

# Trajectory Poisson Multi-Bernoulli Filter for Group Target Tracking

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**Abstract**—This paper presents a new trajectory Poisson multi-Bernoulli (TPMB) filter for group target tracking. Due to the collective behavior and dense spatial distribution, exact trajectory estimation is an extremely challenging task in group target tracking. Aiming for improved performance in group trajectory estimation, the virtual leader-follower model is incorporated into the standard TPMB filter in this paper to address the coordinated motion within groups. Moreover, the Gaussian implementation and  $L$ -scan approximation for the proposed group target trajectory PMB (GTTPMB) filter are also provided. Finally, a simulation scenario with splitting and merging of groups is established to evaluate the proposed GTTPMB filter. The results demonstrate that the proposed filter can effectively estimate the trajectories of group members without introducing additional computational burden.

**Keywords**—group target tracking, leader-follower model, sets of trajectories, trajectory PMB filter

## I. INTRODUCTION

The group target refers to a set of targets with coordinated motion model, where each target occupies a distinct resolution unit. In many applications, there may be targets that are moving with interaction with each other, for instance, a group of geese can fly in a V-formation [1], a swarm of drones may cooperate with each other when carrying out missions [2]–[4], even the pedestrians may not walk alone [5][6]. Such collective behavior can be included in the dynamic model by using the group motion model.

In order to enhance performance in group tracking, numerous scholars have focused their attention on modeling interaction relationships within a group. Several filters combined with collective motion model have been developed for group tracking. The authors in [6] propose a novel approach for pedestrian tracking by integrating the probability hypothesis density (PHD) filter [7] with a social force (SF) model. The proposed SF-PHD filter demonstrates superior performance compared to existing filters that assume independent motion in pedestrian tracking scenarios. A more general approach for modeling the group behavior is proposed in [8] which uses the stochastic differential equations (SDE) to depict the repulsive and restoring forces among group members. Meanwhile, a Markov chain Monte Carlo (MCMC) particle filter is adopted to perform sequential inference. Due to the high computational complexity of MCMC particle filter, the author in [9] proposed a labelled multi-Bernoulli (LMB) [10] based algorithm, which decomposes the joint state transition function modeled by the SDE to derive a single-target state transition function (SSTF). In [11], Li et al. derived such SSTF by integrating the single-target state SDE and considering the coupling relationship between the SSTFs and

group center states. Combined with the multi-Bernoulli (MB) filter [12], the proposed approach greatly improved the performance of group tracking. In [13], the virtual leader-follower model (VLFM) was introduced to the Poisson multi-Bernoulli mixture filter (PMBM) [14] for group tracking. The conjugation of the proposed group target PMBM filter was also rigorously proved by the probability generating functionals (p.g.fl.s).

In many group tracking applications, there is often a demand for obtaining trajectory estimations of the group members due to their dense spatial distribution. One approach to building trajectories from posterior densities is to utilize the labelled RFS filters, which can generate trajectories by connecting the estimates of multiple targets with the same label. The LMB filter and  $\delta$ -generalized labelled multi-Bernoulli ( $\delta$ -GLMB) filter [15] augment the target state with a unique label and provide a corresponding filtering density using labelled multi-Bernoulli birth. Although track building approaches based on labelling can be effective in many cases, they may not always suffice due to the presence of target-to-label association ambiguity. Recently, a new approach to address track building problems involves computing multi-target densities on sets of trajectories [16], rather than using labeled RFS. This approach has led to the following filters: the trajectory PHD (TPHD) filter, the trajectory CPHD (TCPHD) filter [17], the trajectory MB (TMB) filter [18], the trajectory PMB (TPMB) filter [19] and the trajectory PMBM (TPMBM) filter [20]. The TPMB filter introduces an auxiliary variable to achieve the best fit PMB approximation to the PMBM in terms of minimizing the resulting *Kullback-Leibler* divergence which offers a trade-off between computational complexity and accuracy.

In this paper, combined with the virtual leader-follower model, we have proposed a new TPMB filter for tracking all the trajectories of group target at each time step, named group target TPMB (GTTPMB) filter. In addition to deriving the GTTPMB recursion, we have also developed the Gaussian implementation in which case the GTTPMB filter can be implemented in an analytic closed form. To reduce the computational complexity caused by the increasing length of the trajectory over time, the  $L$ -scan approximation technique has been employed that propagates the joint density of the last  $L$  time of trajectories. Finally, the simulation results verify the accurate trajectory tracking performance of the GTTPMB filter in group tracking.

