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A Cardinality Preserving Multitarget Multi-Bernoulli RFS Tracker

Vishal Cholapadi Ravindra

Lennart Svensson, Lars Hammarstrand

Mark Morelande

Flight Mechanics &
Control Division
National Aerospace Laboratories
Bangalore 560017, India
Email: vishalcr@nal.res.in

Department of Signals & Systems
Chalmers University of Technology
Göteborg, Sweden 412 96
Email: lennart.svensson,
lars.hammarstrand@chalmers.se

Department of Electrical & Electronics
University of Melbourne
Victoria 3010
Australia
Email: m.morelande@ee.unimelb.edu.au

Abstract—This paper proposes a novel multitarget multi-Bernoulli (MeMBer) random finite set (RFS) posterior density recursion that preserves the cardinality probability mass function (pmf) upon update. The proposed recursion propagates the posterior density of a MeMBer RFS that is parameterized by target existence probabilities and marginal densities, that are assumed *independent*. At update, the *exact* posterior is derived via marginalization over a set of global (measurement dependent) hypotheses. However, it is shown that the independent existence probability assumption is violated in the exact posterior. In order to alleviate this problem, an approach inspired by the recently proposed set-joint probabilistic data association (SJPDA) filter is proposed to modify the exact posterior to another density within the same RFS family that contains independent existence probabilities. Furthermore, this approach is designed to preserve the cardinality pmf, without affecting mean optimal subpattern assignment (MOSPA) results. The proposed recursion is general, i.e., it does not make any assumptions about target distribution models. Furthermore, it is proved that when the number of existing targets is not more than two, the described modification of the posterior can *always* be made. Future work entails the extension of the proof by relaxing the constraint on the number of targets.

I. INTRODUCTION

Multitarget tracking involves the joint estimation of the states of a (usually unknown) number of targets from a set of measurements. The set of measurements usually consists of both target originated measurements as well as false alarms (clutter) in addition to missed detections, necessitating data association, i.e., association of measurements to targets. Well known data association algorithms are the joint probabilistic data association (JPDA [5]), the multiple hypothesis tracking (MHT [10]) and multidimensional assignment based algorithms (MDA [3]). Furthermore, a class of algorithms that are based on finite set statistics (FISST, [7], [8]) such as the

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probability hypothesis density (PHD [6]) and the cardinalized PHD (CPHD [8]) filter that formulate the multitarget state estimation problem using a Bayesian framework have been proposed and are increasingly popular. FISST provides a good framework for the description of multiple targets, especially when tracking does not require the knowledge of target identity. In such cases a random finite set (RFS) description is suitable — an RFS is a set of multitarget states that are *unlabeled* random vectors, and whose cardinality (number of elements) is a random variable [9].¹

The multitarget multi-Bernoulli (MeMBer) RFS recursion was proposed as a tractable approximation to the Bayes multitarget recursion under low clutter density scenarios [7]. The RFS is statistically represented by a union of independent Bernoulli distributed RFSs, while the cardinality distribution is also assumed distributed as Bernoulli parameterized by independent existence probabilities [13]. Unlike the CPHD recursion, which recursively propagates the first moment and cardinality distributions, the MeMBer recursion propagates the RFS posterior density. The present paper proposes a novel MeMBer RFS recursion that preserves the cardinality pmf upon update. In comparison to the well known cardinalized probability hypothesis density (CPHD) filter [8], which also preserves the cardinality pmf exactly in one update recursion, this new approach is more free in its representation of the marginal posteriors. Both the CPHD filter and the family of MeMBer filters [13] assume that all states are independently distributed, and furthermore, *the CPHD filter in addition assumes that they are identically distributed*. Clearly, the assumptions in the CPHD are limiting and there is a possibility of finding more accurate approximations of the marginal posteriors.

The MeMBer RFS posterior is parameterized by the *marginal posterior and existence probabilities* of the hypothesized tracks, ***both assumed independent***. At each update, the exact multitarget posterior is obtained by marginalization over the global hypotheses (data association and target existence hypotheses). It is however, seen that the independence of

¹For e.g., for an RFS representing two targets; $\{x_1, x_2\} \equiv \{x_2, x_1\}$.

target existence probabilities is lost. In [4], [11], [12], an alternative metric to the mean square error called the mean optimal subpattern assignment (MOSPA) was recommended for problems where the identity of the targets being tracked are not of interest. Furthermore, it was also shown that as long as two densities belong to the same RFS family, switching between them does not change the optimal minimum MOSPA (MMOSPA) estimates. In an approach inspired by the set-JPDA [12], the exact posterior is modified to another posterior within the RFS family where the target existence probabilities are independent. Furthermore, the proposed approach performs the modification in a manner that preserves the cardinality pmf.

Section II provides a background of MeMBer RFS models and RFS families, and outlines the MeMBer RFS posterior recursion parameters. Section III describes the methodology proposed in the paper to obtain the proposed MeMBer RFS recursion. Section IV outlines the derivation of the exact posterior, while Section V discusses the independence of target existences. Section VI details the derivation of the modified posterior. Section VII describes a linear Gaussian model two target implementation of the tracking algorithm proposed in the paper, and describes the optimization framework used to execute the modification of the posterior. Section VIII presents a simulation scenario to demonstrate the application of the proposed tracking algorithm and shows the tracking and cardinality estimation results. Section IX draws conclusions and outlines future work.

