k^{(h)}}}{|T_k^{(h)} \cup T_k'^{(h)}|} \quad (35)$$

as an indicator for amount of cumulative information stored in the hypotheses $(I, (\xi, \theta)), \theta \in \Theta(I)$ which are generated by hypothesis (I, ξ) during the filtering time. Therefore the parameter set is denoted by

$$\{I_k^{(h)}, \xi_k^{(h)}, w_k^{(h)}, p_k^{(h)}, Y_k^{(h)}\}_{h=1}^H \quad (36)$$

$Y^{(h)}$ is a history matrix which keeps the last N cumulative information stored in hypothesis (h) .

$$Y_k^{(h)} = [v_{k-N+1}^{(h)}, \dots, v_{k-1}^{(h)}, v_k^{(h)}] \quad (37)$$

where

$$v_k^{(h)} = \frac{\sum_{j=1}^{T_k^{(h)} \cup T_k'^{(h)}} [\eta_Z^{(\xi_k^{(h)}, \theta_k^{(h,j)})}]_{I_k^{(h)}}}{|T_k^{(h)} \cup T_k'^{(h)}|}. \quad (38)$$

In the rest of this section, according to newly defined parameter Y a new truncation algorithm for the update phase of the δ -GLMB filter is presented which is more immune to uncertain conditions.

The overall steps of proposed truncation method is summarised as follows.

The initialisation and Y propagation steps are almost the same as the N-scan method with the history vector, $Y_0^{(h)} = [0, 0, 0, \dots, 0, 0, v_0^{(h)}]$ where $|Y_k^{(h)}| = N$. An ordered enumeration of association maps θ is obtained after solving the ranked optimal assignment problem which its cost matrix is $C_Z^{(I, \xi)}$. This enumeration is sorted according to the value of $[\eta_Z^{(\xi, \theta)}]^I$ which relates directly with weight of a hypothesis $w^{(I, \xi, \theta)}(Z) \propto w^{(I, \xi)}[\eta_Z^{(\xi, \theta)}]^I$.

Analogous to [40], the hypotheses which satisfy the condition $[\eta_Z^{(\xi, \theta)}]^I \geq \eta^{Threshold}$ (the set T) are chosen for being extracted in the next prediction step. Although the elements of the set T are selected, there might be hypotheses in the set T' which their value of $[\eta_Z^{(\xi, \theta)}]^I$ is under a certain threshold however, selecting them benefits the filtering procedure due to uncertainty reasons.

In the following, utilising the parameter Y , a method for detecting some candidates $C \subseteq T'$ which are probable to be victims of uncertainty reasons that causes the value $[\eta_Z^{(\xi, \theta)}]^I$ of a hypothesis decreases, is proposed.

A hypothesis (h) is added to the candidate set C if satisfies either one of the following conditions, Condition 1:

$$\sum_{i=0}^{|Y_k^{(h)}|-1} \frac{Y_k^{(h)}[i]}{|Y_k^{(h)}|} \geq v_{Mean} \quad (39)$$

and

$$Var(Y_k^{(h)}[0 : |Y_k^{(h)}| - 1]) - \quad (40)$$

$$Var(Y_k^{(h)}[0 : |Y_k^{(h)}| - 2]) \geq v_{Var}$$

and

$$Y_k^{(h)}[|Y_k^{(h)}| - 2] \geq Y_k^{(h)}[|Y_k^{(h)}| - 1] \quad (41)$$

and

$$[\eta_Z^{(\xi, \theta)}]^I \geq \eta^{Relaxed_Threshold} \quad (42)$$

where v_{Mean} is a threshold for the mean of information indicator in the windowing size of Y . $Var(\cdot)$ is a variance operator and $Y[\zeta : \zeta']$ stands for a subset of Y which its elements consist of ζ^{th} element of vector Y to the ζ'^{th} element. v_{Var} is a threshold for difference between variance of the vector Y before and after adding the last element. $\eta^{Relaxed_Threshold}$ is a threshold for amount of the η which $\eta^{Relaxed_Threshold} \leq \eta^{Threshold}$. Note that satisfying the condition 1 means the hypothesis is suspicious for being under an uncertain circumstance, from the point of the experience some time it is beneficial to select some random hypothesis from the set T' and put them in the set C .

If a hypothesis satisfies the condition 1 then $C = C \cup h$ and $\mathcal{U}^{(h)} = 1$ which this parameter can be stored among other parameters of a hypothesis. This parameter shows whether a hypothesis satisfied condition 1 or not, if a hypothesis does not satisfy condition 1 (even once) then $\mathcal{U} = 0$.

Condition 2:

$$\sum_{i=0}^{|Y_k^{(h)}|-1} \frac{Y_k^{(h)}[i]}{|Y_k^{(h)}|} \geq v_{Mean} \quad (43)$$

and

$$\mathcal{U}^{(h)} = 1 \quad (44)$$

and

$$\left| Y_k^{(h)}[|Y_k^{(h)}| - 2] - Y_k^{(h)}[|Y_k^{(h)}| - 1] \right| \leq v_{Thresh} \quad (45)$$

and

$$[\eta_Z^{(\xi, \theta)}]^I \geq \eta^{Relaxed_Threshold} \quad (46)$$

where $|\zeta|$ is absolute value of ζ and v_{Thresh} is a threshold for difference between values of elements of vector Y . If a hypothesis satisfies the condition 2 then $C = C \cup h$ and $\mathcal{U}^{(h)} = 1$. The hypotheses inside the set C are considered as a set of candidates which its elements are possibly afoul with the uncertainties. Intuitively, the above algorithm seeks for those components which their $v_k^{(h)}$ drops momentarily. The obtained set C is given a second chance along side the set T , hence the truncated version of the prediction density is denoted in the following. Equation 15 can be written as

$$\pi(X|Z) = \sum_{h=1}^H \pi^{(h)}(X|Z) \quad (47)$$

where

$$\pi^{(h)}(X|Z) = \Delta(X) \sum_{j=1}^{|\Theta(I^{(h)})|} w^{(I^{(h)}, \xi^{(h)}, \theta^{(h,j)})}(Z) \delta_{I^{(h)}}(\mathcal{L}(X)) [p^{(\xi^{(h)}, \theta^{(h,j)})}(\cdot|Z)]^X \quad (48)$$