This paper is organized as follows. Section II provides the background information about the trajectory RFS, the PMBM Conjugate Prior and TPMB filter. The group motion model, the recursion of proposed GTTPMB filter, Gaussian implementation and  $L$ -scan approximation are provided in Section III. The simulation results and the conclusions are given in Section IV and Section V respectively.

## II. BACKGROUND

In this section, we take a brief review of the RFSs of trajectories, PMBM conjugate prior and the TPMB filter, which are the background knowledge of this paper.

### A. Random Finite Sets of Trajectories

The trajectory of a target is consist of a finite sequence of target states which can start at any time step and end at any time later on. In this paper, the state of a single target is represented by  $x \in \mathbb{R}^{n_x}$  which contains the position and velocity information. Therefore, a trajectory can be represented as  $X=(t, x^{1:v})$  where  $t$  is the start time,  $v$  is the length of the trajectory and  $x^{1:v} = (x^1, \dots, x^v)$  is a finite states sequence.

Consider a trajectory  $X=(t, x^{1:v})$  up to the current time step  $k$ , the variable  $(t, v)$  therefore belongs to the set  $I_{(k)} = \{(t, v): 0 \leq t \leq k \text{ and } 1 \leq v \leq k-t+1\}$ . Then, the trajectory state  $X$  up to current time step belongs to the space

$$T_{(k)} = \biguplus_{(t, v) \in I_{(k)}} \{t\} \times \mathbb{R}^{v n_x} \quad (1)$$

where  $\biguplus$  denotes the union of disjoint sets. Moreover, a set of trajectories up to time step  $k$  is defined as  $\mathbf{X} \in \mathcal{F}(T_{(k)})$ . The integral of a real-valued function  $\pi(\cdot)$  on the single trajectory space  $T_{(k)}$  is given as

$$\int \pi(X) dX = \sum_{(t, v) \in I_{(k)}} \int \pi(t, x^{1:v}) dx^{1:v} \quad (2)$$

The integral encompasses all possible birth times, durations, and target states of the trajectory. Given a real-valued function  $\pi(\cdot)$  defined on the space  $\mathcal{F}(T_{(k)})$  of trajectory sets, its set integral is computed as

$$\int \pi(\mathbf{X}) \delta \mathbf{X} = \sum_{n=0}^{\infty} \frac{1}{n!} \int \pi(\{X_1, \dots, X_n\}) dX_{1:n} \quad (3)$$

If  $\pi(\cdot) \geq 0$  and its integral over the set equals one, The function  $\pi(\cdot)$  will be considered as a multi-trajectory density of a RFS of trajectories.

### B. PMBM Conjugate Prior

Given the measurements up to time step  $k$ , the densities for the set of all trajectories at time step  $k' \in \{k, k+1\}$  are modeled as PMBMs. The PMBM density is denoted as [14]

$$f_{k'|k}(\mathbf{X}_{k'}) = \sum_{\mathbf{Y} \uplus \mathbf{W} = \mathbf{X}_{k'}} f_{k'|k}^p(\mathbf{Y}) f_{k'|k}^{mbm}(\mathbf{W}) \quad (4)$$

$$f_{k'|k}^p(\mathbf{X}_{k'}) = e^{-\int \lambda_{k'|k}(X) dX} [\lambda_{k'|k}(\cdot)]^{\mathbf{X}_{k'}} \quad (5)$$

$$f_{k'|k}^{mbm}(\mathbf{X}_{k'}) = \sum_{a \in \mathcal{A}_{k'|k}} w_{k'|k}^a \sum_{\substack{\mathbf{X}' \in \mathcal{A}_{k'|k} \\ \mathbf{X}' \uplus \mathbf{X}_{k'} = \mathbf{X}_{k'}}} \prod_{i=1}^{n_{k'|k}} f_{k'|k}^{i,a}(\mathbf{X}^i) \quad (6)$$

From Eq. (4), it could be seen that the PMBM is consist of two RFSs: a Poisson RFS with density  $f_{k'|k}^p(\cdot)$  which has intensity  $\lambda_{k'|k}(X)$ , representing undetected targets, and a mixture of Multi-Bernoulli RFS  $f_{k'|k}^{mbm}(\cdot)$  which denotes the targets that have been detected at some point up to time step  $k$ . The number of Bernoulli components is  $n_{k'|k}$ . Each component is indexed by variable  $i \in \{1, \dots, n_{k'|k}\}$  and

corresponds to a global hypothesis  $a$ , with a weight  $w_{k'|k}^a$ . The  $i$ -th Bernoulli component has density