II. BACKGROUND & PROBLEM FORMULATION

In this article we study the tracking of multiple, but unknown number of targets, given independently generated measurements from targets as well as sources of clutter. Suppose, at time k , there are n_k hypothesized tracks and m_k measurements then the set of states representing the tracks and the set of measurements can be formalized as the following random finite sets (RFS),² $X_k = \{x_k^{(1)}, \dots, x_k^{(n_k)}\} \in \mathcal{F}(\mathcal{X})$ and $Z_k = \{z_k^{(1)}, \dots, z_k^{(m_k)}\} \in \mathcal{F}(\mathcal{Z})$, respectively. For the possibility that no target exists at k , i.e., $n_k = 0$, then RFS is denoted by the empty set $X_k = \emptyset$. Here, $\mathcal{F}(\mathcal{X})$ and $\mathcal{F}(\mathcal{Z})$ denotes the space of finite subsets on $\mathcal{X} \subseteq \mathbb{R}^{n_x}$ and $\mathcal{Z} \subseteq \mathbb{R}^{n_z}$. Furthermore, we denote all measurements up to and including time k as $Z^k = \bigcup_{l=1}^k Z_l$.

The problem at hand is to recursively calculate the RFS density of the multitarget state X_k given the super set of sensor observations Z^k . From this posterior density the idea is to calculate estimates of the number of targets (cardinality pmf) as well as their states. The target labels are not of interest for the tracking algorithm introduced in the paper, hence, the MOSPA metric is used to evaluate the results. The modeling assumptions regarding the multitarget state and measurements are stated in the following subsections.

² $x_k^{(i)}$ does not necessarily represent the state of target i , hence, making it an unordered set. An ordered set is represented by, for e.g., $\mathbf{x}_k = (x_k^{(1)}, x_k^{(2)})$, while an unordered set is represented by $X_k = \{x_k^{(1)}, x_k^{(2)}\}$.

A. MeMBer RFS Model

Given a multitarget RFS X_{k-1} , it is assumed that each target state $x_{k-1} \in X_{k-1}$, either continues to exist at time k with a (survival) probability $p_{S,k}(x_{k-1})$ and transitions to the new state modeled by a prior (prediction) density $q_{k|k-1}(x_k)$, or dies with probability $1-p_{S,k}(x_{k-1})$. The state transition (using the notations from [13]) is given by

$$X_k = \underbrace{\left[\bigcup_{x_{k-1} \in X_{k-1}} S_{k|k-1}(x_{k-1}) \right]}_{\text{existing targets}} \bigcup \underbrace{\Gamma_k}_{\text{new targets}} \quad (1)$$

where the multi-Bernoulli RFS $S_{k|k-1}(x_{k-1})$ models the state transition at time k , and is parameterized by the existence (survival) probability $p_{S,k}(x_{k-1})$ and the prior (prediction) density $q_{k|k-1}(x_k)$. New targets are modeled by the multi-bernoulli RFS Γ_k described by the union of $n_{b,k}$ independent Bernoulli RFSs all with birth probability $p_{\Gamma,k}$ and density $f_b(\cdot)$. As the individual RFSs are modeled as independent, the new RFS X_k resulting from the union in (1) is a multi-Bernoulli RFS conditional on X_{k-1} [13].

The measurements are modeled in such a way that each target, at time k , represented by its state $x_k \in X_k$, generates measurements independently and is detected with probability $p_{D,k}(x_k)$ to generate an observation z_k with likelihood $\Lambda_k(z_k|x_k)$, or is missed with probability $1-p_{D,k}(x_k)$. Hence, each state $x_k \in X_k$ in (1) generates a Bernoulli RFS $R_k(x_k)$ parameterized by $r = p_{D,k}(x_k)$ and the likelihood $\Lambda_k(z_k|x_k)$ [13]. In addition, the RFS of measurements at time k , Z_k , also consists of false alarms or measurements generated by clutter. These are modeled by RFS K_k . Hence, at time k the measurement set Z_k is denoted by the union

$$Z_k = \underbrace{\left[\bigcup_{x_k \in X_k} R_k(x_k) \right]}_{\text{target generated measurements}} \bigcup \underbrace{K_k}_{\text{clutter}} \quad (2)$$

Similar to (1), the RFS in (2) constitutes a multi-Bernoulli RFS, conditional on X_k .

B. MeMBer Parameterization

As such, the posterior MeMBer RFS density $\pi_{k|k}(X_k)$ is constructed using a set of $n_{k|k}$ hypothesized tracks where the i^{th} hypothesized track is parameterized by its existence probability $r_{k|k}^{(i)} \in (0, 1)$ and the marginal posterior density conditioned on its existence, $q_{k|k}^{(i)}(\cdot)$. The MeMBer RFS posterior is expressed as [13]

$$\pi_{k|k}(X_k) = \pi_{k|k}(\emptyset) \sum_{1 \leq j_1 \neq \dots \neq j_{n_k} \leq n_{k|k}} \prod_i \frac{r_{k|k}^{(j_i)} q_{k|k}^{(j_i)}(x_k^{(j)})}{1 - r_{k|k}^{(j_i)}} \quad (3)$$

where $\pi_{k|k}(\emptyset) = \prod_i^{n_{k|k}} (1 - r_{k|k}^{(i)})$.

As the posterior (3) is completely defined by its parameter set, it is sufficient to update the marginal probability of existence $r_{k|k}^{(i)}$ and marginal density $q_{k|k}^{(i)}(\cdot)$ of each hypothesized track i [13].

The MeMBer RFS X_k is constructed by the union of a set of hypothesized tracks, $X_k = \bigcup_{i=1}^{n_{k|k}} X^{(i)}$, where $X^{(i)}$ is an independent Bernoulli RFS on \mathcal{X} , parameterized by $(r_{k|k}^{(i)}, q_{k|k}^{(i)}(\cdot))$. From this construction and the structure of (3), it follows that the expected number of targets (mean cardinality of a MeMBer RFS) is $\sum_{i=1}^{n_{k|k}} r_{k|k}^{(i)}$ [13] and that the cardinality³ probability mass function (pmf) is formed as

$$\Pr\{|X_k| = n | Z^k\} = \pi_{k|k}(\emptyset) \sum_{1 \leq j_1 \neq \dots \neq j_n \leq n_{k|k}} \prod_{i=1}^n \frac{r_{k|k}^{(j_i)}}{1 - r_{k|k}^{(j_i)}}. \quad (4)$$

It is inherent in the description of the MeMBer RFS posterior in (3) that the hypothesized tracks have both *independent states and existences probabilities*.