In order to keep the parallel-ability of the truncation, the density of each hypothesis (h) is truncated separately. Each hypothesis (h) generates $|\Theta(I^{(h)})|$ components for filtering density which considering solving ranked optimal assignment with the mentioned cost matrix, yields $\theta^{(h,j)}$, $j = 1, \dots, |T|$ (The hypotheses are sorted in decreasing order). Since the candidate set C also produce association maps $\theta^{(h,j)}$, $j \in \mathfrak{S}(C)$ (hypotheses in C is not ordered) then the truncated version of $\pi^{(h)}(\cdot|Z)$ is

$$\pi^{(h)}(X|Z) = \Delta(X) \sum_{j \in \mathfrak{S}(T \cup C)} w^{(I^{(h)}, \xi^{(h)}, \theta^{(h,j)})}(Z) \delta_{I^{(h)}}(\mathcal{L}(X)) [p^{(\xi^{(h)}, \theta^{(h,j)})}(\cdot|Z)]^X \quad (49)$$

where $\mathfrak{S}$ is an operator which shows the association maps indices of a set of hypotheses. i.e $\mathfrak{S}(T) = \{1, \dots, |T|\}$

3.4. Enhanced Predict phase

Using K-shortest path algorithm, [40] presents a δ -GLMB prediction implementation which truncates predicted hypotheses without computing all of them and their weights. Analogous to the update, a hypothesis (I, ξ) generates a set of hypotheses $((J \cup L), \xi)$ which J is set of surviving labels and L is set of birth labels with weights $w_S^{(I, \xi)}(J)$ and $w_B(L)$ respectively.

For a hypothesis (I, ξ) the weight of surviving label $J \subseteq I$ is denoted as following

$$w_S^{(I, \xi)}(J) = w^{(I, \xi)} [1 - \eta_S^{(\xi)}]^I \left[\frac{\eta_S^{(\xi)}}{1 - \eta_S^{(\xi)}} \right]^J \quad (50)$$

In order to avoid exhaustively computing all the survival hypotheses weights, the surviving label set are generated in decreasing order of $[\frac{\eta_S^{(\xi)}}{1 - \eta_S^{(\xi)}}]^J$ using K-shortest path algorithm with a cost vector $C^{(I, \xi)} = [C^{(I, \xi)}(\ell_1), \dots, C^{(I, \xi)}(\ell_{|I|})]$, where (More details are available in [40])

$$C^{(I, \xi)}(\ell_j) = -\ln \left[\frac{\eta_S^{(\xi)}(\ell_j)}{1 - \eta_S^{(\xi)}(\ell_j)} \right]. \quad (51)$$

After sorting the hypotheses in decreasing order the highest weighted survival for (I, ξ) is selected. It is analogous to consider selection of those which $[\frac{\eta_S^{(\xi)}}{1 - \eta_S^{(\xi)}}]^J \geq \eta'^{Threshold}$

According to this setting it is possible to truncate the prediction phase analogous to the update phase with a slight differences. $v_k^{(h)}$ which is an indicator for amount of information stored in the hypothesis is altered as denoted below

$$v_k^{(h)} = \left[\frac{\eta_S^{(\xi^{(h)})}}{1 - \eta_S^{(\xi^{(h)})}} \right]^{J^{(h)}} \quad (52)$$

where $J^{(h)} \subseteq I^{(h)}$ is the set of survival hypotheses of the $I^{(h)}$. Satisfying the condition $[\eta_S^{(\xi)} / (1 - \eta_S^{(\xi)})]^J \geq \eta_{Relaxed_Threshold}$ is not essential.

Note that enhanced prediction does not interfere with new born targets truncation due to their small amount of weight and the difficulty of the keeping their history.

3.5. Refined δ -GLMB

Using a fixed value for probability of survive is a prevalent scenario in δ -GLMB filters as it is used in [40], [49]. Adopting the idea in [50] the following section introduces an adaptive probability of survive which is based on a pre-defined survival model which can be defined based on different scenarios, for example existence of a solid object in the scene can be defined for the filtering system (e.g a wall, a door or a window). Afterwards, this survival model is utilised to present a new method for detecting the hypotheses which their measurements are likely uncertain.