$$f_{k'|k}^{i,a}(\mathbf{X}) = \begin{cases} 1 - r_{k'|k}^{i,a} & \mathbf{X} = \emptyset \\ r_{k'|k}^{i,a} p_{k'|k}^{i,a}(X) & \mathbf{X} = \{X\} \\ 0 & \text{otherwise} \end{cases} \quad (7)$$

where  $r_{k'|k}^{i,a}$  denotes the existence probability and  $p_{k'|k}^{i,a}(\cdot)$  is the single-trajectory density. A global hypothesis is  $a = (a^1, \dots, a^{n_{k'|k}})$ , where  $a^i \in \{1, \dots, h^i\}$  is the index to local hypothesis for the  $i$ -th Bernoulli and  $h^i$  is the number of local hypotheses.  $\mathcal{A}_{k'|k}$  represents the set of all global hypotheses.

### C. TPMB Filter

Instead of propagating the PMBM density, the TPMB filter introduces an auxiliary variable to achieve the best fit PMB approximation to the PMBM in terms of minimizing the resulting *Kullback-Leibler* divergence. The prediction and update processes of the TPMB filter [19] are briefly outlined below.

**TPMB prediction:** If the density on the set of trajectories at time step  $k-1$  is a PMB as

$$f_{k|k-1}(\mathbf{X}_{k'}) = \sum_{\substack{\mathbf{Y} \uplus \mathbf{W} = \mathbf{X}_{k'} \\ \mathbf{Y} \in \mathcal{A}_{k|k-1}}} f_{k|k-1}^p(\mathbf{Y}) \prod_{i=1}^{n_{k|k-1}} [f_{k|k-1}^i(\mathbf{X}^i)] \quad (8)$$

the predicted density is also a PMB with  $n_{k|k-1} = n_{k-1|k-1}$  and

$$\lambda_{k|k-1}(X) = \lambda_{k-1|k-1}^B(X) + \langle \lambda_{k-1|k-1}, g_k(X|\cdot) p^S(\cdot) \rangle \quad (9)$$

$$r_{k|k-1}^i = r_{k-1|k-1}^i \langle p_{k-1|k-1}^i, p^S \rangle \quad (10)$$

$$p_{k|k-1}^i(X) = \frac{\langle p_{k-1|k-1}^i, g_k(X|\cdot) p^S(\cdot) \rangle}{\langle p_{k-1|k-1}^i, p^S \rangle} \quad (11)$$

where  $g_k(\cdot|\cdot)$  is the transition density,  $\lambda_{k-1|k-1}^B(\cdot)$  is the intensity of new born trajectories and  $p^S(\cdot)$  is the survival probability of a trajectory  $X$ .

**TPMB update:** If the predicted density on the set of trajectories at time step  $k$  is a PMB, given the measurement set  $\mathbf{z}_k = \{z_k^1, \dots, z_k^{m_k}\}$ , the update density is a PMBM where  $n_{k|k} = n_{k|k-1} + m_k$  and

$$\lambda_{k|k}(X) = (1 - p_k^D(X)) \lambda_{k|k-1}(X) \quad (12)$$

Each Bernoulli component  $i \in \{1, \dots, n_{k|k-1}\}$  in predicted density has  $h^i = m_k + 1$  local hypotheses. The misdetection hypothesis is given by  $\mathcal{M}(i, 1) = \emptyset$

$$w_{k|k}^{i,1} = 1 - r_{k|k-1}^i \langle p_{k|k-1}^i, p_k^D \rangle \quad (13)$$

$$r_{k|k}^{i,1} = \frac{r_{k|k-1}^i \langle p_{k|k-1}^i, 1 - p_k^D \rangle}{1 - r_{k|k-1}^i \langle p_{k|k-1}^i, p_k^D \rangle} \quad (14)$$

$$p_{k|k}^{i,1}(X) = \frac{(1-p_k^D(X))p_{k|k-1}^i(X)}{\langle p_{k|k-1}^i, 1-p_k^D \rangle} \quad (15)$$

The hypothesis for  $i$ -th Bernoulli component update with measurement  $z_k^j$  is given by  $\mathcal{M}(i, j) = \{j\}$ ,  $r_{k|k}^{i,1+j} = 1$ ,

$$w_{k|k}^{i,1+j} = r_{k|k-1}^i \langle p_{k|k-1}^i, l(z_k^j|\cdot) p_k^D(\cdot) \rangle \quad (16)$$

$$p_{k|k}^{i,1+j}(X) = \frac{l(z_k^j|X) p_k^D(X) p_{k|k-1}^i(X)}{\langle p_{k|k-1}^i, l(z_k^j|\cdot) p_k^D(\cdot) \rangle} \quad (17)$$