C. RFS Family

The concept of RFS families formalizes the equivalence between RFS densities and ordered densities. Any density can be replaced by any other density within its RFS family without changing the MMOSPA estimates [11], [12]. Furthermore, all densities in an RFS family represent the same RFS density.

Definition 2.1: An RFS family $\mathcal{R}_{p(\mathbf{x})}$ of an ordered density $p(\mathbf{x})$ is given by [12]

$$\mathcal{R}_{p(\mathbf{x})} = \left\{ f(\mathbf{x}) : \sum_{\pi \in \Pi_n} p(\mathbf{x} = \boldsymbol{\alpha}^\pi) = \sum_{\pi \in \Pi_n} f(\mathbf{x} = \boldsymbol{\alpha}^\pi) \right\} \quad (5)$$

where Π_n is the set of all permutation matrices corresponding to an \mathbf{x} of dimension n and $\boldsymbol{\alpha} = (\alpha^{(1)}, \dots, \alpha^{(n)})$ is a point in the joint target state space [12].

Svensson *et al.* in [4], [11], [12] provide three key insights from the RFS family concept: the first is that, for $n > 1$ number of targets there is a many-to-one mapping from the ordered densities to RFS densities⁴

$$p\left(\{x_k^{(1)}, \dots, x_k^{(n)}\} = \{\alpha^{(1)}, \dots, \alpha^{(n)}\}\right) = \sum_{\pi \in \Pi_n} p(\mathbf{x}_k = \boldsymbol{\alpha}^\pi) \quad (6)$$

where $\mathbf{x}_k = (x_k^1, \dots, x_k^n)^T$ is an ordered set of states. Hence, an RFS density is the sum of all the ordered densities that arise from the permutations of the multitarget state vector. The second insight is that all densities within an RFS family yield the same MMOSPA estimates. This insight leads to the idea of posterior modification via switching within the RFS family [12], as the modified posterior also yields the same MMOSPA estimates, while satisfying the desired properties, that necessitate the switch in the first place, such as less multimodality and independent existence probabilities, etc. The third insight is that, at any given time, a posterior can be replaced by any other posterior as long as it is within the RFS family, without affecting any current or future MMOSPA estimates [12].

³ $|X|$ denotes the cardinality or the number of elements of the RFS X .

⁴An ordered density is represented by $p(\cdot)$ and an RFS (unordered) density is denoted by $p(\{\cdot\})$.

III. RECURSION METHODOLOGY

The proposed structure of the posterior in (3) assumes that the marginal distributions and existence probabilities of the hypothesized tracks are independent. The methodology used to derive the (exact) posterior in the paper is via marginalization over the set of global hypotheses, i.e., the combined data association as well as target existence hypotheses. However, if different hypothesized tracks have the possibility to share measurements, then both their states and existences will become correlated after the measurement update. Hence, the marginal densities and existence probabilities, if approximated from the exact posterior will not be independent, and as identified in [13] the cardinality estimate will be biased.

The main idea of the presented approach is to modify the exact posterior to another distribution within the RFS family where the independence assumptions will hold. Importantly, as of yet we have not been bound to any specific assumption on the parametrization of the marginal posteriors, $q_{k|k}^{(i)}(\cdot)$, and are thus free to choose any parametrization that fits the problem at hand, i.e., it could be Gaussian, a Gaussian mixture, a swarm of particles or something completely different.

The proposed recursion rests on two key steps to arrive at the structure proposed in (3):

- (a) *Derivation of the exact posterior:* The independence assumptions are clearly invalid in the exact posterior.
- (b) *Marginals approximation from a modified posterior:* The exact posterior is modified to another posterior within the RFS family such that the independence assumptions hold, *without affecting the MMOSPA estimates, or the cardinality pmf*.

A. Prior Densities

The prior MeMBer RFS, at time $k-1$, is parameterized by the existence probabilities and the marginal densities of each hypothesized track at $k-1$. The representation of the MeMBer RFS posterior at $k-1$ is given as

$$\pi_{k-1|k-1}(X_{k-1}) = \left\{ \left(r_{k-1|k-1}^{(i)}, q_{k-1|k-1}^{(i)} \right) \right\}_{i=1}^{n_{k-1|k-1}} \quad (7)$$

where X_{k-1} denotes the multi-target state at time $k-1$, described by the $n_{k-1|k-1}$ hypothesized targets.

B. Prediction

The prediction is a union of individual RFSs consisting of surviving targets from $k-1$, and newly born targets at k . The predicted RFS density can be expressed as

$$\begin{aligned} \pi_{k|k-1}(X_k) &= \left\{ \left(p_{S,k-1}^{(i)} r_{k-1|k-1}^{(i)}, q_{k|k-1}^{(i)} \right) \right\}_{i=1}^{n_{k-1|k-1}} \\ &\cup \left\{ \left(p_{\Gamma,k}^{(i)}, f_b^{(i)} \right) \right\}_{i=1}^{n_{b,k}} \end{aligned} \quad (8)$$

where the cardinality of the predicted RFS is $n_{k|k-1} = n_{k-1|k-1} + n_{b,k}$, where $n_{b,k}$ denotes the number of “birthed” tracks at k . Hence, the predicted RFS density can be rewritten as

$$\pi_{k|k-1}(X_k) = \left\{ \left(r_{k|k-1}^{(i)}, q_{k|k-1}^{(i)} \right) \right\}_{i=1}^{n_{k|k-1}} \quad (9)$$

