

A fast implementation of the generalized labeled multi-Bernoulli filter with joint prediction and update

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Abstract—This paper proposes a new implementation for the delta generalized labeled multi-Bernoulli (δ -GLMB) filter by combining prediction and update into a single step. In contrast to the original implementation which requires different truncation procedures for each component in the prediction and update, the joint strategy involves only one truncation per component in the filtering density, thus drastically reduces the number of computations. Performance comparison with the original implementation is presented through numerical studies.

I. INTRODUCTION

Multi-object tracking refers to the problem of jointly estimating the number of objects and their trajectories from sensor data. Driven by aerospace applications in the 1960's, today multi-object tracking lies at the heart of a diverse range of application areas, see for example the texts [1]–[5]. The most popular approaches to multi-object tracking are the joint probabilistic data association filter [1], multiple hypothesis tracking [2], and more recently, random finite set (RFS) [3], [5].

The RFS approach has attracted significant attention as a general systematic treatment of multi-object systems and provides the foundation for the development of novel filters such as the Probability Hypothesis Density (PHD) filter [6]–[8], Cardinalized PHD (CPHD) filter [9], [10], and multi-Bernoulli filters [3], [11]. While these filters were not designed to estimate the trajectories of objects, they have been successfully deployed in many applications including radar/sonar [12], [13], [14], computer vision [15], [16], cell biology [17], autonomous vehicle [18], [19], automotive safety [20], [21], sensor scheduling [22]–[25] and sensor network [26], [27].

The introduction of the generalized labeled multi-Bernoulli (GLMB) RFS in [28] has led to the development of the first tractable RFS-based multi-object tracker - the δ -GLMB filter. The δ -GLMB filter is attractive in that it exploits the conjugacy of the GLMB family to propagate forward in time the (labeled) multi-object filtering density exactly [28]. Each iteration of this filter involves an update operation and a prediction operation, both of which result in weighted sums of multi-target exponentials with intractably large number of terms. The first

implementation of the δ -GLMB filter truncate these sums by using the K -shortest path and ranked assignment algorithms, respectively, in the prediction and update to determine the most significant components [29].

While the original two-staged implementation is intuitive and highly parallelizable, it is structurally inefficient as it requires many intermediate truncations of the δ -GLMB densities, and does not fully exploit the statistical independence of target motions and detection measurements. Specifically, in the prediction, truncation is performed by solving two different K -shortest path problems, one for existing tracks and the other one for birth tracks. On the other hand, in the update, truncation is performed by solving a ranked assignment problem for each predicted δ -GLMB component. Since truncation of the predicted δ -GLMB sum is performed separately from the update, in general, a significant portion of the predicted components would generate updated components with negligible weights. Hence, computations are wasted in solving a large number of ranked assignment problems, each of which has cubic complexity in the number of measurements.

In this paper, we present a new implementation by formulating a joint prediction and update that eliminates inefficient truncation procedures in the original approach. The key innovation is the exploitation of the direct relationship between the components of the δ -GLMB filtering densities at consecutive iterations so that only one truncation is required for each component in the filtering density. Importantly, this formulation still allows for the truncation to be executed in polynomial time without having to explicitly enumerate all components. Consequently, the new implementation yields considerable computational savings while preserving the filtering performance.

The paper is organized as follows. Background on labeled RFS and the δ -GLMB filter is provided in section II. Section III presents the joint prediction and update implementation. Numerical results are presented in Section IV and concluding remarks are given in Section V.

II. BACKGROUND

This section summarizes the labeled RFS and the GLMB filter implementation. We refer the reader to the original work [28], [29] for detailed expositions.

For the rest of the paper, single-object states are represented by lowercase letters, e.g. x , \mathbf{x} while multi-object states are represented by uppercase letters, e.g. X , \mathbf{X} , symbols for labeled states and their distributions are bolded to distinguish them from unlabeled ones, e.g. \mathbf{x} , \mathbf{X} , π , etc, spaces are represented by blackboard bold e.g. \mathbb{X} , \mathbb{Z} , \mathbb{L} , \mathbb{N} , etc, and the class of finite subsets of a space \mathbb{X} is denoted by $\mathcal{F}(\mathbb{X})$. We use the standard inner product notation $\langle f, g \rangle \triangleq \int f(x)g(x)dx$, and the following multi-object exponential notation $h^{\mathbf{X}} \triangleq \prod_{x \in \mathbf{X}} h(x)$, where h is a real-valued function, with $h^\emptyset = 1$ by convention. We denote a generalization of the Kronecker delta that takes arbitrary arguments such as sets, vectors, etc, by

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

and the inclusion function, a generalization of the indicator function, by

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

We also write $1_Y(x)$ in place of $1_Y(\{x\})$ when $X = \{x\}$.

A. Labeled RFS

A labeled RFS is simply a finite set-valued random variable where each single-object dynamical state is augmented with a unique label that can be stated concisely as follows

Definition 1. A labeled RFS with state space \mathbb{X} and (discrete) label space \mathbb{L} is an RFS on $\mathbb{X} \times \mathbb{L}$ such that each realization has distinct labels.

Let $\mathcal{L} : \mathbb{X} \times \mathbb{L} \rightarrow \mathbb{L}$ be the projection $\mathcal{L}((x, \ell)) = \ell$, then a finite subset set \mathbf{X} of $\mathbb{X} \times \mathbb{L}$ has distinct labels if and only if \mathbf{X} and its labels $\mathcal{L}(\mathbf{X}) = \{\mathcal{L}(\mathbf{x}) : \mathbf{x} \in \mathbf{X}\}$ have the same cardinality, i.e. $\delta_{|\mathbf{X}|}(|\mathcal{L}(\mathbf{X})|) = 1$. The function $\Delta(\mathbf{X}) \triangleq \delta_{|\mathbf{X}|}(|\mathcal{L}(\mathbf{X})|)$ is called the *distinct label indicator*.