A new Bernoulli component  $i \in \{n_{k|k-1} + j\}$ ,  $j \in \{1, \dots, m_k\}$  initiated by  $z_k^j$  has  $h^i=2$  local hypotheses

$$\mathcal{M}(i, 1) = \emptyset, w_{k|k}^{i,1} = 1, r_{k|k}^{i,1} = 0, \mathcal{M}(i, 2) = \{j\} \quad (18)$$

$$w_{k|k}^{i,2} = \lambda^C(z_k^j) + \langle \lambda_{k|k-1}, l(z_k^j|\cdot) p_k^D(\cdot) \rangle \quad (19)$$

$$r_{k|k}^{i,2} = \frac{\langle \lambda_{k|k-1}, l(z_k^j|\cdot) p_k^D(\cdot) \rangle}{\lambda^C(z_k^j) + \langle \lambda_{k|k-1}, l(z_k^j|\cdot) p_k^D(\cdot) \rangle} \quad (20)$$

$$p_{k|k}^{i,2}(X) = \frac{l(z_k^j|X) p_k^D(X) \lambda_{k|k-1}(X)}{\langle \lambda_{k|k-1}, l(z_k^j|\cdot) p_k^D(\cdot) \rangle} \quad (21)$$

Finally, the projection of this PMBM density to a PMB density is obtained by Proposition 1 in [19]. Compared with the TPMBM filter, the TPMB filter offers a trade-off between computational complexity and accuracy. However, it still hold the assumption that targets appearing in the surveillance area move independently, which may not be applicable for tracking group targets.

### III. GROUP TARGET TPMB FILTER

In this section, by adopting the classical virtual leader-follower model, we propose a new TPMB filter for group tracking, referred as the group target TPMB (GTPMB) filter. The group transition density is introduced in Section III-A. The recursion of the GTPMB filter is derived in Section III-B. The Gaussian implementation and  $L$ -scan approximation are provided in Section III-C and III-D.

#### A. Group Target Transition Densities

The dynamics of group target are considerably more complex than those of multi-target. In the context of multi-target tracking, it is common for targets to be close in spatial distribution while moving largely independently of each other. However, group targets are strategically organized, implying that the knowledge of a group member can provide additional information about the motion of other targets within the same group. Due to such collective behavior of group targets, the transition density of the group target deviates from that of independently moving multi-target.

In this paper, we focus on the group transition density based on the virtual leader-follower model. The basic assumption underlying the virtual leader-follower model (VLFM) is that the deterministic state of any target in the group is a translational offset of the average state (centroid) of the group. Fig.1 illustrates the concept.

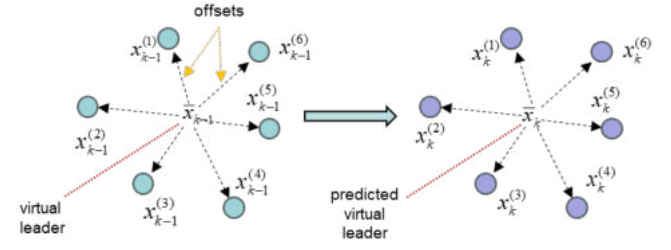


Fig. 1. The virtual leader-follower model

Let  $\mathbf{x}_{k-1} = \{x_{k-1}^{(1)}, \dots, x_{k-1}^{(n)}\}$  be the multi-target states at time step  $k-1$  and  $\bar{x}_{k-1}$  denotes the average single-target state (i.e., virtual leader). The translational offset of each target from the center is denoted as  $\Delta x_{k-1}^{(i)} = x_{k-1}^{(i)} - \bar{x}_{k-1}$ . Assumed that no targets appear or disappear from the group, then, the predicted state set has the form

$$\mathbf{x}_{k|k-1} = \{\varphi_{k|k-1}(\bar{x}_{k-1}) + \Delta x_{k-1}^{(1)} + V_1, \dots, \varphi_{k|k-1}(\bar{x}_{k-1}) + \Delta x_{k-1}^{(n)} + V_n\} \quad (22)$$

where  $V_1, \dots, V_n$  are zero-mean random state vectors which are independent and identical distribution. The offsets of the targets in the group from the predicted centroid remain consistent with the previous centroid in the VLFM, except for random variations. The belief-mass function for the VLFM is [21]