C. Measurement Update

The approximated RFS posterior, on the arrival of measurements Z_{k+1} , is expressed as

$$\pi_{k|k}(X_k) = \left\{ \left(r_{k|k}^{(i)}, q_{k|k}^{(i)} \right) \right\}_{i=1}^{n_{k|k}} \quad (10)$$

The RFS posterior given in (10) is parameterized by individual *independent* target existence probabilities and marginal posteriors that are assumed independent [12].⁵

IV. EXACT POSTERIOR

In the present section, we describe the methodology proposed to arrive at the parameters of the RFS posterior given in (10). The first step is the derivation of the exact posterior. The exact RFS posterior is derived via marginalization over the set of global hypotheses. The set of global hypotheses is a combination of both data association as well as existence hypotheses.⁶

A. Local Hypotheses

The set of measurements at k is denoted by $Z_k = \{z_k^{(j)}\}_{j=1}^{m_k}$. For each hypothesized track there exist three possibilities at update; either the concerned target does not exist, it exists but is not detected, or it exists and is detected and generates measurement $j \in \{1, \dots, m_k\}$.

The hypotheses described above, that are associated with each hypothesized track is known as a *local hypothesis*. Let us denote these local hypotheses with the discrete variable h , where $h = -1$ implies the non-existence of the concerned target, $h = 0$ represents a missed detection, and $h = 1, \dots, m_k$ denotes that measurement j originated from the concerned target. The updated marginal posterior⁷ of target i is then given by

$$\tilde{q}_{k|k}^{(i,h)}(x_k) = \begin{cases} \emptyset; & \text{if } h = -1 \\ q_{k|k-1}^{(i)}(x_k); & \text{if } h = 0 \\ \frac{1}{c} \Lambda(z_k^{(h)} | x_k) q_{k|k-1}^{(i)}(x_k) & \text{if } h = 1, \dots, m_k \end{cases} \quad (11)$$

where $\Lambda(\cdot)$ denotes the likelihood function or the stochastic sensor model and c is a proportionality constant. The updated individual local hypothesis probabilities are given up to a proportionality constant by

$$\tilde{\ell}_{k|k}^{(i,h)} \propto \begin{cases} 1 - r_{k|k-1}^{(i)}; & \text{if } h = -1 \\ (1 - P_D) r_{k|k-1}^{(i)}; & \text{if } h = 0 \\ \frac{P_D}{\mu} \Lambda(z_k^{(h)} | x_k = x_k^{(i)}) r_{k|k-1}^{(i)} & \text{if } h = 1, \dots, m_k \end{cases} \quad (12)$$

where μ is the clutter intensity.

⁵Upon update, targets whose updated existence probabilities fall below a pre-set threshold can be considered as candidates to be pruned for the next recursion.

⁶The SJPDAF [12] considered only data association hypotheses, while the present paper can be thought of as a track management augmentation to the SJPDAF, in addition, also considers the target existence hypotheses.

⁷The marginal densities are ordered densities.

B. Global Hypotheses

The set of global hypotheses can be denoted as $\mathcal{H} \in \{\mathbf{h}_1, \dots, \mathbf{h}_{\mathcal{N}_{\mathcal{H}}}\}$, where each global hypothesis $\mathbf{h}_{\lambda}; \lambda = 1, \dots, \mathcal{N}_{\mathcal{H}}$ can be thought of as a set of mutually exclusive local hypotheses $h_{\lambda}^{(i)}$ ⁸

$$\mathbf{h}_{\lambda} = \left[h_{\lambda}^{(1)}, \dots, h_{\lambda}^{(n_{k|k})} \right]^T; \quad \forall \lambda \quad (13)$$

constructed such that no tracks share the same measurement, and where $h_{\lambda}^{(i)}; i = 1, \dots, n_{k|k}$ takes values within $\{-1, \dots, m_k\}$. To simplify the notation in subsequent expressions, we introduce λ_i to represent the value $h_{\lambda}^{(i)}$. Using this notation, the updated probability of each local hypothesis is

$$\Pr\{\mathbf{h}_{\lambda} | Z_k\} \propto \prod_{i=1}^{n_{k|k}} \tilde{\ell}_{k|k}^{(i,\lambda_i)} \quad (14)$$

where the proportionality constant is found by ensuring that the sum of all global hypotheses is one.

C. Updated Densities and Existence Probabilities

The *exact* marginal updated existence probability is given by

$$\tilde{r}_{k|k}^{(i)} = \sum_{\mathcal{H}} \Pr\{\mathbf{h}_{\lambda} | Z_k\} \cdot \delta_{\lambda_i} \quad (15)$$

where δ_{λ_i} is an indicator function

$$\delta_{\lambda_i} = \begin{cases} 1; & \text{if target } i \text{ exists in hypothesis } \mathbf{h}_{\lambda} \\ 0; & \text{otherwise} \end{cases}$$

The summation index \mathcal{H} represents the set of all global hypotheses and λ_i represents the i^{th} element of the global hypothesis \mathbf{h}_{λ} . The *exact* marginal posterior for hypothesized track i is described as

$$\tilde{q}_{k|k}^{(i)}(x_k) = \frac{1}{\tilde{r}_{k|k}^{(i)}} \sum_{\mathcal{H}} \tilde{q}_{k|k}^{(i,\lambda_i)}(x_k) \Pr\{\mathbf{h}_{\lambda} | Z_k\} \cdot \delta_{\lambda_i} \quad (16)$$

V. INDEPENDENCE OF TARGET EXISTENCES

From the formulation of the exact posterior it is apparent that the target states are dependent, as each hypothesized track in X_k has the possibility to share measurements. Furthermore, it can be shown that the target existences are also dependent. Let us denote by $\mathcal{R}_{p(x)}$, the RFS family that the exact posterior belongs to. We need to prove that there always exists a subset of densities $\mathcal{B}_{\tilde{p}(x)} \subset \mathcal{R}_{p(x)}$, such that all densities in $\mathcal{B}_{\tilde{p}(x)}$ have independent track existence probabilities. The idea is to select a density in $\mathcal{B}_{\tilde{p}(x)}$ that can be accurately approximated. In the present paper, we provide a proof that when the number of existing targets **does not exceed two**, then such a subset $\mathcal{B}_{\tilde{p}(x)}$ can always be found. Future work entails expanding the proof to a more general scenario, where the constraint on the number of existing targets is relaxed.