The set integral defined for any function $\mathbf{f} : \mathcal{F}(\mathbb{X} \times \mathbb{L}) \rightarrow \mathbb{R}$ is given by

$$\int \mathbf{f}(\mathbf{X}) \delta \mathbf{X} = \sum_{i=0}^{\infty} \frac{1}{i!} \int \mathbf{f}(\{\mathbf{x}_1, \dots, \mathbf{x}_i\}) d(\mathbf{x}_1, \dots, \mathbf{x}_i).$$

where the integral of a function $\mathbf{f} : \mathbb{X} \times \mathbb{L} \rightarrow \mathbb{R}$ is:

$$\int \mathbf{f}(\mathbf{x}) d\mathbf{x} = \sum_{\ell \in \mathbb{L}} \int_{\mathbb{X}} \mathbf{f}((x, \ell)) dx,$$

The notion of labeled RFS enables the incorporation of individual object identity into multi-object system and the Bayes filter to be used as a tracker of these multi-object states.

B. Bayes filter for labeled RFS

Suppose that at time k , there are N_k target states $\mathbf{x}_{k,1}, \dots, \mathbf{x}_{k,N_k}$, each taking values in the (labeled) state space $\mathbb{X} \times \mathbb{L}$. In the random finite set formulation the set of targets is treated as the *multi-object state*

$$\mathbf{X}_k = \{\mathbf{x}_{k,1}, \dots, \mathbf{x}_{k,N_k}\}. \quad (1)$$

Each state $(x_k, \ell) \in \mathbf{X}_k$ either survives with probability $p_S(x_k, \ell)$ and evolves to a new state (x_{k+1}, ℓ) or dies with probability $1 - p_S(x_k, \ell)$. The dynamics of the survived targets are encapsulated in the multi-object transition density $\mathbf{f}_{k+1|k}(\mathbf{X}|\mathbf{X}_k)$.

For a given multi-object state \mathbf{X}_k , each state $(x_k, \ell) \in \mathbf{X}_k$ at time k is either detected with probability $p_D(x_k, \ell)$ and generates an observation z with likelihood $g(z|x_k, \ell)$ or missed with probability $1 - p_D(x_k, \ell)$. The *multi-object observation* at time k , $Z_k = \{z_{k,1}, \dots, z_{k,M_k}\}$, is the superposition of the observations from detected states and Poisson clutters with intensity κ . Assuming that, conditional on \mathbf{X}_k , detections are independent, and that clutter is independent of the detections, the multi-object likelihood is given by [28], [29]

$$g(Z_k|\mathbf{X}_k) = e^{-\langle \kappa, 1 \rangle} \kappa^{Z_k} \sum_{\theta_k \in \Theta(\mathcal{L}(\mathbf{X}_k))} [\psi_Z(\cdot; \theta_k)]^{\mathbf{X}_k} \quad (2)$$

where $\theta_k : \mathbb{L} \rightarrow \{0, 1, \dots, |Z_k|\}$ is a function such that $\theta_k(i) = \theta_k(i') > 0$ implies $i = i'$, and

$$\psi_Z(x, \ell; \theta) = \begin{cases} \frac{p_D(x, \ell) g(z_{\theta_k(\ell)} | x, \ell)}{\kappa(z_{\theta_k(\ell)})}, & \text{if } \theta_k(\ell) > 0 \\ 1 - p_D(x, \ell), & \text{if } \theta_k(\ell) = 0 \end{cases} \quad (3)$$

Remark. θ_k is called an *association map* since it provides the mapping between tracks and observations, i.e. which track generates which observation, with undetected tracks assigned to 0. The condition $\theta_k(i) = \theta_k(i') > 0$ implies $i = i'$ ensures that a track can generate at most one measurement at any point in time. The set $\Theta(L)$ denotes the collection of all possible association maps on domain L .

Given a multi-object system as described above, the objective is to find the *multi-object filtering density*, denoted by $\pi_{k+1}(\mathbf{X}|Z_{k+1})$ ¹, which captures all information on the number of targets and individual target states at time $k+1$. In multi-object Bayesian filtering, the multi-object filtering density is computed recursively in time according to the following prediction and update, commonly referred to as *multi-object Bayes recursion* [3]

$$\pi_{k+1|k}(\mathbf{X}|Z_k) = \int \mathbf{f}_{k+1|k}(\mathbf{X}|\mathbf{X}_k) \pi_k(\mathbf{X}_k|Z_k) \delta \mathbf{X}_k, \quad (4)$$

$$\pi_{k+1}(\mathbf{X}|Z_{k+1}) = \frac{g(Z_{k+1}|\mathbf{X}) \pi_{k+1|k}(\mathbf{X}|Z_k)}{\int g(Z_{k+1}|\mathbf{X}) \pi_{k+1|k}(\mathbf{X}|Z_k) \delta \mathbf{X}}. \quad (5)$$

Note, however, that the Bayes filter is intractable since the set integrals in (4)-(5) have no analytic solution in general.

¹For convenience, we drop the dependence on past measurements upto time k

C. Delta generalized labeled multi-Bernoulli RFS

The δ -GLMB RFS, a special class of labeled RFS, provides an exact solution to (4)-(5). This is because the δ -GLMB RFS is closed under the multi-object Chapman-Kolmogorov equation with respect to the multi-object transition kernel and is conjugate with respect to the multi-object likelihood function [28].

Definition 2. A δ -GLMB RFS is a labeled RFS with state space \mathbb{X} and (discrete) label space \mathbb{L} , distributed according to

$$\pi(\mathbf{X}) = \Delta(\mathbf{X}) \sum_{(I, \xi) \in \mathcal{F}(\mathbb{L}) \times \Xi} \omega^{(I, \xi)} \delta_I(\mathcal{L}(\mathbf{X})) \left[p^{(\xi)} \right]^{\mathbf{X}}, \quad (6)$$

where Ξ is a discrete space while $\omega^{(I, \xi)}$ and $p^{(\xi)}$ satisfy

$$\sum_{(I, \xi) \in \mathcal{F}(\mathbb{L}) \times \Xi} \omega^{(I, \xi)} = 1, \quad (7)$$

$$\int p^{(\xi)}(x, \ell) dx = 1. \quad (8)$$

Remark. The δ -GLMB density is essentially a mixture of multi-object exponentials, in which each component is identified by a pair (I, ξ) . Each $I \in \mathcal{F}(\mathbb{L})$ is a set of tracks labels while $\xi \in \Xi$ represents a history of association maps $\xi = (\theta_1, \dots, \theta_k)$. The pair (I, ξ) can be interpreted as the hypothesis that the set of tracks I has a history of ξ association maps and corresponding kinematic state densities $p^{(\xi)}$. The weight $\omega^{(I, \xi)} \delta_I(\mathcal{L}(\mathbf{X}))$, therefore, can be considered as the probability of the hypothesis (I, ξ) .