$$\begin{aligned} \beta_{k|k-1}(\mathbf{s} | \mathbf{x}_{k-1}) &= \Pr(\mathbf{x}_{k|k-1} \subseteq \mathbf{s} | \mathbf{x}_{k-1}) \\ &= \Pr(V_1 \in \mathbf{s} - \varphi_{k|k-1}(\bar{x}_{k-1}) - \Delta x_{k-1}^{(1)} | \mathbf{x}_{k-1}) \\ &\quad \dots \Pr(V_n \in \mathbf{s} - \varphi_{k|k-1}(\bar{x}_{k-1}) - \Delta x_{k-1}^{(n)} | \mathbf{x}_{k-1}) \\ &= p_{k|k-1}^1(\mathbf{s} | \mathbf{x}_{k-1}) \dots p_{k|k-1}^n(\mathbf{s} | \mathbf{x}_{k-1}) \end{aligned} \quad (23)$$

where,

$$p_{k|k-1}^i(\mathbf{s} | \mathbf{x}_{k-1}) \triangleq \int_{\mathbf{s}} g_{k|k-1}^i(x_k | \mathbf{x}_{k-1}) dx_k \quad (24)$$

$$g_{k|k-1}^i(x_k | \mathbf{x}_{k-1}) \triangleq f_V(x_k - \varphi_{k|k-1}(\bar{x}_{k-1}) - \Delta x_{k-1}^{(i)}) \quad (25)$$

Thus, the multi-target Markov density can be written as

$$g_k(\mathbf{x}_k | \mathbf{x}_{k-1}) = \sum_{\sigma} g_k^{\sigma 1}(x_k^{(1)} | \mathbf{x}_{k-1}) \dots g_k^{\sigma n}(x_k^{(n)} | \mathbf{x}_{k-1}) \quad (26)$$

The uncertainty of the VLFM model is determined by the independent and identically distributed zero-mean random state vectors, denoted as  $V_1, \dots, V_n$ . Based on this condition, the group target belief-mass function can be expressed in a separable form, resulting in a Markov transition density with a product form (26).

#### B. The GTPMB Filter Recursion

Combined with the group transition density, the standard TPMB is improved to the GTPMB for group target tracking. The set of all trajectories evolves according to the group Markov transition density.

The predicted set  $\mathbf{X}_{k+1}$  is the union of new birth trajectories and surviving trajectories. Due to the uncertainty about the motion of the newborn trajectories, we suppose that they are born independently following a Poisson Point Process (PPP) with intensity

$$\lambda_{k+1}^B(t, x^{1:v}) = \delta_{k+1}[t] \delta_1[v] \lambda^B(x^v) \quad (27)$$

Given the set  $\mathbf{X}_k$  of all trajectories up to time step  $k$ , each single trajectory  $X=(t, x^{1:v})$ , where  $t+v-1 \leq k$ , survives with probability 1, with a transition density

$$g_{k+1}(t_y, y^{1:v_y} | \mathbf{X}_k) = \delta_t[t_y] \times \begin{cases} \delta_v[v_y] \delta_{x^{1:v_y}}(y^{1:v_y}) & \omega_y < k \\ \delta_v[v_y] \delta_{x^{1:v_y}}(y^{1:v_y}) (1 - p^S(x^v)) & \omega_y = k \\ \delta_{v+1}[v_y] \delta_{x^{1:v_y}}(y^{1:v_y-1}) p^S(x^v) & \omega_y = k+1 \\ \times g(y^{v_y} | \mathbf{x}_k) & \omega_y = k+1 \end{cases} \quad (28)$$

where  $\omega_y = t_y + v_y - 1$ ,  $\delta_i[u] = 1$  if  $u=i$  and  $\delta_i[u] = 0$ , otherwise.  $\mathbf{x}_k$  represents the set of the states of all alive trajectories at the current time step  $k$ , denoted as

$$\mathbf{x}_k = \{x^v : (t, x^{1:v}) \in \mathbf{X}_k, t+v-1 = k\} \quad (29)$$

When  $\omega_y = k+1$ , the transition density is modeled by VLFM model. Compared with the standard transition density of TPMB filter (e.g., Eq. (21) in [19]), Eq. (28) employs the states of all alive trajectories as conditions, while original density only relies on the state of a single trajectory.

However, in the context of a multi-group scenario, not all members of  $\mathbf{x}_k$  will exert an influence on the transition density of individual trajectory  $X=(t, x^{1:v})$ . Here we need to partition the set of current states  $\mathbf{x}_k$  to determine the applicable scope of the group motion model.