In this work, a simple survival model $\mathcal{S}(\cdot)$ is defined which can be altered according to the existing conditions. $\mathcal{S}(\cdot)$ is utilised to adaptively calculate the survival probability of a hypothesis according to its position and its direction of movement. The probability of survive for a hypothesis (h) is shown by $P_{S,k}^{(h)}$ which is equal to $\mathcal{S}(x_k^{(h)})$ where $x_k^{(h)}$ is an indicator for the position that a hypothesis (h) presents and is calculated as following

$$x_k^{(h)} = \int y p(\hat{h}_j)(y, \cdot) dy \quad (53)$$

$$(\hat{h}, \hat{j}) = \underset{(\hat{h}, \hat{j})}{\operatorname{argmax}} w^{(h,j)} \delta_{\hat{N}}(|I^{(h,j)}|) \quad (54)$$

$$\hat{N} = \underset{\rho}{\operatorname{argmax}} \rho \quad (55)$$

$$\rho(n) = \sum_{j=1}^T w^{(h,j)} \delta_n(|I^{(h,j)}|); n = 0, \dots, N_{Max} \quad (56)$$

More details are available in [40] in the state estimation section.

Each survival model is constructed from a set of boundary lines (linear, quadratic or any desired form) which are shown as $b^1, b^2, \dots, b^j, \dots, b^{N_B}$ where N_B is the number of boundaries in a survival model. Hence, the probability of survive for a hypothesis can be re-written as

$$P_{S,k}^{(h)} = \mathcal{S}(x_k^{(h)}) = \min_j (P_{S,k}^{(h,j)}) \quad (57)$$

where $P_{S,k}^{(h,j)}$ is defined as

$$P_{S,k}^{(h,j)} = \begin{cases} 0, & \text{dist}(x_k^{(h)}, b^j) < d_2 \ \& \ D_h(b^j) > 0 \\ \frac{\text{dist}(x_k^{(h)}, b^j) + d_1}{d_1 - d_2}, & d_2 \leq \text{dist}(x_k^{(h)}, b^j) < d_1 \ \& \ D_h(b^j) > 0 \\ P_{S_{Max}}, & \text{Otherwise} \end{cases} \quad (58)$$

where $D_h(b^j)$ is positive if the corresponding position of the h is moving toward the boundary b^j and is negative vice versa. Note that the movement direction of a hypothesis can be inferred from the intrinsic kinematic state vector (by checking sign of velocity stored in state vector along any existing axis X,Y or Z). d_1 and d_2 stands for distance thresholds and $\text{dist}(\cdot, \cdot)$ shows the positional distance between its entrances. $P_{S_{Max}}$ is the maximum value considered for the survival portability which is at most equal to 1.

In the δ -GLMB filtering procedure, the weight $w^{(h)}$ denotes the probability of hypothesis (h). In practice, missing the measurement of a target affects the weights of corresponding hypotheses and therefore the estimation might be lost. In this section, inspiring from [50] a new parameter PC (which is abbreviated for Probability of Confirm) is added to hypothesis parameter set. The parameter PC is responsible for showing the amount of confidence of a hypothesis during the filtering period. PC is an adaptive parameter which is calculated separately for each hypothesis based on a reward and punishment schema. The parameter PC is then utilised in truncation step in order to decrease the effect of miss-detection and similar uncertainties by preventing the truncation of informative hypotheses which their measurements are uncertain momentarily.

Considering the parameter set (w.r.t newly defined parameter PC) as

$$\{I_k^{(h)}, \tilde{\mathbf{z}}_k^{(h)}, w_k^{(h)}, p_k^{(h)}, PC_K^{(h)}\}_{h=1}^H, \quad (59)$$

$PC_k^{(h)}$ shows the probability of confirm for hypothesis (h) at the k^{th} step of filtering. At the birth time of each hypothesis the value of PC is set to a value less than pre-defined threshold PC_{Thresh} , i.e

$$PC_0^{(h)} = PC_{Thresh} - \epsilon. \quad (60)$$

where $\epsilon > 0$.

During the life time of each hypothesis (h), whenever the weight of corresponding hypothesis drops below PC_{Thresh} (after performing update/prediction phase) the hypothesis is considered as a probable chance of being affected by a uncertain condition like miss-detection, hence the hypothesis is punished by the means of penalising the $PC_k^{(h)}$. Penalising of the PC occurs using a penalty coefficient τ_p

$$PC_k^{(h)} = PC_{k-1}^{(h)} \times \tau_p \quad (61)$$

where $0 < \tau_p < 1$. In contrast, if the weight of a hypothesis exceeds PC_{Thresh} then the hypothesis is rewarded as

$$PC_k^{(h)} = \min(1, PC_{k-1}^{(h)} \times \tau_r) \quad (62)$$

where $\tau_r > 1$.

If the measurement uncertainties continues for multi consecutive period of time ($k - n, \dots, k + m$) (e.g a long time occlusion) most of hypotheses relative to the corresponding target might perish cruelly. In order to alleviate this flaw a hypothesis pool refinement method is proposed which utilises the concept of adaptive probability of survive and adaptive probability of confirm. The base idea of this method is that if a hypothesis exists in step $k - 1$ and $P_{S,k}^{(h)} > 0$ then the corresponding track is expected to survive at the next time step k . Therefore, in truncation section a refinement step is added. In the refinement step the hypotheses which their probability of survive is a non-zero positive value and their probability of confirm exceeds a predefined threshold PC_{Refine} are added to the hypotheses pool and given a second chance to confront the probable occurrence of uncertainty.

4. Experimental Results and Discussion

In this section the performance and effectiveness of the proposed methods which intend to confront the measurement uncertainty drawback of δ -GLMB filtering are verified using both simulated and real world datasets. The example and scenarios are based on linear Gaussian and hence Gaussian mixture implementation is used. The experimental results on simulated scenario utilises a Monte Carlo simulation with 100 runs. Some scenarios with different probability of detection and various subsequent miss-detection rate are employed to show the effectiveness of the proposed methods comparing with standard version of δ -GLMB filter, GM-PHD filter and N-Scan GM-PHD filter [43] in order to compare with methods of tracking which are designed to encounter uncertainties in measurements.