Denote the collection of all label sets with n unique elements by $\mathcal{F}_n(\mathbb{L})$, the cardinality distribution of a δ -GLMB RFS is given by

$$\rho(n) = \sum_{(I, \xi) \in \mathcal{F}_n(\mathbb{L}) \times \Xi} \omega^{(I, \xi)}. \quad (9)$$

A δ -GLMB is completely characterized by the set of parameters $\{(\omega^{(I, \xi)}, p^{(\xi)}) : (I, \xi) \in \mathcal{F}(\mathbb{L}) \times \Xi\}$. For implementation it is convenient to consider the set of parameters as an enumeration of all δ -GLMB components (with positive weight) together with their associated weights and track densities $\{(I^{(h)}, \xi^{(h)}, \omega^{(h)}, p^{(h)})\}_{h=1}^H$, as shown in Figure 1, where $\omega^{(h)} \triangleq \omega^{(I^{(h)}, \xi^{(h)})}$ and $p^{(h)} \triangleq p^{(\xi^{(h)})}$.

$I^{(1)} =$ $\{\ell_1^{(1)}, \dots, \ell_{ I^{(1)}}^{(1)}\}$	$I^{(2)} =$ $\{\ell_1^{(2)}, \dots, \ell_{ I^{(2)}}^{(2)}\}$...	$I^{(h)} =$ $\{\ell_1^{(h)}, \dots, \ell_{ I^{(h)}}^{(h)}\}$...
$\xi^{(1)}$	$\xi^{(2)}$...	$\xi^{(h)}$...
$\omega^{(1)}$	$\omega^{(2)}$...	$\omega^{(h)}$...
$p^{(1)}(\cdot, \ell_1^{(1)})$	$p^{(2)}(\cdot, \ell_1^{(2)})$...	$p^{(h)}(\cdot, \ell_1^{(h)})$...
\vdots	\vdots	...	\vdots	...
$p^{(1)}(\cdot, \ell_{ I^{(1)}}^{(1)})$	$p^{(2)}(\cdot, \ell_{ I^{(2)}}^{(2)})$...	$p^{(h)}(\cdot, \ell_{ I^{(h)}}^{(h)})$...

Fig. 1. An enumeration of a δ -GLMB parameter set with each component indexed by an integer h . The hypothesis for component h is $(I^{(h)}, \xi^{(h)})$ while its weight and associated track densities are $\omega^{(h)}$ and $p^{(h)}(\cdot, \ell)$, $\ell \in I^{(h)}$.

Given a δ -GLMB initial density, all subsequent multi-object densities are δ -GLMBs and can be computed exactly by a tractable filter called the δ -GLMB filter.

D. Delta generalized labeled multi-Bernoulli filter

The δ -GLMB filter recursively propagates a δ -GLMB density forward in time via the Bayes recursion equations (4) and (5). Closed form solutions to the prediction and update of the δ -GLMB filter are given in the following propositions [28].

Proposition 1. If the multi-target posterior at time $k-1$ is a δ -GLMB of the form (6), i.e.

$$\pi_{k-1}(\mathbf{X}|Z_{k-1}) = \Delta(\mathbf{X}) \sum_{(I_{k-1}, \xi_{k-1}) \in \mathcal{F}(\mathbb{L}) \times \Xi} \omega_{k-1}^{(I_{k-1}, \xi_{k-1})} \times \delta_{I_{k-1}}(\mathcal{L}(\mathbf{X})) \left[p_{k-1}^{(\xi_{k-1})}(\cdot|Z_{k-1}) \right]^{\mathbf{X}}, \quad (10)$$

and the birth density \mathbf{f}_B is defined on $\mathcal{F}(\mathbb{X} \times \mathbb{B})$ according to

$$\mathbf{f}_B(\mathbf{Y}) = \Delta(\mathbf{Y}) \omega_B(\mathcal{L}(\mathbf{Y})) [p_B(\cdot)]^{\mathbf{Y}}, \quad (11)$$

then the multi-target prediction density to the next time is a δ -GLMB given by

$$\pi_{k|k-1}(\mathbf{X}|Z_{k-1}) = \Delta(\mathbf{X}) \times \sum_{(I_k, \xi_{k-1}) \in \mathcal{F}(\mathbb{L} \cup \mathbb{B}) \times \Xi} \omega_{k|k-1}^{(I_k, \xi_{k-1})} \delta_{I_k}(\mathcal{L}(\mathbf{X})) \left[p_{k|k-1}^{(\xi_{k-1})}(\cdot|Z_{k-1}) \right]^{\mathbf{X}}, \quad (12)$$

where

$$\omega_{k|k-1}^{(I_k, \xi_{k-1})} = \omega_{k-1}^{(I_{k-1}, \xi_{k-1})} \omega_S^{(\xi_{k-1})}(I_k \cap \mathbb{L}) \omega_B(I_k \cap \mathbb{B}) \quad (13)$$

$$\omega_S^{(\xi_{k-1})}(L) = \left[\eta_S^{(\xi_{k-1})} \right]^L \sum_{I_{k-1} \supseteq L} \left[1 - \eta_S^{(\xi_{k-1})} \right]^{I_{k-1} - L} \quad (14)$$

$$\eta_S^{(\xi_{k-1})}(\ell) = \left\langle p_S(\cdot, \ell), p_{k-1}^{(\xi_{k-1})}(\cdot, \ell) \right\rangle \quad (15)$$

$$p_{k|k-1}^{(\xi_{k-1})}(x, \ell) = 1_{\mathbb{L}}(\ell) p_S^{(\xi_{k-1})}(x, \ell) + 1_{\mathbb{B}}(\ell) p_B(x, \ell) \quad (16)$$

$$p_S^{(\xi_{k-1})}(x, \ell) = \frac{\left\langle p_S(\cdot, \ell) f_{k|k-1}(x|\cdot, \ell), p_{k-1}^{(\xi_{k-1})}(\cdot, \ell) \right\rangle}{\eta_S^{(\xi_{k-1})}(\ell)} \quad (17)$$