A simple approach is to adopt undirected graph theory where the states are regarded as vertex, and the relationship between trajectories are denoted by the edges. We first calculate the Mahalanobis distance  $d_{ij}$  between members in  $\mathbf{x}_k$ . Then we can obtain the adjacency matrix by comparing the calculated Mahalanobis distance with a predefined threshold  $\varepsilon$ . More details about the undirected graph theory can be found in [11], [13]. Substituting Equation (28) into Equation (11), the resulting predicted density is still a PMB. Therefore, we use the standard TPMB update process in the GTTPMB filter.

$$d_{ij} = \sqrt{(x_{k,i} - x_{k,j})(P_{k,i} + P_{k,j})^{-1}(x_{k,i} - x_{k,j})^T} \quad (30)$$

$$D_k = \begin{bmatrix} 0 & \eta_k(1,2) & \cdots & \eta_k(1,n) \\ \eta_k(2,1) & 0 & \cdots & \eta_k(2,n) \\ \vdots & \vdots & \ddots & \vdots \\ \eta_k(n,1) & \eta_k(n,2) & \cdots & 0 \end{bmatrix} \quad (31)$$

$$\eta_k(i, j) = \eta_k(j, i) = \begin{cases} 1 & d_{ij} < \varepsilon \\ 0 & \text{otherwise} \end{cases} \quad (32)$$

In [8], the partitions of targets were described by the term “group structure”. Meanwhile, the authors proposed a group structure transition model to correctly infer the group structure. However, the number of partitions of a finite set is a *Bell number* which is computational expensive. Besides, the group structure is a variable describing the kinematic

feature of the whole set which is hard to be decomposed into a separable form. As far as we know, no RFS-based group target filter can recursively estimate the group structure. The focus of this paper is to discuss the tracking performance of group target between trajectory RFS-based filters and standard RFS-based filters, so we will not discuss the processing of group structure too much, and only use a clustering algorithm which is highly efficient and easily implementable.

### C. The Gaussian Implementation

In this section, we consider the Gaussian implementation of the proposed GTTPMB filter for all trajectories. The intensity of PPP and the  $i$ -th Bernoulli component have the form as

$$\lambda_{k|k}(X) = \sum_{q=1}^{n_{k|k}^p} w_{k|k}^{p,q} \mathcal{N}(X; t_{k|k}^{p,q}, \bar{x}_{k|k}^{p,q}, P_{k|k}^{p,q}) \quad (33)$$

$$p_{k|k}^i(X) = \sum_{l=t^i}^{k'} \beta_{k|k}^i(l) \mathcal{N}(X; t^i, \bar{x}_{k|k}^i(l), P_{k|k}^i(l)) \quad (34)$$

where  $n_{k|k}^p$  represents the number of components,  $w_{k|k}^{p,q}$  denotes the weight of the  $q$ -th component,  $t_{k|k}^{p,q}$  denotes the initiating time,  $\bar{x}_{k|k}^{p,q}$  and  $P_{k|k}^{p,q}$  are the mean and covariance matrix. In Eq.(34),  $\beta_{k|k}^i(l)$  represents the probability that the corresponding trajectory terminates at time step  $l$ , and

$$\bar{x}_{k|k}^i(l) \in \mathbb{R}^{m_x}, P_{k|k}^i(l) \in \mathbb{R}^{m_x \times m_x} \text{ where } l = k - t^i + 1.$$

Assumed that the PMB filtering density for all trajectories with  $p_{k-1|k-1}^i(\cdot)$  and  $\lambda_{k-1|k-1}(\cdot)$  is given by (33) and (34), then, the predicted density is a PMB with

$$r_{k|k-1}^i = r_{k-1|k-1}^i \quad (35)$$

$$\lambda_{k|k-1}(X) = \sum_{q=1}^{n_{k|k-1}^p} w_{k|k-1}^{b,q} \mathcal{N}(X; k, \bar{x}_{k|k-1}^{b,q}, P_{k|k-1}^{b,q}) + p^S \sum_{q=1}^{n_{k|k-1}^p} w_{k|k-1}^{p,q} \mathcal{N}(X; t_{k|k-1}^{p,q}, \bar{x}_{k|k-1}^{p,q}, P_{k|k-1}^{p,q}) \quad (36)$$

$$\bar{x}_{k|k-1}^i(l) = \begin{cases} \bar{x}_{k-1|k-1}^i(l), l \in \{t^i, \dots, k-1\} \\ \left[ \left( \bar{x}_{k-1|k-1}^i(l-1) \right)^T, \left( \bar{F}_i \bar{x}_{k-1|k-1}^i(l-1) + B u_{k-1,i} \right)^T \right]^T, l = k \end{cases} \quad (37)$$