4.1. Simulated Dataset Results

A typical scenario is considered as a set of multi-target trajectories on two dimensional region $[-1000,1000]m \times [-1000,1000]m$ as shown in Figure 1 with duration of $K = 100s$. The number of targets may change during the time as an outcome of births and deaths. The kinematic target state is a 4-D vector which contains planar position and constant velocity (target velocities are constant and may differ from each other) $x_k = [p_{x,k}, p_{y,k}, \dot{p}_{x,k}, \dot{p}_{y,k}]^T$. Noisy vectors of 2-D planar position $z_k = [z_{x,k}, z_{y,k}]^T$ are showing the measurements. The single-target state space model is linear Gaussian with $f_{k|k-1}(x_k|x_{k-1}) = \mathcal{N}(x_k; F_k x_{k-1}, Q_k)$ and Gaussian likelihood $g_k(z_k|x_k) = \mathcal{N}(z_k; H_k x_k, R_k)$ where F, H are state and observation transition matrices respectively and R, Q are noise matrices which are represented by

$$F_k = \begin{bmatrix} 1 & 1 & \Delta & \Delta \\ 1 & 1 & \Delta & \Delta \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 1 & 1 \end{bmatrix}, H_k = \begin{bmatrix} 1 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 \end{bmatrix}, Q_k = \sigma_v^2 \begin{bmatrix} \frac{\Delta^4}{4} & \frac{\Delta^4}{4} & \frac{\Delta^3}{2} & \frac{\Delta^3}{2} \\ \frac{\Delta^4}{4} & \frac{\Delta^4}{4} & \frac{\Delta^3}{2} & \frac{\Delta^3}{2} \\ \frac{\Delta^3}{2} & \frac{\Delta^3}{2} & \Delta^2 & \Delta^2 \\ \frac{\Delta^3}{2} & \frac{\Delta^3}{2} & \Delta^2 & \Delta^2 \end{bmatrix}, R_k = \sigma_\epsilon^2 \begin{bmatrix} 1 & 1 \\ 1 & 1 \end{bmatrix}$$

where $\Delta = 1s$ is the sampling period, $\sigma_v = 5m/s^2$ and $\sigma_\epsilon = 10m$ are standard deviations of the process and measurement noise. The survival probability is $P_{S,k} = 0.97$ (Except the RGM version which the probability of survive is adaptive) and the birth model is a Labeled Multi-Bernoulli RFS with parameters $\pi_B = \{r_B^{(i)}, p_B^{(i)}\}_{i=1}^4$ where $r_B^{(i)} = 0.03$ and $p_B^{(i)}(x) = \mathcal{N}(x; m_B^{(i)}, P_B)$ with $m_B^{(1)} = [0.1, 0, 0.1, 0]^T$, $m_B^{(2)} = [400, 0, -600, 0]^T$, $m_B^{(3)} = [-800, 0, -200, 0]^T$, $m_B^{(4)} = [-200, 0, 800, 0]^T$, $P_B = \text{diag}([10, 10, 10, 10]^T)^2$. Clutter follows a Poisson RFS giving an average of 65 false alarm per scan. The δ -GLMB filter is capped to 12000 components and results are shown for 100 Monte Carlo trials. The comparison criteria for the methods is Optimal Sub-Pattern Assignment (OSPA) [51,52] with cut-off $c = 100$ and order $p = 1$. OSPA formulation is calculated as

$$OSPA^{c,p}(X_k, \hat{X}_k) = \left[\frac{1}{|\hat{X}_k|} \left(\min_{\pi \in \Pi_{|\hat{X}_k|}} \sum_{i=1}^{|X_k|} (d_c(x^i, \hat{x}^{\pi(i)}))^p + c^p \times (|\hat{X}_k| - |X_k|) \right) \right]^{\frac{1}{p}} \quad (63)$$

The results shown for N-scan method is obtained considering fixed values for N-scan parameters. Length of history window $N = 5$, $N_{Init} = 3$ and $N_{Surv} = 2$.

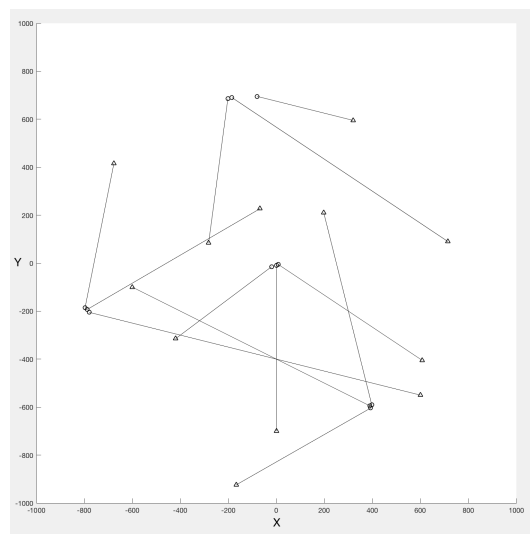


Figure 1. Multiple trajectories in the XY plane which are inputs for tracking simulation procedure. Start/Stop positions for each track are shown with o/Δ. Notice that at same time there are at most 10 target in the system according to different time of birth and death of targets. The targets are occluded and they cross each other in certain locations shown in the figure.

Figure 2 shows result for standard δ -GLMB filter, N-scan δ -GLMB filter, N-scan δ -GLMB filter with enhanced update and prediction steps and Refined δ -GLMB. These results are obtained in detection rate of 80% and the average OSPA in this situation is brought here in Figure 1.