Proposition 2. Given the prediction density in (12), the multi-target posterior is a δ -GLMB given by

$$\pi_k(\mathbf{X}|Z_k) = \Delta(\mathbf{X}) \sum_{(I_k, \xi_{k-1}, \theta_k) \in \mathcal{F}(\mathbb{L} \cup \mathbb{B}) \times \Xi \times \Theta(I_k)} \omega_k^{(I_k, \xi_{k-1}, \theta_k)}(Z_k) \times \delta_{I_k}(\mathcal{L}(\mathbf{X})) \left[p_k^{(\xi_{k-1}, \theta_k)}(\cdot|Z_k) \right]^{\mathbf{X}}, \quad (18)$$

where

$$\omega_k^{(I_k, \xi_{k-1}, \theta_k)}(Z_k) \propto \omega_{k|k-1}^{(I_k, \xi_{k-1})} \left[\eta_{Z_k}^{(\theta_k)}(\cdot) \right]^{I_k}, \quad (19)$$

$$\eta_{Z_k}^{(\theta_k)}(\ell) = \left\langle p_{k|k-1}^{(\xi_{k-1})}(\cdot, \ell), \psi_{Z_k}(\cdot, \ell; \theta_k) \right\rangle, \quad (20)$$

$$p_k^{(\xi_{k-1}, \theta_k)}(x, \ell|Z_k) = \frac{p_{k|k-1}^{(\xi_{k-1})}(x, \ell) \psi_{Z_k}(x, \ell; \theta_k)}{\eta_{Z_k}^{(\theta_k)}(\ell)}. \quad (21)$$

The propagations of δ -GLMB components through prediction and update are illustrated in Fig. 2 and Fig. 3, respectively.

It is clear that the the number of components grows exponentially with time. Specifically, a component in the filtering density at time $k - 1$ generates a large number of predicted components, of which each one in turn produces a new set of multiple δ -GLMB components in the filtering density at time k . Hence, it is necessary to reduce the number of δ -GLMB components in both prediction and update densities at every time step.

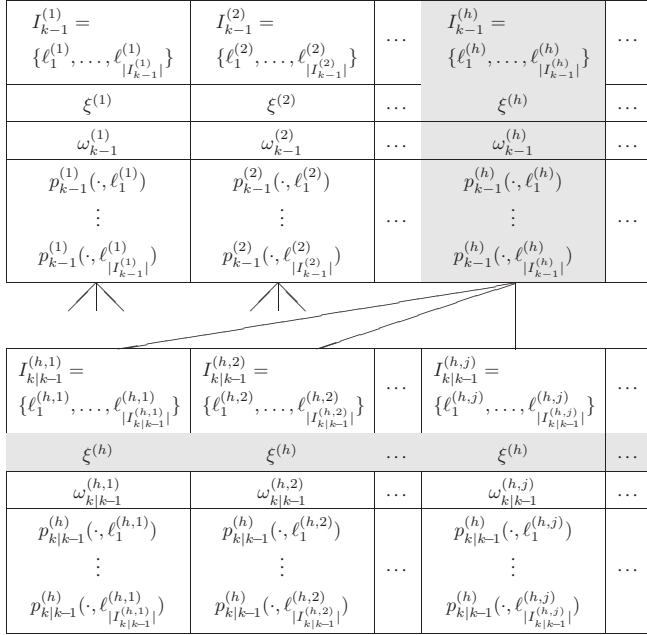


Fig. 2. The δ -GLMB prediction [29]: component h in the prior generates a large set of predicted components with $I_k^{(h,j)} \subseteq I_{k-1}^{(h)} \cup \mathbb{B}$, i.e. $j = 1, \dots, 2^{|I_{k-1}^{(h)}| + |\mathbb{B}|}$, and $\omega_{k|k-1}^{(h,j)} \triangleq \omega_{k|k-1}^{(I_k^{(h,j)}, \xi_{k-1}^{(h)})}$.

The simplest way to truncate a δ -GLMB density is discarding components with smallest weights. The following proposition asserts that this strategy minimizes the L_1 -distance between the true density and the truncated one [29]

Proposition 3. Let $\|\mathbf{f}\|_1 \triangleq \int |\mathbf{f}(\mathbf{X})| \delta \mathbf{X}$ denote the L_1 -norm of $\mathbf{f} : \mathcal{F}(\mathbb{X} \times \mathbb{L}) \rightarrow \mathbb{R}$, and for a given $\mathbb{H} \subseteq \mathcal{F}(\mathbb{L}) \times \Xi$ let

$$\mathbf{f}_{\mathbb{H}}(\mathbf{X}) = \Delta(\mathbf{X}) \sum_{(I, \xi) \in \mathbb{H}} \omega^{(I, \xi)} \delta_I(\mathcal{L}(\mathbf{X})) \left[p^{(\xi)} \right]^{\mathbf{X}}$$

be an unnormalized δ -GLMB density. If $\mathbb{T} \subseteq \mathbb{H}$ then

$$\|\mathbf{f}_{\mathbb{H}} - \mathbf{f}_{\mathbb{T}}\|_1 = \sum_{(I, \xi) \in \mathbb{H} - \mathbb{T}} \omega^{(I, \xi)},$$

$$\left\| \frac{\mathbf{f}_{\mathbb{H}}}{\|\mathbf{f}_{\mathbb{H}}\|_1} - \frac{\mathbf{f}_{\mathbb{T}}}{\|\mathbf{f}_{\mathbb{T}}\|_1} \right\|_1 \leq 2 \frac{\|\mathbf{f}_{\mathbb{H}}\|_1 - \|\mathbf{f}_{\mathbb{T}}\|_1}{\|\mathbf{f}_{\mathbb{H}}\|_1}.$$

III. JOINT PREDICTION AND UPDATE FOR THE δ -GLMB FILTER

In this section, we briefly review the original implementation of the δ -GLMB filter in subsection III-A and propose a new implementation strategy with joint prediction and update in subsection III-B.