⁸ $\mathcal{N}_{\mathcal{H}}$ should really be $\mathcal{N}_{\mathcal{H}_k}$, but the time notation is omitted for simplicity of notation.

A. Discrete Existence Events

We introduce the vector $\mathbf{e} = [e_{n_{k|k}} \ e_{n_{k|k}-1} \ \dots \ e_1]^T$, where each element $e_i \in (0, 1)$ represents the existence of target i

$$e_i = \begin{cases} 1; & \text{if target } i \text{ exists} \\ 0; & \text{otherwise} \end{cases}$$

Furthermore, we introduce an additional notation to “order” the existence events. Consider

$$\sum_{i=1}^{n_{k|k}} 2^{i-1} e_i = j, \quad (17)$$

this has the effect of allotting a decimal value to each possible set of existence events. Hence, each set of existence events can be denoted by $\mathbf{e}_j; j = 0, \dots, 2^{n_{k|k}} - 1$. Let us denote by $p(j)$ the probability of the existence event \mathbf{e}_j , with the goal of finding atleast one other probability $\tilde{p}(j)$ within the RFS family of $p(j)$ for which the target existences are independent $\forall j$.

B. Cardinality pmf

Consider the example with $n_{k|k} \leq 2; \forall k$. From a set perspective, the two existence events⁹

$$\mathbf{e}_1 = [1 \ 0]^T \quad \text{and} \quad \mathbf{e}_2 = [0 \ 1]^T$$

are identical as the number of targets in each event is the same. However, $\mathbf{e}_0 = [0 \ 0]^T$ and $\mathbf{e}_3 = [1 \ 1]^T$ are not, as they represent two different cardinalities. Therefore, $p(j)$ and $\tilde{p}(j)$ belong to the same RFS family if

$$\sum_{j: \sum_i \mathbf{e}_j(i) = k} p(j) = \sum_{j: \sum_i \mathbf{e}_j(i) = k} \tilde{p}(j); \quad \text{for } k = 0, 1, \dots, n_{k|k}$$

where we denote the probability of having a cardinality k as

$$c(k) = \sum_{j: \sum_i \mathbf{e}_j(i) = k} p(j) = \sum_{j: \sum_i \mathbf{e}_j(i) = k} \tilde{p}(j) \quad (18)$$

within the RFS family. From (18), it is clear that we have $2^{n_{k|k}} - 1$ equality constraints on $p(j)$, shown below for $n_{k|k} = 2$

$$c(0) = p(0); c(1) = p(1) + p(2); c(2) = p(3) \quad (19)$$

Similarly, the constraints on $\tilde{p}(j)$ to be in the same RFS family as $p(j)$ are

$$c(0) = \tilde{p}(0); c(1) = \tilde{p}(1) + \tilde{p}(2); c(2) = \tilde{p}(3) \quad (20)$$

Hence, by comparing (19) and (20), it can be seen that there is one degree of freedom to maintain the cardinality pmf upon switching

$$\tilde{p}(1) + \tilde{p}(2) = p(1) + p(2) \quad (21)$$

while $\tilde{p}(0) = p(0)$ and $\tilde{p}(3) = p(3)$. Hence, mass can be switched between $p(1)$ and $p(2)$, while satisfying (21).

⁹Each existence event may correspond to several data association hypotheses.

C. Independence Constraints

The goal is to find a pmf $\tilde{p}(j)$ such that target existences are independent, while maintaining the cardinality pmf, as described in (21). The set of independence constraints for the two-target scenario can be expressed by

$$\Pr\{\mathbf{e}_j\} = \prod_{i=1}^2 \Pr\{\mathbf{e}_j(i)\}; \quad j = 0, \dots, 3 \quad (22)$$

The set of constraints for the two target scenario is as follows:

$$\begin{aligned} \tilde{p}(0) &= (\tilde{p}(0) + \tilde{p}(2))(\tilde{p}(0) + \tilde{p}(1)) \\ \tilde{p}(1) &= (\tilde{p}(1) + \tilde{p}(3))(\tilde{p}(0) + \tilde{p}(1)) \\ \tilde{p}(2) &= (\tilde{p}(0) + \tilde{p}(2))(\tilde{p}(2) + \tilde{p}(3)) \\ \tilde{p}(3) &= (\tilde{p}(1) + \tilde{p}(3))(\tilde{p}(2) + \tilde{p}(3)) \end{aligned} \quad (23)$$

The proof that $\tilde{p}(j)$, satisfying the conditions in (23), can **always** be found for a *two target scenario*, such that it is a part of the same RFS family as the original pmf $p(j)$, and maintains the cardinality pmf, is given in Appendix A.

VI. MODIFIED POSTERIOR

In this section we describe a methodology inspired by the SJPDAF [11], [12] where mass is switched from the local distribution of one target to another target, in such a way that the resulting target existence probabilities calculated from the modified posterior are independent. The marginal modified posteriors and the marginal modified updated existence probabilities will constitute the RFS recursion in (10).

The modified updated existence probabilities are given by

$$r_{k|k}^{(i)} = \sum_{\mathcal{H}} \sum_{j=1}^{n_{k|k}} \phi_{i,j}^{\lambda} \Pr\{\mathbf{h}_{\lambda} | Z_k\} \cdot \delta_{\lambda_j} \quad (24)$$

where $\phi_{i,j}^{\lambda}$ represents the mass switched from the local distribution of target j to target i , under hypothesis λ .