Table 1. AVG OSPA of different methods in 100 filtering iteration

Method($P_D = 0.8$)	OSPA(AVG)(# of targets)
GM-PHD	47.46(5.17)
N-Scan GM-PHD	39.71(5.88)
δ -GLMB	33.4375(6.13)
N-scan δ -GLMB	31.1589(6.71)
Enhanced N-scan δ -GLMB	29.4330(6.94)
Refined N-scan δ -GLMB	27.0017(7.26)

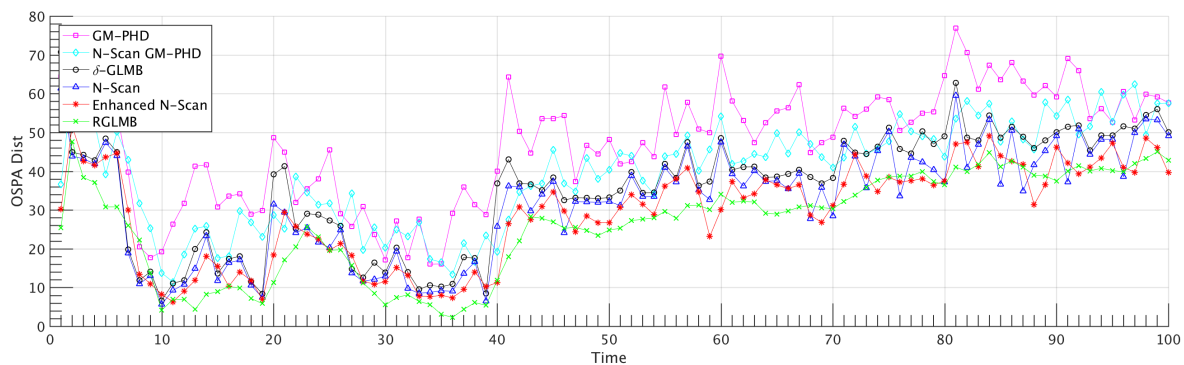


Figure 2. The figure shows OSPA of different methods in 100 filtering iteration (100 Monte Carlo trials). $P_D = 0.80$ and 65 clutter per frame is used. As it is clear in the figure the area under lines of proposed methods are lower than δ -GLMB method which results in a lower average of OSPA in time and consequently shows a better result obtained.

Figure 3 shows result for different detection probability rate versus average of OSPA in time. This result shows that the effects of miss detection is decreased using proposed methods. Notice that in higher rate of miss detection situation, proposed methods diverge from the standard δ -GLMB which shows the proposed methods operates better in uncertain conditions. Figure 4 shows the analysis of the methods in different clutter rate and Figure 5 shows result in the scenario which some targets are forced to be miss-detected for a certain number of frames in a sequence. The results demonstrate that proposed N-scan and refined δ -GLMB method improved the estimation performance of the δ -GLMB in uncertain conditions since the OSPA of proposed methods are decreased comparing to the other methods, specially when the uncertainty rate increases. For example the OSPA distance between our proposed method and other methods gets a higher value in lower rates of detection which shows a better performance in uncertain conditions. The proposed refined method also outperforms other methods in the sequenced miss detection. Notice that some proposed methods like Marginalized δ -GLMB [53] which are recently proposed, performs analogous to the δ -GLMB from the aspect of estimation in uncertain conditions. The proposed methods of this paper focus on enhancing the performance of the δ -GLMB filters family, hence this idea and methods can be used on other form of the δ -GLMB.

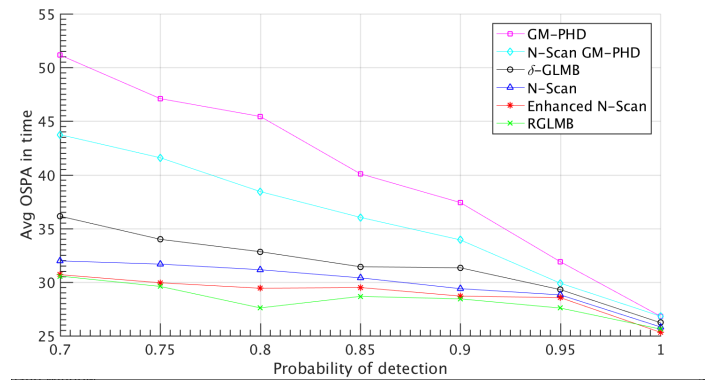


Figure 3. Different probability of detection (100 Monte Carlo trials). As clear in the figure the proposed methods are outperforming the δ -GLMB method in the presence of miss detection. With higher rate of miss detection (lower probability of detection) the divergence between different methods increase which shows the power of proposed method in more uncertain conditions like presence of clutter.

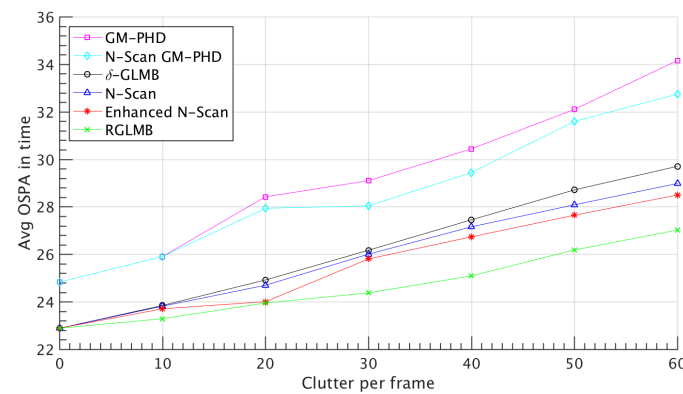


Figure 4. Different clutter per frame with probability of detection 0.95 (100 Monte Carlo trials). As clear in the figure the proposed methods are outperforming the δ -GLMB method in the presence of clutter. With higher rate of clutter the divergence between different methods increase which shows the power of proposed method in more uncertain conditions like presence of miss detection.