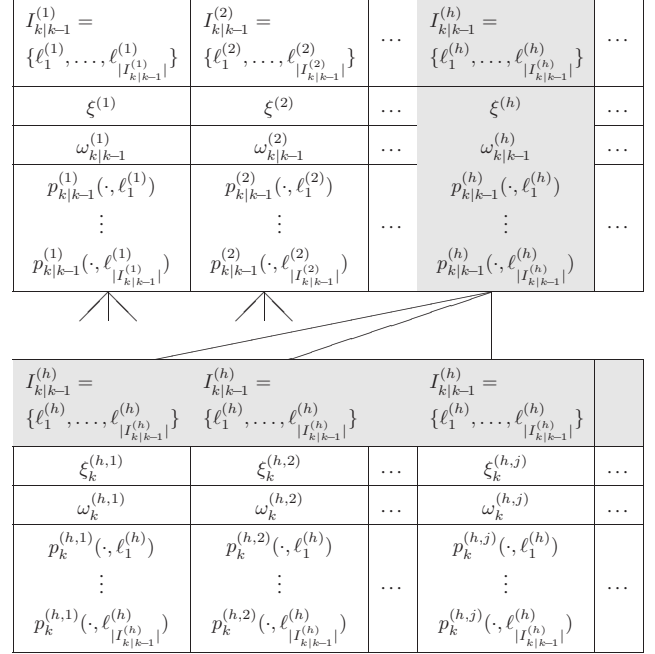


Fig. 3. The δ -GLMB update [29]: component h in the predicted density generates a (large) set of update components with $\xi_k^{(h,j)} \triangleq (\xi_{k-1}^{(h)}, \theta_k^{(h,j)})$ and weights $\omega_k^{(h,j)} \triangleq \omega_k^{(I_k^{(h,j)}, \xi_{k-1}^{(h)}, \theta_k^{(h,j)})}$, $j = 1, \dots, |\Theta(I_k^{(h)})|$.

A. The original implementation

The first implementation of the δ -GLMB filter, detailed in [29], recursively calculates the filtering density by sequentially computing the predicted and update densities at each iteration based on Proposition 1 and Proposition 2. Since direct implementation of equations (12) and (18) is difficult due to the sum over supersets in (14), the predicted and update densities are rewritten as (22) and (23), respectively, with

$$\omega_S^{(I_{k-1}, \xi_{k-1})}(L) = \left[1 - \eta_S^{(\xi_{k-1})} \right]^{I_{k-1} - L} \left[\eta_S^{(\xi_{k-1})} \right]^L.$$

In the prediction stage (22), each component (I_{k-1}, ξ_{k-1}) with weight $\omega_{k-1}^{(I_{k-1}, \xi_{k-1})}$ generates a set of prediction components $(L \cup J, \xi_{k-1})$ with weight

$$\omega_{k|k-1}^{(L \cup J, \xi_{k-1})} = \omega_{k-1}^{(I_{k-1}, \xi_{k-1})} \omega_S^{(I_{k-1}, \xi_{k-1})}(L) \omega_B(J),$$

where L and J represent two disjoint label sets of survival and birth tracks, respectively. Since the weight of the prediction component can be factorized into two factors $\omega_S^{(I_{k-1}, \xi_{k-1})}(L)$ and $\omega_B(J)$ that operates on two mutually exclusive sets, truncating the predicted density is performed by solving two separate K -shortest path problems for each set of tracks. This is because running only one instance of the K -shortest path based on the augmented set of existing and birth tracks generally favours the selection of survival tracks over new births and typically results in poor track initiation.

In the update stage (23), each prediction component $(L \cup J, \xi_{k-1})$ generates a (large) set of update components $(L \cup$

$$\pi_{k|k-1}(\mathbf{X}|Z_{k-1}) = \Delta(\mathbf{X}) \sum_{I_{k-1}, \xi_{k-1}, L, J} 1_{\mathcal{F}(I_{k-1})}(L) 1_{\mathcal{F}(\mathbb{B})}(J) \omega_{k-1}^{(I_{k-1}, \xi_{k-1})} \omega_S^{(I_{k-1}, \xi_{k-1})}(L) \omega_B(J) \delta_{L \cup J}(\mathcal{L}(\mathbf{X})) \left[p_{k|k-1}^{(\xi_{k-1})}(\cdot|Z_{k-1}) \right]^{\mathbf{X}} \quad (22)$$

$$\pi_k(\mathbf{X}|Z_k) = \frac{\Delta(\mathbf{X}) \sum_{I_{k-1}, \xi_{k-1}, L, J, \theta_k} 1_{\mathcal{F}(I_{k-1})}(L) 1_{\mathcal{F}(\mathbb{B})}(J) 1_{\Theta(L \cup J)}(\theta_k) \omega_{k-1}^{(I_{k-1}, \xi_{k-1})} \omega_S^{(I_{k-1}, \xi_{k-1})}(L) \omega_B(J) \left[\eta_{Z_k}^{(\theta_k)} \right]^{L \cup J} \delta_{L \cup J}(\mathcal{L}(\mathbf{X})) \left[p_k^{(\xi_{k-1}, \theta_k)}(\cdot|Z_k) \right]^{\mathbf{X}}}{\sum_{I_{k-1}, \xi_{k-1}, L, J, \theta_k} 1_{\mathcal{F}(I_{k-1})}(L) 1_{\mathcal{F}(\mathbb{B})}(J) 1_{\Theta(L \cup J)}(\theta_k) \omega_{k-1}^{(I_{k-1}, \xi_{k-1})} \omega_S^{(I_{k-1}, \xi_{k-1})}(L) \omega_B(J) \left[\eta_{Z_k}^{(\theta_k)} \right]^{L \cup J}} \quad (23)$$

$J, (\xi_{k-1}, \theta_k)$. These update components are truncated without having to exhaustively compute all the components by solving a ranked assignment problem.

Although the original two-staged implementation is intuitive and highly parallelizable, it has several drawbacks. First, since truncation of the predicted δ -GLMB density is performed separately from the update based purely on *a priori* knowledge (e.g. survival and birth probabilities), in general, a significant portion of the predicted components would generate updated components with negligible weights. Hence, computations are wasted in solving a large number of ranked assignment problems, each of which has cubic complexity in the number of measurements. Second, it would be very difficult to determine the final approximation error of the truncated filtering density as the implementation involves least three separate truncating processes: one for existing tracks, one for birth tracks, and one for predicted tracks.

In the following subsections, we will introduce the joint prediction and update as a better alternative to the original two-staged approach. The joint strategy eliminates the need for separate prediction truncating procedures, thus involves only one truncation per each iteration. Consequently, the new implementation yields considerable computational savings while preserving the filtering performance as well as the parallelizability of the original implementation.