$$P_{k|k-1}^i(l) = \begin{cases} P_{k-1|k-1}^i(l), l \in \{t^i, \dots, k-1\} \\ \left[ \begin{array}{cc} P_{k-1|k-1}^i(l-1) & P_{k-1|k-1}^i(l-1) \bar{F}_i^T \\ \bar{F}_i P_{k-1|k-1}^i(l-1) & \bar{F}_i P_{k-1|k-1}^i(l-1) \bar{F}_i^T + Q \end{array} \right], l = k \end{cases} \quad (38)$$

$$\bar{F}_i = [0_{1,t^i-1}, 1] \otimes F \quad (39)$$

$$F = \begin{bmatrix} 1 & \tau/n_g & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & \tau/n_g \\ 0 & 0 & 0 & 1 \end{bmatrix} B = \begin{bmatrix} 0 & \tau/n_g & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \tau/n_g \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (40)$$

$$u_{k-1,i} = \frac{1}{n_g} \sum_{j \in \Gamma_g(i)} x_{k-1,j} \quad (41)$$

where  $t^i = \dim(\bar{x}_{k-1|k-1}^i(l)) / n_x$ ,  $\bar{x}_{k|k-1}^{p,q}$  and  $P_{k|k-1}^{p,q}$  are computed by (37) and (38) using  $\bar{x}_{k|k-1}^{p,q}$  and  $P_{k|k-1}^{p,q}$  instead of  $\bar{x}_{k-1|k-1}^i(l-1)$  and  $P_{k-1|k-1}^i(l-1)$ .  $n_g$  represents the number of members in the  $g$ -th group. Moreover,  $\Gamma_g(i)$  represents the index set of other members in the  $g$ -th group corresponding to the  $i$ -th Bernoulli component. Finally, the prediction of terminating probability corresponding to the trajectory at time step  $l$  is

$$\beta_{k|k-1}^i(l) = \begin{cases} \beta_{k-1|k-1}^i(l) & l \in \{t^i, \dots, k-2\} \\ (1-p^S) \beta_{k-1|k-1}^i(l) & l = k-1 \\ p^S \beta_{k-1|k-1}^i(k-1) & l = k. \end{cases} \quad (42)$$

The update step is same with the standard TPMB filter which could be found in [19].

#### D. L-Scan approximation

Due to the increasing length of trajectories, the GTTPMB filter becomes computationally demanding. To solve the problem, we consider the  $L$ -scan implementation in the prediction step which approximates the covariance matrices of PPP and Bernoulli components as

$$P_{k|k} \approx \text{diag}(\tilde{P}_{k|k}^k, \tilde{P}_{k|k}^{k+1}, \dots, \tilde{P}_{k|k}^{k-L}, \tilde{P}_{k|k}^{k-L+1:k}) \quad (43)$$

where  $\tilde{P}_{k|k}^{k-L+1:k} \in \mathbb{R}^{L \cdot n_x \times L \cdot n_x}$  is the joint covariance matrix of the last  $L$  time steps and  $\tilde{P}_{k|k}^k \in \mathbb{R}^{n_x \times n_x}$  is the covariance matrix of target at time step  $k$ . This approximation method makes the states outside the  $L$ -scan window independent and unchanged with new measurements. More details for pruning and  $L$ -scan implementation could be found in [19]. Finally, the pseudocodes of the proposed GTTPMB filter is given in Algorithm 1.

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#### Algorithm1: The GTTPMB Filter Pseudocode

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**Set**  $\lambda_{0|0} = 0$ ,  $n_{0|0} = 0$

**for**  $k=1$  to ending time step do

-Group trajectory grouping  $\rightarrow \{n_{g,k}, \Gamma_{g,k}\}_{g \in G_k}$

-Perform prediction:

- Prediction for PPP: use Eq. (35)
- Prediction for MB with VLFM:
  - predicted mean: Eq. (36)
  - predicted covariance: Eq. (37)
  - predicted terminating probability: Eq. (41)
- Apply  $L$ -scan approximation: use Eq. (42)