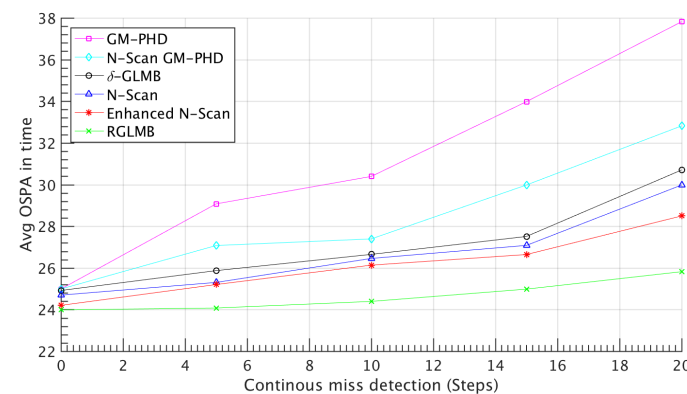


Figure 5. Different forced consequent miss detection with $P_D = 0.95$ (100 Monte Carlo trials). This figure shows the examination of proposed method in a condition that miss detection happens consequentially which as it is clear in the figure refined GLMB out performs other methods.

Figure 6 shows another scenario with a vivid high amount of uncertainty in the measurements and also dense occlusion in both X and Y axis. The discussed methods are performed on this scenario and results are brought in the Table 2 which shows the effectiveness of our proposed methods in a heavily uncertain conditions.

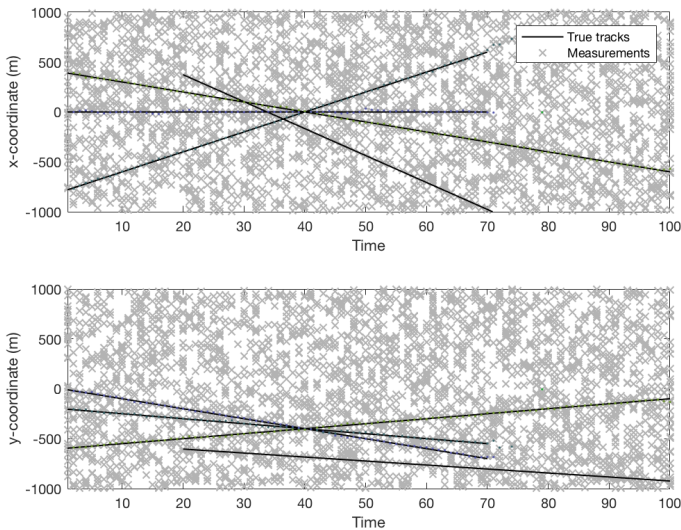


Figure 6. Multiple trajectories in X-Time and Y-Time plane which are highly occluded and the amount of uncertainty in the measurements are clearly intense.

Table 2. AVG OSPA of different methods in 100 filtering iteration for the scenario defined in [Figure 6](#)

Method	OSPA(AVG)
GM-PHD	39.03
N-Scan GM-PHD	34.51
δ -GLMB	32.28
N-scan δ -GLMB	28.67
Enhanced N-scan δ -GLMB	26.44
Refined N-scan δ -GLMB	24.10

4.2. Visual Dataset Results

Here, the PETS09-S2L1 and GRAM-RTM [54] datasets are utilised in order to verify the functionality of proposed methods. We have chosen PETS09-S2L1 as a dataset which is crowded with people (presents a proper multi-object tracking environment) and contains certain obstacles in the scene which causes momentary and continuous occlusions. The GRAM-RTM dataset is chosen because of loads of vehicle crossing, in the scene and consequently, the high amount of occlusion. The GRAM-RTM dataset has a low quality which also causes miss-detection. Hence, it is possible to verify proposed methods performance in a challenging environment with uncertainties in measurement. [Figure 7](#) shows the quality of different methods in a sub sample of the PETS09-S2L1 and GRAM-RTM datasets. As it is clear in the [Figure 7](#) the δ -GLMB fails to track the targets which are behind the obstacle at the middle of the scene, however other three proposed methods shows progress in tracking. The scene shown by [Figure 7](#) is a frame which two different object move from different locations, come across each other, stay for moments (which is mostly miss-detected because of the presence of solid obstacles in the scene) and leave the scene in different directions. The qualitative results shown in [Figure 7](#) shows that the proposed methods are more successful in tracking targets rather than the original δ -GLMB method since they track the targets in more frames and confront the miss detection effect.