B. The joint prediction and update implementation

Instead of computing the filtering density in two steps, the new strategy aims to generate the components of the filtering density in one combined step by formulating a direct relationship between the component of the current filtering density with those of the previous density. Specifically, we will derive a new formulation for $\pi_k(\mathbf{X}|Z_k)$ that does not involve prediction induced variables L and J . This can be done via an extended measurement mapping, denoted by $\tilde{\theta}$, and defined as follows

Definition 3. The extended measurement mapping $\tilde{\theta} : \mathbb{L} \cup \mathbb{B} \rightarrow \{0, 1, \dots, |Z_k|, |Z_k|+1\}$ is a function such that $\tilde{\theta}(i) = \tilde{\theta}(i')$ for $0 < \tilde{\theta}(i) < |Z_k|+1$ implies $i = i'$.

Remark. The new mapping, in essence, only extends the original mapping to include a new association, $|Z_k|+1$. In particular, $\tilde{\theta}$ is identical to θ except for non-survival and

unconfirmed birth tracks, i.e.

$$\tilde{\theta}_k(\ell) = \begin{cases} \theta_k(\ell) & \forall \ell \in L \cup J, \\ |Z_k| + 1 & \forall \ell \in (I_{k-1} - L) \cup (\mathbb{B} - J). \end{cases} \quad (24)$$

Using the extended mapping $\tilde{\theta}$, the following proposition establishes the direct relationship between two consecutive filtering densities at time k and $k-1$. For simplicity, we assume that target births are modeled by (labeled) multi-Bernoulli RFS's, i.e. $\omega_B(J) = [1 - r(\cdot)]^{\mathbb{B}-J} [r(\cdot)]^J$ with $r(\ell)$ denotes the existence probability of track ℓ .

Proposition 4. *If the multi-target posterior at time $k-1$ is a δ -GLMB of the form (10) and the set of targets born at the next time is distributed as a labeled multi-Bernoulli RFS, then the multi-target posterior at the next time is a δ -GLMB given by*

$$\pi_k(\mathbf{X}|Z_k) \propto \Delta(\mathbf{X}) \sum_{I_{k-1}, \xi_{k-1}, \tilde{\theta}_k} 1_{\Theta(I_{k-1} \cup \mathbb{B})}(\tilde{\theta}_k) \omega_{k-1}^{(I_{k-1}, \xi_{k-1})} \left[\gamma_{Z_k}^{(\tilde{\theta}_k)} \right]^{I_{k-1} \cup \mathbb{B}} \times 1_{\{0, \dots, |Z_k|\}}(\tilde{\theta}(\mathcal{L}(\mathbf{X}))) \left[p_k^{(\xi_{k-1}, \tilde{\theta}_k)}(\cdot|Z_k) \right]^{\mathbf{X}} \quad (25)$$

where $p_k^{(\xi_{k-1}, \tilde{\theta}_k)}(\ell|Z_k) \equiv p_k^{(\xi_{k-1}, \theta_k)}(\ell|Z_k)$, $\forall \ell : \tilde{\theta}(\ell) < |Z_k|+1$ and

$$\gamma_{Z_k}^{(\tilde{\theta}_k)}(\ell) = \begin{cases} 1 - \eta_S^{(\xi_{k-1})}(\ell) & \forall \ell \in I_{k-1} : \tilde{\theta}(\ell) = |Z_k|+1, \\ \eta_S^{(\xi_{k-1})}(\ell) \eta_{Z_k}^{(\theta_k)}(\ell) & \forall \ell \in I_{k-1} : \tilde{\theta}(\ell) < |Z_k|+1, \\ 1 - r(\ell) & \forall \ell \in \mathbb{B} : \tilde{\theta}(\ell) = |Z_k|+1, \\ r(\ell) \eta_{Z_k}^{(\theta_k)}(\ell) & \forall \ell \in \mathbb{B} : \tilde{\theta}(\ell) < |Z_k|+1. \end{cases} \quad (26)$$

We now proceed to detail an efficient implementation of the δ -GLMB filter based on the result in Proposition 4. Let the sets of existing tracks, birth tracks, and measurements be enumerated by $I_{k-1}^{(h)} = \{\ell_1, \dots, \ell_N\}$, $\mathbb{B} = \{\ell_{N+1}, \dots, \ell_P\}$, and $Z_k = \{z_1, \dots, z_M\}$, respectively. Given the h -th component of the previous filtering density, the set of all possible values of $\gamma_{Z_k}^{(\theta_k)}(\ell)$ is represented by a $P \times (M+2P)$ matrix, denoted by $\Gamma_{Z_k}^{(h)}$, as depicted in Fig. 4. The objective is to exploit $\Gamma_{Z_k}^{(h)}$ to find the mappings $\tilde{\theta}_k$ for all the existing and birth tracks that yield high update component weights without exhaustively computing all of them. The simplest way to achieve this objective is to adopt the ranked assignment approach in the original implementation [29].

Denote by $S_{\tilde{\theta}_k}^-$ a $P \times (M+2P)$ matrix whose entries are either 1 or 0 such that the sum of each row is exactly 1

		Detected			Misdetected					Died						
		z_1	...	z_M	\emptyset	...	\emptyset	\emptyset	...	\emptyset	\emptyset	...	\emptyset	\emptyset	...	\emptyset
Existing tracks	$p(\cdot, \ell_i)$	$\gamma_1(\ell_i)$...	$\gamma_M(\ell_i)$	$\gamma_0(\ell_i)$...	0	0	...	0	$\gamma_{M+1}(\ell_i)$...	0	0	...	0
	\vdots	\vdots	\ddots	\vdots	\vdots	\ddots	\vdots	\vdots	\ddots	\vdots	\vdots	\ddots	\vdots	\vdots	\ddots	\vdots
	$p(\cdot, \ell_N)$	$\gamma_1(\ell_N)$...	$\gamma_M(\ell_N)$	0	...	$\gamma_0(\ell_N)$	0	...	0	0	...	$\gamma_{M+1}(\ell_N)$	0	...	0
Births	$p(\cdot, \ell_{N+1})$	$\gamma_1(\ell_{N+1})$...	$\gamma_M(\ell_{N+1})$	0	...	0	$\gamma_0(\ell_{N+1})$...	0	0	...	0	$\gamma_{M+1}(\ell_{N+1})$...	0
	\vdots	\vdots	\ddots	\vdots	\vdots	\ddots	\vdots	\vdots	\ddots	\vdots	\vdots	\ddots	\vdots	\vdots	\ddots	\vdots
	$p(\cdot, \ell_T)$	$\gamma_1(\ell_T)$...	$\gamma_M(\ell_T)$	0	...	0	0	...	$\gamma_0(\ell_T)$	0	...	0	0	...	$\gamma_{M+1}(\ell_T)$