Similarly, the individual modified posteriors are given by

$$q_{k|k}^{(i)}(x_k) = \frac{1}{r_{k|k}^{(i)}} \sum_{\mathcal{H}} \sum_{j=1}^{n_{k|k}} \phi_{i,j}^{\lambda} \tilde{q}_{k|k}^{(j,\lambda_j)}(x_k) \Pr\{\mathbf{h}_{\lambda} | Z_k\} \cdot \delta_{\lambda_j} \quad (25)$$

No assumptions have been made on the distributions of the target states thus far. The proposed recursion entails the following key steps:

- 1) At each update k , derive the exact posterior using the prediction.
- 2) Modify the exact posterior to another density within the RFS family, by switching of mass from each target to the local distribution of another, such that the modified density has independent target existence probabilities.
- 3) Approximate the marginalized posteriors as independent, while the existence probabilities of the hypothesized tracks obtained from the modified posterior are independent. The marginalized posteriors and existence probabilities are inputs for the next recursion.
- 4) Recursively repeat from step 1).

The switching weights $\phi_{i,j}^\lambda$ are chosen in such a way that the target existences are independent. The calculation of weights for the implementation shown in the paper is described in the next section.

VII. IMPLEMENTATION

The recursion presented in Section III is general, i.e., it does not depend on any particular model for the target state distributions. We now present an implementation of the tracking algorithm by assuming a linear Gaussian model for the targets. Hence, the exact marginal posterior (11) of each hypothesized track is a weighted sum of individual Gaussians, i.e., a Gaussian mixture (GM). The marginalized posterior densities of all the targets are approximated as independent Gaussians; the state estimates and covariances are calculated to be the first and second moments of the approximated Gaussians. In order to improve the accuracy of the approximation it is desired that the GM is not too multimodal. Hence, the switching weights are calculated by solving an optimization problem [12], so that the modified posterior is less multimodal and suited to accurate Gaussian approximations. Furthermore, the optimized switching weights ensure that the target existence probabilities are independent. The following subsections describe the target state transition and measurement models, the target birth process, the optimization problem formulation and the update steps for the state density and existence probabilities.

A. State models

In the implementation presented in this paper, each surviving target with state vector x_k is assumed to follow a linear Gaussian nearly constant velocity [1] process model

$$x_k = F_{k-1}x_{k-1} + D_{k-1}v_{k-1} \quad (26)$$

where F_k and D_k are the constant velocity state transition matrix and process noise gain matrix, respectively, and $v_{k-1} \sim \mathcal{N}(0, Q_{k-1})$ is the process noise with a covariance Q_k . Newly appearing targets are described by a multi-Bernoulli birth process with density $\pi_{\Gamma_k} = \{r_{\Gamma_k}^{(i)}, q_{\Gamma_k}^{(i)}\}_{i=1}^{n_{b,k}}$ where $r_{\Gamma_k}^{(i)} = p_{\Gamma_k}$ is the birth probability and $q_{\Gamma_k}^{(i)} = \mathcal{N}(x; \mu_{\Gamma}, P_{\Gamma})$ is the marginal density, both are assumed to be equal $\forall i$. To limit the computational complexity of the implementation we have limited the number of birth tracks at each scan to an upper bound n_{\max} .

Each existing target can give rise to a measurement with probability of detection P_D that is described by a linear Gaussian measurement model [1],

$$z_k = H_k x_k + w_k \quad (27)$$

where H_k is the measurement matrix and $w_k \sim \mathcal{N}(0, R_k)$ is the measurement noise with covariance R_k . The process and measurement noise are white noise processes and are mutually uncorrelated. It is also assumed that the target states are independent, and the measurements generated by each target are independent. Furthermore, measurements due to clutter are modeled as Poisson RFS with intensity λ . The standard

linear Gaussian Kalman filter [1] is applied to update the local posterior of each target under each hypothesis.

B. Calculation of Switching Weights

The weights $\phi_{i,j}^\lambda$ in the modified posterior in (25) are calculated at each update by solving an optimization problem. The goal function and the constraints, chosen to reduce the multimodality of the GM and to ensure independence of existence probabilities, are given below.

1) *Goal Function:* In this implementation, similar to the SJPDAF [12], the trace of the updated covariance is considered as the cost function to be minimized¹⁰

$$J(\phi) = - \sum_{i=1}^{n_{k|k}} r_{k|k}^{(i)} \hat{x}_k^{(i)T} \hat{x}_k^{(i)} \quad (28)$$

where $r_{k|k}^{(i)}$ is the existence probability of hypothesized track i given by (24) and

$$\hat{x}_k^{(i)} = \frac{1}{r_{k|k}^{(i)}} \sum_{\mathcal{H}} \sum_{j=1}^{n_{k|k}} \phi_{i,j}^\lambda \hat{x}_k^{(j,\lambda_j)} \Pr\{\mathbf{h}_\lambda | Z_k\} \cdot \delta_{\lambda_j} \quad (29)$$

where $\hat{x}_k^{(j,\lambda_j)}$ is the mean of the local distribution $\tilde{q}_{k|k}^{(j,\lambda_j)}(x_k)$.

According to [4], [12], minimizing the trace of the posterior is equivalent to minimizing the MOSPA, given that the expected value is used as the estimate and the entire space of densities within the RFS family forms the search space. Furthermore, it was observed in [12] that minimizing the trace of the covariance results in a less multimodal density, hence, resulting in better marginal density approximations. In the present implementation, the search space is limited to the family of Gaussian mixtures, with independent existence probabilities, within the RFS family.