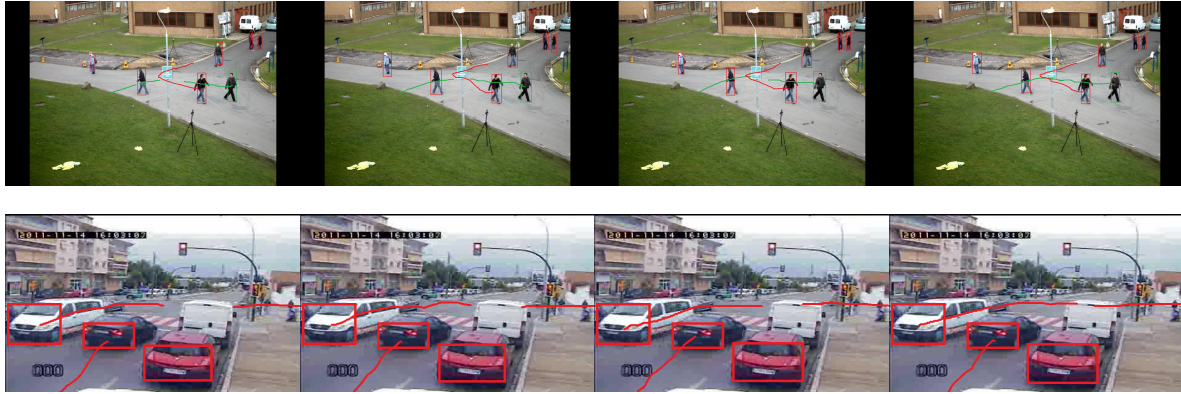


Figure 7. Results on PETS09-S2L1 (first row) and GRAM-RTM (Urban1) (second row). For simplicity just two targets trajectories are drawn in the pictures. Col one) Trajectory for δ -GLMB method. Col two) Trajectory for N-scan method. Col three) Trajectory for Enhanced method. Col four) Trajectory for Refined δ -GLMB.

The quantitative results for PETS09-S2L1 and GRAM-RTM are shown in Table 3 and Table 4, respectively which popular CLEAR MOT metrics are used to evaluate the performance of the trackers [55,56]. The MOT metrics used here are MOTA and MOTP. MOTA or Multiple Object Tracking Accuracy measure, combines three error sources: false positives, missed targets and identity switches, calculated as:

$$MOTA = 1 - \frac{\sum_k (FalseNegative_k + FalsePositive_k + NS_k)}{\sum_k ng_k} \quad (64)$$

where k is frame number and nb_k is the number of estimated bounding boxes at frame k . MOTP or Multiple Object Tracking Precision measure, is a criteria for how the tracker performs in situation of misalignment between the annotated and the predicted bounding boxes, calculated as:

$$\left(\sum_{t \in targets, k} \frac{Area(groundTruth_k^t \cap estimated_k^t)}{Area(groundTruth_k^t \cup estimated_k^t)} \right) / \sum_k nb_k \quad (65)$$

where ng_k denotes the number of ground truth at frame k and NS_k is number of target identity switches. The results also contains four other numerical metrics. Recall Rate (ReR) metric which is brought to verify the ability of the filters for true estimations. The False Alarm Rate (FAR) which is utilised to investigate the effect of the uncertainty. The Missed Trajectory Rate (MTR) and the Missed Occlusion rate (MOR) which evaluate the amount of improvement for handling occlusion. These criteria are calculated as:

$$ReR = \frac{\# \text{ true estimations}}{\# \text{ totoal ground truth targets}}, FAR = \frac{\# \text{ false estimations}}{\# \text{ total estimations}},$$

$$MTR = \frac{\# \text{ missed trajectories}}{\# \text{ total trajectories}}, MOR = \frac{\# \text{ missed occlusions}}{\# \text{ total occlusions}}$$

Table 3. Results of different methods on PETS09-S2L1

Method	MOTA	MOTP	ReR	FAR	MTR	MOR
GM-PHD	42.62	54.02	0.45	0.12	0.57	0.71
N-Scan GM-PHD	46.78	58.49	0.51	0.10	0.46	0.57
δ -GLMB	51.05	63.62	0.57	0.10	0.42	0.64
N-scan δ -GLMB	54.53	65.28	0.62	0.07	0.34	0.42
Enhanced N-scan δ -GLMB	55.60	65.91	0.62	0.07	0.34	0.35
Refined N-scan δ -GLMB	56.79	66.38	0.71	0.05	0.26	0.28

Table 4. Results of different methods on GRAM-RTM

Method	MOTA	MOTP	ReR	FAR	MTR	MOR
GM-PHD	27.91	32.59	0.31	0.17	0.68	0.78
N-Scan GM-PHD	31.20	36.17	0.46	0.12	0.56	0.66
δ -GLMB	30.83	37.55	0.48	0.14	0.53	0.64
N-scan δ -GLMB	35.41	40.06	0.58	0.07	0.46	0.56
Enhanced N-scan δ -GLMB	36.26	41.74	0.60	0.07	0.41	0.53
Refined N-scan δ -GLMB	39.32	43.45	0.68	0.04	0.34	0.43

As it is clear in the results, our proposed methods improve the mentioned considered criteria. The criteria MOTA and MOTP are improved which shows that the proposed methods improve the tracking accuracy and precision of other discussed trackers. The criteria ReR, FAR, MTR and MOR are improved which are criteria for verifying the performance of the trackers in uncertain conditions. For example decreasing MTR shows that the number of missed trajectories are significantly decreased in our proposed methods comparing with other verified methods. Totally, these results shows that utilising the information stored in history of filtering performance, causes a better performance for trackers. For example when a person detected in the scene is not detected for a while, knowing that this person existed and has been moved in a certain direction, can help the tracker to expect that person be seen again in a rational (due to its history of appearance in the scene) area.