Fig. 4. The matrix $\Gamma_{Z_k}^{(h)}$ contains all possible values of the update factor $\gamma_j(\ell_i) \triangleq \gamma_{Z_k}^{(j)}(\ell_i)$, $j = \tilde{\theta}_k(\ell_i)$, $i = 1, \dots, P$. The cost matrix $C_{Z_k}^{(h)}$ is formed by taking negative logarithm on $\Gamma_{Z_k}^{(h)}$, i.e. $C_{Z_k}^{(h)} = [-\log(\gamma_j(\ell_i))]_{(i,j)=(1,1)}^{(P, M+2P)}$.

while the sum of each column is at most 1. $S_{\tilde{\theta}_k}$ is called an assignment matrix since it represents legitimate outcomes that a mapping $\tilde{\theta}_k$ assigns for each individual track. Therefore, a valid mapping $\tilde{\theta}_k$ is completely determined through its associated assignment. To find the most significant assignments, it is necessary to design a cost function such that the cost of each assignment is proportional to the corresponding update weight given in (25).

Let the cost matrix $C_Z^{(h)}$ be a $P \times (M + 2P)$ matrix whose entries are negative logarithm of $\gamma^{(h, \tilde{\theta})}(\ell)$, i.e. $C_Z^{(h)} = -\log(\Gamma_Z^{(h)})$. The cost function for an assignment $S_{\tilde{\theta}}$ is defined as follows

$$f_c(S_{\tilde{\theta}}) \triangleq -\text{tr}(S_{\tilde{\theta}}^T C_Z^{(h)}). \quad (27)$$

It is straightforward to show that the (unnormalized) weight of the $S_{\tilde{\theta}}$ -induced j -th component in the filtering density at time k by is

$$\omega_k^{(h, j)} \propto \exp[-f_c(S_{\tilde{\theta}})]. \quad (28)$$

Taking a positive integer $T^{(h)}$ and (27) as the objective function, the Murty's algorithm will generate a sequence of $T^{(h)}$ assignment matrices that yield lowest costs (or equivalently, highest update weights) without exhaustively navigating the whole assignment space. The pseudo code for the joint prediction and update algorithm is presented in Algorithm 1.

Similar to the original implementation, the joint prediction and update also operates independently on each components in the filtering density, thereby is highly parallelizable.

IV. SIMULATION

In this section we compare the performance of the joint prediction and update implementation with that of the original separated prediction and update strategy. For illustration purpose, we use the same numerical example as that in [29], where a varying number targets travel in straight paths and with different but constant velocities on the two dimensional region $[1000, 1000]m \times [1000, 1000]m$. The duration of the scenario is $K = 100s$. There is a crossing of 3 targets at the origin at time $k = 20$, and a crossing of two pairs of targets at position $(\pm 300, 0)$ at time $k = 40$. The region and tracks are shown in Figure 5.

Algorithm 1 δ -GLMB joint prediction and update

Inputs: $\{(I_{k-1}^{(h)}, \xi^{(h)}, \omega_{k-1}^{(h)}, p_{k-1}^{(h)}, T^{(h)})\}_{h=1}^H, Z$

Outputs: $\{(I_k^{(h, j)}, \xi_k^{(h, j)}, \omega_k^{(h, j)}, p_k^{(h, j)})\}_{(h, j)=(1, 1)}^{(H, T^{(h)})}$

- 1: **for** $h \leftarrow 1, H$ **do**
- 2: compute $\Gamma_{Z_k}^{(h)}$ according to (26)
- 3: $C_{Z_k}^{(h)} \leftarrow -\log(\Gamma_{Z_k}^{(h)})$
- 4: $(I_k^{(h, j)}, \xi_k^{(h, j)}) \leftarrow \text{ranked_assignment}(C_{Z_k}^{(h)}, T^{(h)})$
- 5: **for** $j \leftarrow 1, T^{(h)}$ **do**
- 6: compute $\omega_k^{(h, j)}$ according to (28)
- 7: compute $p_k^{(h, j)}$ according to (21)
- 8: **end for**
- 9: **end for**
- 10: **normalize weights** $\{\omega_k^{(h, j)}\}_{(h, j)=(1, 1)}^{(H, T^{(h)})}$

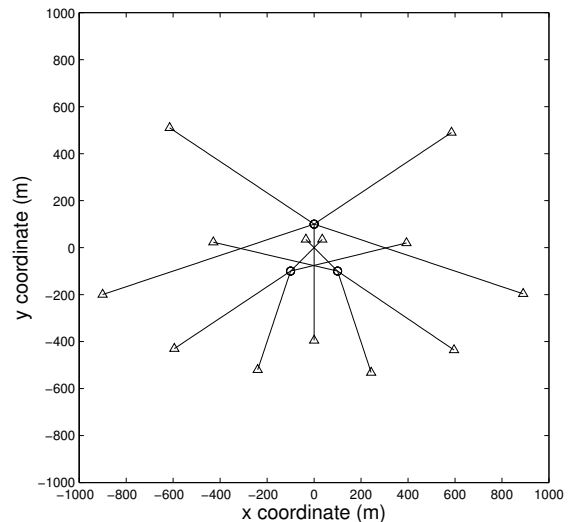


Fig. 5. Multiple trajectories in the xy plane. Start/Stop positions for each track are shown with \circ/Δ .