2) *Constraints:* There are two groups of constraints: basic constraints, and independence constraint. The basic constraints are as follows:

1. Each weight must be non-negative; $\phi_{i,j}^\lambda \geq 0, \forall i, j, \lambda$, where $i, j \in \{1, \dots, n_{k|k}\}$ represents the indices of hypothesized tracks and $\lambda \in \{1, \dots, \mathcal{N}_{\mathcal{H}}\}$ represents the indices of the global hypotheses.
2. Under each global hypothesis λ , every target must be associated with exactly one local distribution, i.e., $\sum_j \phi_{i,j}^\lambda = 1; \forall i, \lambda$.
3. Under each global hypothesis λ , every local distribution must be associated with exactly one target, i.e., $\sum_i \phi_{i,j}^\lambda = 1; \forall j, \lambda$.

The independence constraint is enforced as follows:

4. The existence probabilities, after switching, must meet the following constraint

$$r_{k|k}^{(i)} = \sum_{\mathcal{H}} \sum_{j=1}^{n_{k|k}} \phi_{i,j}^\lambda \Pr\{\mathbf{h}_\lambda | Z_k\} \cdot \delta_{\lambda_j} \quad (30)$$

The desired independent existence probabilities $r_{k|k}^{(i)}$ after switching are calculated *a priori* as roots of a polynomial (described, for the two target case, in Appendix A).

¹⁰See [12] for simplification of the trace expression to the form in (28).

C. Update

Given the set of switching weights from the optimization algorithm, the resultant marginal posteriors in (25), which are GMs, are approximated as independent single Gaussians from the modified posterior by moment matching [11], [12]. Note that this approximation benefits from the fact that the objective function of the optimization algorithm is chosen so as to reduce the multimodality of densities in the modified posterior. The independent target existence probabilities are calculated for each updated track using the weights, obtained from the solution to the optimization problem, in (24). The approximated marginal Gaussians and the independent existence probabilities are recursively propagated according to the recursion outlined in Section III. Finally, to reduce computational complexity, hypothesized tracks whose existence probabilities fall below a certain pruning threshold are disregarded and not propagated to the next time instance.

VIII. SIMULATION SCENARIO & RESULTS

The scenario considered in the paper consists of two targets, one of whom appears later and stops earlier, as shown in Figure 1. The entire scenario considered lasts for 41 s. Target 1, that starts at (-9 m, 5 m) and ends at (29 m, -5 m) in Cartesian coordinates, lasts the entire scenario while Target 2, that starts at (-5 m, 3.5 m) and ends at (24 m, 3 m), appears at $t_0 + 4$ s and ends at $t_0 + 36$ s, where t_0 is the start time of the scenario. The two targets travel with a constant speed of 1 m/s and measurements of position in Cartesian are obtained at the rate of 1 Hz. The state vector consists of position and velocity in Cartesian coordinates. The matrices F_{k-1} and D_{k-1} in (26) are chosen according to the nearly constant velocity model given in [1], while the measurement noise standard deviations are set at $\sigma_x = \sigma_y = 0.25$ m/s. Targets are detected with a probability of detection $P_D = 0.97$, and the clutter intensity used is $\lambda = 0.001$ m⁻². The process noise acceleration standard deviations used are 0.07 m/s². The birth probability for new tracks is set at $p_\Gamma = 0.1$, while the birth model is set up to limit the maximum number of tracks at any given time to be not more than 3. The survival probability for existing tracks is set to be $p_S(x) = 0.98$, while the existence probability threshold for pruning tracks is set at 0.03. *For 180 Monte Carlo runs, it was observed that the optimization problem always had a solution, i.e., a modification to obtain independent existence probabilities was always possible.*

Figure 1 illustrates the state estimation results for a single run of the algorithm. The state estimates are plotted against the true trajectories in Cartesian coordinates. The state estimates shown in the figure are from hypothesized tracks that have an existence probability ≥ 0.2 . It can be noticed from the middle portion of the scenario, where the targets move close together, that the tracks are reasonably well separated.

Figure 2 shows the cardinality estimates, calculated from updated track existence probabilities, obtained from 180 Monte Carlo runs. It is observed that the cardinality estimate takes close to 2 s to pick up a new target after its birth, and a

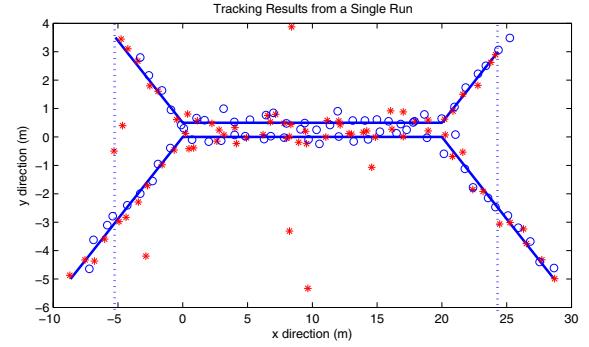


Figure 1. State (position) estimates ('o') of hypothesized tracks whose existence probability ≥ 0.2 , true trajectories ('-') and measurements generated in a single run ('*').

similar amount of time to adjust to an existing target leaving the scenario.

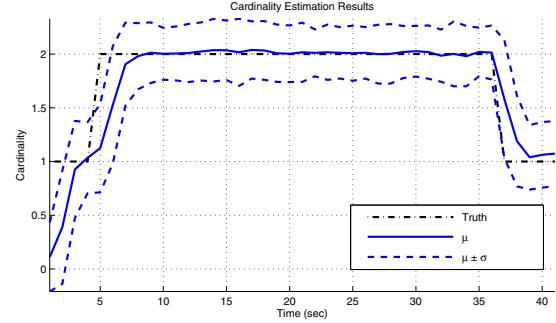


Figure 2. Cardinality estimates along with true cardinality and $\pm 1\sigma$ bounds on the expected number of targets, from 180 Monte Carlo runs.