5. Conclusions

In practice δ -GLMB filter performance may decrease in uncertain conditions due to truncation of the informative components which have lost information at the moment of occurrence of the uncertainty. In this paper, we proposed methods that aims improving the performance of the filtering via guessing the components which are under the mentioned circumstances and keeping them from being removed form the filtering procedure. The main idea is utilising the information stored in the history of the filtering procedure. We benefit information stored in last N iteration of filtering to guess the components which are truncating wrongly according to their behaviour during the time of their existence (w.r.t to the N value). Then we use a survival model and a reward and punishment scheme to make sure that a component is confirmed to be truncated or to survive. The performance of proposed methods is verified via a simulated scenario and multiple conditions in term of different probabilities of detection, different clutter rates and a subsequent miss-detection scenario which in that, targets was forced to be miss detect for a coherent sequenced frames. The proposed methods has been compared with the standard δ -GLMB filter and the results show that proposed methods outperforms it in presence of random uncertainties.

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Conflicts of Interest: The authors declare no conflicts of interest.

Appendix A. Supplementary Background

A.1 The probability density of a Multi-Bernoulli RFS X on $\mathbb{X}$ is denoted by [44]

$$\pi(\{x_1, \dots, x_n\}) = \prod_{j=1}^M \left(1 - r^{(j)}\right) \sum_{1 \leq i_1 \neq \dots, \neq i_n \leq M} \prod_{j=1}^n \frac{r^{(i_j)} p^{(i_j)}(x_j)}{1 - r^{(i_j)}}$$

A.2 The probability density of a labelled Multi-Bernoulli (LMB) RFS X on $\mathbb{X}$ which has a finite parameter set $\left\{ (r^{(\zeta)}, p^{(\zeta)}) : \zeta \in \Psi \right\}$ and is augmented with $\ell \in \mathbb{L}$ is denoted by

$$\pi(\{(x_1, \ell_1), \dots, (x_n, \ell_n)\}) = \delta_n(|\{\ell_1, \dots, \ell_n\}|) \times \prod_{\zeta \in \Psi} \left(1 - r^{(\zeta)}\right) \prod_{j=1}^n \frac{1_{\alpha(\Psi)}(\ell_j) r^{(\alpha^{-1}(\ell_j))} p^{(\alpha^{-1}(\ell_j))}(x_j)}{1 - r^{(\alpha^{-1}(\ell_j))}}$$

A.3 The set integral is defined as

$$\int f(X) \delta(X) = \sum_{i=0}^{\infty} \frac{1}{i!} \int f(\{x_1, \dots, x_i\}) d(x_1, \dots, x_i)$$

Appendix B. The L_1 -Error of N-Scan Method and Traditional Method of Discarding

In proposition 5 of the [40] it is proved that the L_1 -error between a δ -GLMB density and its truncated (traditional truncation) version is denoted by

$$\|f_{\mathbb{H}} - f_{\mathbb{T}}\|_1 = \sum_{(I, \xi) \in \mathbb{H} - \mathbb{T}} w^{(I, \xi)}$$

only if $\mathbb{T} \subseteq \mathbb{H}$, where $\|f\|_1 \triangleq \int |f(X)| dX$ denotes the L_1 -norm and

$$f_{\mathbb{H}} = \Delta(X) \sum_{(I, \xi) \in \mathbb{H}} w^{(I, \xi)} \delta_I(\mathcal{L}(X)) [p^{(\xi)}]^X. \quad (\text{A1})$$

Now, let the $\mathbb{T}'$ present δ -GLMB density truncated via N-scan version, since $\mathbb{T}' \subseteq \mathbb{H}$, then

$$\|f_{\mathbb{H}} - f_{\mathbb{T}'}\|_1 = \sum_{(I, \xi) \in \mathbb{H} - \mathbb{T}'} w^{(I, \xi)} = \sum_{(I, \xi) \in \mathbb{C}^F} w^{(I, \xi)}$$

Since $\mathbb{C}^F \subseteq \mathbb{C}$, $\mathbb{C} \cap \mathbb{T} = \emptyset$, $\mathbb{C} \subseteq \mathbb{H}$ and $\mathbb{T} \subseteq \mathbb{H}$, then

$$\begin{aligned} \mathbb{C} \cup \mathbb{T} \subseteq \mathbb{H} &\Rightarrow (\mathbb{C} \cup \mathbb{T}) \cap \neg \mathbb{T} \subseteq \mathbb{H} \cap \neg \mathbb{T} \Rightarrow \\ \mathbb{C} \cap \neg \mathbb{T} \subseteq \mathbb{H} \cap \neg \mathbb{T} &\Rightarrow \mathbb{C} \subseteq \mathbb{H} - \mathbb{T} \Rightarrow \mathbb{C}^F \subseteq \mathbb{H} - \mathbb{T} \end{aligned}$$

then

$$\sum_{(I, \xi) \in \mathbb{H} - \mathbb{T}} w^{(I, \xi)} \geq \sum_{(I, \xi) \in \mathbb{C}^F} w^{(I, \xi)}$$

So

$$\|f_{\mathbb{H}} - f_{\mathbb{T}}\|_1 \geq \|f_{\mathbb{H}} - f_{\mathbb{T}'}\|_1.$$

which shows that the L_1 -error of N-scan method is less than traditional truncation method.

Potential Extension In recent years, self-supervised learning [57,58] has demonstrated strong capabilities in representation learning without requiring labeled data. Techniques such as contrastive learning [59], and kernel-based dependency minimization [60] have shown promise in learning robust embeddings. In the context of multi-target tracking, SSL could enhance feature learning by enabling the model to extract invariant representations of targets across different observations, reducing the impact of clutter, occlusion, and missing detections. By integrating it with the δ -GLMB filtering process, tracking robustness could be improved, particularly in scenarios where measurement uncertainty is high.

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