The kinematic target state is a vector of planar position and velocity $x_k = [p_{x,k}, p_{y,k}, \dot{p}_{x,k}, \dot{p}_{y,k}]^T$. Measurements are

noisy vectors of planar position only $z_k = [z_{x,k}, z_{y,k}]^T$. The single-target state space model is linear Gaussian according to transition density $f_{k|k-1}(x_k|x_{k-1}) = \mathcal{N}(x_k; F_k x_{k-1}, Q_k)$ and likelihood $g_k(z_k|x_k) = \mathcal{N}(z_k; H_k x_k, R_k)$ with parameters

$$F_k = \begin{bmatrix} I_2 & \Delta I_2 \\ 0_2 & I_2 \end{bmatrix} \quad Q_k = \sigma_\nu^2 \begin{bmatrix} \frac{\Delta^4}{4} I_2 & \frac{\Delta^3}{2} I_2 \\ \frac{\Delta^2}{3} I_2 & \Delta^2 I_2 \end{bmatrix}$$

$$H_k = \begin{bmatrix} I_2 & 0_2 \end{bmatrix} \quad R_k = \sigma_\epsilon^2 I_2$$

where I_n and 0_n denote the $n \times n$ identity and zero matrices respectively, $\Delta = 1s$ is the sampling period, $\sigma_\nu = 5m/s^2$ and $\sigma_\epsilon = 10m$ are the standard deviations of the process noise and measurement noise. The survival probability is $p_{S,k} = 0.99$ and the birth model is a Labeled Multi-Bernoulli RFS with parameters $\pi_B = \{r_B^{(i)}, p_B^{(i)}\}_{i=1,\dots,3}$ where $r_B^{(i)} = 0.04$ and $p_B^{(i)}(x) = \mathcal{N}(x; m_B^{(i)}, P_B)$ with $m_B^{(1)} = [0, 0, 100, 0]^T$, $m_B^{(2)} = [100, 0, 100, 0]^T$, $m_B^{(3)} = [100, 0, 100, 0]^T$, $P_B = [\text{diag}([10, 10, 10, 10]^T)]^2$. The detection probability is $p_{D,k} = 0.88$ and clutter follows a Poisson RFS with an average intensity of $\lambda_c = 6.6 \times 10^{-5} m^{-2}$ giving an average of 66 false alarms per scan.

For a fair comparison, both approaches are capped to the same maximum components. Results are shown over 100 Monte Carlo trials. Figures 6 shows the mean and standard deviation of the estimated cardinality versus time. Figures 7 and 8 show the OSPA distance [30] and its localization and cardinality components for $c = 100m$ and $p = 1$.

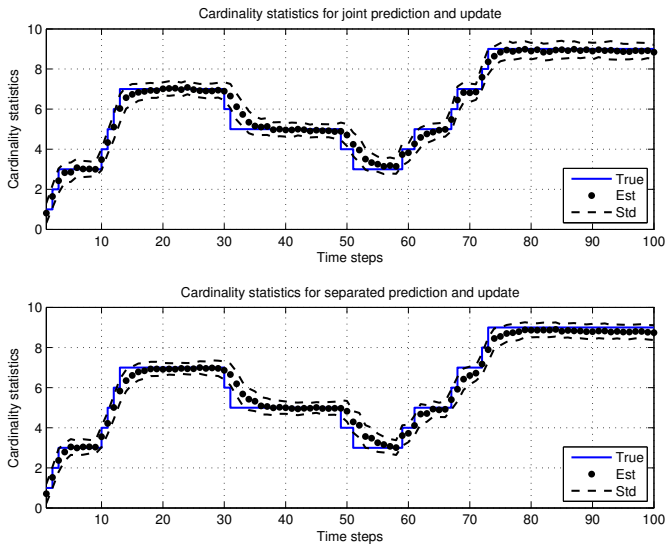


Fig. 6. Cardinality statistics comparison

It can be seen that both approaches estimate the cardinality equally well. Similarly, in terms of OSPA distance, the performance of the two approaches is virtually the same. As expected, however, the joint implementation average run time is typically between 1 and 2 order of magnitude faster than that of the original implementation.

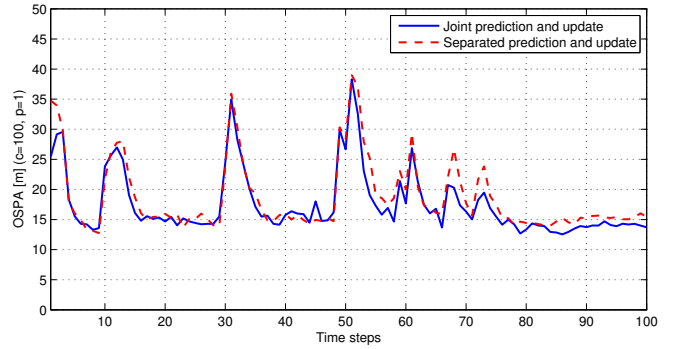


Fig. 7. OSPA distance comparison

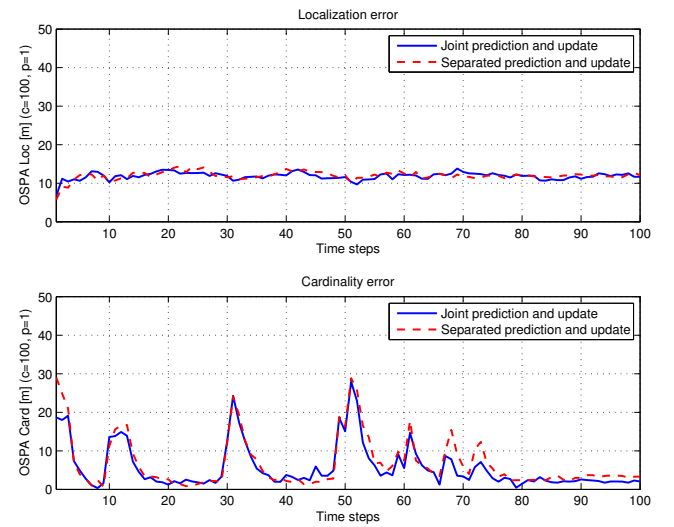


Fig. 8. Comparison of localization and cardinality errors

V. CONCLUSIONS

In this paper we propose a new implementation scheme for the δ -GLMB filter that allows joint prediction and update. In contrast to the conventional two-staged implementation, the joint approach use *a posteriori* information to construct cost matrices for every individual track, thereby requires only one truncation in each iteration. Consequently, the filter run time is significantly improved without affecting the filtering performance. The joint implementation scheme is also applicable to approximations of the δ -GLMB filter such as the labeled multi-Bernoulli (LMB) filter [31]. It is possible to further reduce the computational complexity in our proposed joint prediction and update by replacing the ranked assignment algorithm with Markov Chain Monte Carlo methods. In fact using a Gibbs sampler, a multi-target tracking algorithm, with linear complexity in the number of measurements and quadratic in the number of targets, was proposed in [32].

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