IX. CONCLUSION & FUTURE WORK

This paper proposed a novel multitarget multi-Bernoulli (MeMBer) random finite set (RFS) recursion that retains the cardinality probability mass function (pmf). At each update, the proposed approach builds the exact posterior by marginalizing over global hypotheses, that depend on both existence as well as data association hypotheses. However, if different hypothesized tracks have the possibility to share measurements, then both their states and existences will become correlated after the measurement update. The key to the recursion proposed in the paper lies in the idea to modify the exact posterior to another density within the same RFS family, in such a manner that the existence probabilities are independent in the modified posterior. Furthermore, the modification that is carried out by switching probability mass from local distributions of targets to other hypothesized tracks, maintains the cardinality pmf within the update. This paper proves that when there are a maximum of two existing targets, at least one density can be found within the RFS family that has independent existence probabilities, while maintaining the cardinality pmf. Future work entails the extension of the proof to a general case without constraints on the maximum number of existing targets.

APPENDIX A
PROOF OF INDEPENDENT EXISTENCES — $n_{k|k} \leq 2$
EXISTING TARGETS

The equations (23) are the four independence constraints for the two target problem. The four original equations are reduced to $\tilde{p}(0) = (\tilde{p}(0) + \tilde{p}(1))(\tilde{p}(0) + \tilde{p}(2)) = \tilde{p}(0)(1 - \tilde{p}(1) - \tilde{p}(3)) + \tilde{p}(1)(\tilde{p}(0) + \tilde{p}(2))$ which is equivalent to the *single* constraint

$$\tilde{p}(0)\tilde{p}(3) = \tilde{p}(1)\tilde{p}(2) \quad (31)$$

The idea is to prove that the constraint (31) is always holds. As mentioned in (21), the cardinality pmf can *only* be maintained if the switching of mass is *only* done between $p(1)$ and $p(2)$, i.e., a mass a is switched between $p(1)$ and $p(2)$ in the following manner

$$\tilde{p}(0)\tilde{p}(3) = \tilde{p}(1)\tilde{p}(2) = (p(1) - a)(p(2) + a) \quad (32)$$

This maintains the cardinality constraints as $p(0) = \tilde{p}(0)$, $p(3) = \tilde{p}(3)$, and $\tilde{p}(1) + \tilde{p}(2) = p(1) - a + p(2) + a = p(1) + p(2)$, as given in (21).

The proof is complete if we can show that there always exists a mass “ a ” in (32) such that (31) is always valid. Solving for a from the quadratic equation (32), we have

$$a = \frac{p(1) - p(2)}{2} \pm \frac{\sqrt{(p(1) - p(2))^2 - 4(p(0)p(3) - p(1)p(2))}}{2} \quad (33)$$

There are two criteria to show the feasibility of the solution a ; the first is, we need to prove that $(p(1) - p(2))^2 - 4(p(0)p(3) - p(1)p(2)) \geq 0$, and the second is, from (32), a has to be bounded

$$0 \leq a \leq p(1) \quad (34)$$

If the following is true,

$$p(0)p(3) \leq p(1)p(2) \quad (35)$$

then we can show that $(p(1) - p(2))^2 - 4(p(0)p(3) - p(1)p(2)) \geq 0$, as $(p(1) - p(2))^2 \geq 0$. We prove (35) as a conjecture.

Conjecture A.1: Given the nature of the measurements, and given that the target existences are independent *a priori* (before update)

$$\Pr\{\mathbf{e}(1) = 1 | \mathbf{e}(2) = 1\} \leq \Pr\{\mathbf{e}(1) = 1 | \mathbf{e}(2) = 0\} \quad (36)$$

$$\Pr\{\mathbf{e}(1) = 0 | \mathbf{e}(2) = 0\} \leq \Pr\{\mathbf{e}(1) = 0 | \mathbf{e}(2) = 1\} \quad (37)$$

where $\mathbf{e} = [e_1 \ e_2]^T$ is a generic existence event for two targets. Expanding the left and right hand terms of the inequality in (35), respectively, we have

$$\begin{aligned} p(0)p(3) &= \Pr\{\mathbf{e}(1) = 0 | \mathbf{e}(2) = 0\} \Pr\{\mathbf{e}(2) = 0\} \\ &\quad \cdot \Pr\{\mathbf{e}(1) = 1 | \mathbf{e}(2) = 1\} \Pr\{\mathbf{e}(2) = 1\} \end{aligned} \quad (38)$$

and

$$\begin{aligned} p(1)p(2) &= \Pr\{\mathbf{e}(1) = 1 | \mathbf{e}(2) = 0\} \Pr\{\mathbf{e}(2) = 0\} \\ &\quad \cdot \Pr\{\mathbf{e}(1) = 0 | \mathbf{e}(2) = 1\} \Pr\{\mathbf{e}(2) = 1\} \end{aligned} \quad (39)$$

Substituting for (38) and (39) in (35), one can straightaway notice that the $\Pr\{\mathbf{e}(2) = 0\}$ and $\Pr\{\mathbf{e}(2) = 1\}$ terms cancel out. Furthermore, using (37) in (38) and (39), it is shown that the inequality in (35) is true.

Proposition A.2: The upper bound in (34) is always valid for any feasible solution for a given in (33).

Proof: By substituting for a from (33), in the upper bound inequality in (34), and by squaring both sides and by further simplifying, we obtain

$$-p(0)^2 \leq 0 \quad (40)$$

which is always true.

Proposition A.3: The lower bound in (34) is always valid for any feasible solution for a given in (33).

Proof: By substituting for a from (33), in the upper bound inequality in (34), and by squaring both sides and by further simplifying, we obtain

$$p(0)p(3) \leq p(1)p(2) \quad (41)$$

which was shown to be true in Conjecture A.1.

Hence, it is proved that a *feasible* mass a always exists in each recursion so that the independence constraints can be enforced upon switching.

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