-Update based on measurement set

-Perform projection of PMBM to PMB density

-Estimate the set of trajectories

**end for**

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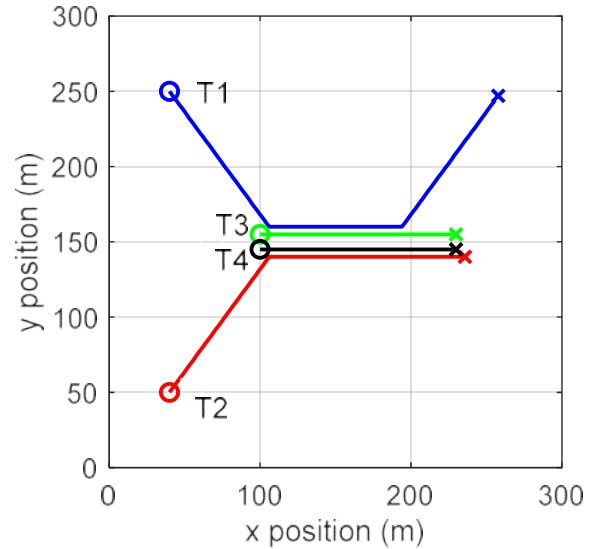
## IV. SIMULATION RESULTS

In this section, the performance of the proposed group target trajectory PMB filter is analyzed in comparison with the standard TPMB filter. The GTTPMB and TPMB are implemented with the following parameters: threshold for pruning the PPP weights  $\Gamma_p = 10^{-5}$ , Maximum number of hypotheses  $N_h = 200$ , existence threshold for Bernoulli components  $\Gamma_b = 10^{-5}$ ,  $L$ -Scan length  $L = 5$ , estimation threshold for estimator  $\Gamma_d = 0.5$  and threshold for ending alive trajectories  $\Gamma_a = 10^{-4}$ .

The PMBM filter [14] and the group target PMBM (GTPMBM) filter [13] are also considered, which do not exploit trajectory smoothing. The trajectory estimates of these filters are formed by linking target state estimates that originate from the same Bernoulli component. The PMBM based filters have a threshold for pruning multi-Bernoulli mixture weights  $\Gamma_g = 10^{-4}$ .

As shown in Fig. 2, the two-dimensional surveillance area of  $300m \times 300m$  contains four targets, and the state of a target is considered as  $x = [p_x, \dot{p}_x, p_y, \dot{p}_y]^T$  which contains both position ( $m$ ) and velocity ( $m/s$ ). The initial states of these targets are shown in Table I. The duration is  $K=100s$  and the time varying group targets are set as follows

- Phase 1 (1~30s): the two targets {T1,T2} move independently and get close to each other.
- Phase 2 (31~70s): the other two targets {T3,T4} appear at 31s. The four targets {T1,T2,T3,T4} are merged into one group.
- Phase 3 (71~100s): Target {T1} is split from the group and move independently at 71s. The other targets still move in a group {T2,T3,T4} and disappear at 90s.



**Fig. 2.** Ground truth trajectories in the scenario. Starting/ending points are marked with  $\circ/\times$

TABLE I  
INITIAL STATE OF TARGETS

Target ID	Initial state $x$	Survival time(s)
T1	$[40, 2.2, 250, -3]^T$	1~100
T2	$[40, 2.2, 50, 3]^T$	1~90
T3	$[100, 2.2, 155, 0]^T$	31~90
T4	$[100, 2.2, 145, 0]^T$	31~90

The kinematic model used in the group target filters (GTPMB and GTPMBM) is the virtual leader-follower model, while the kinematic model used in the standard filters (TPMB and PMBM) is the constant velocity model

$$F_{cv} = I_2 \otimes \begin{pmatrix} 1 & \tau \\ 0 & 1 \end{pmatrix}, \quad Q = qI_2 \otimes \begin{pmatrix} \tau^3/3 & \tau^2/2 \\ \tau^2/2 & \tau \end{pmatrix} \quad (44)$$

where  $\tau = 1s$  and  $q = 0.02m/s^2$ . Under linear observation conditions, target positions are measured with

$$H = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{pmatrix}, \quad R = \sigma^2 I_2 \quad (45)$$

where  $\sigma^2 = 5m^2$  and the detection probability of the target is  $p_D = 0.9$ . The clutter intensity is  $\lambda_c(z) = \bar{\lambda}_c u_A(z)$ , where,  $u_A(z)$  is a uniform density in  $\bar{\lambda}_c = 10$  and  $A = [0m, 300m] \times [0m, 300m]$ . For the four filters, the survival probability for each target is  $p_s = 0.99$  and the birth intensity is Gaussian with  $\bar{x}_k^{b,1} = [100, 0, 100, 0]^T$  and  $P_k^{b,1} = \text{diag}([150^2, 1, 150^2, 1])$  with weight  $w_1^{b,1} = 3$  and  $w_k^{b,1} = 0.005$  for  $k > 1$ .

We assess the performance of the four filters using Monte Carlo simulation with 100 runs. In our scenario, when the four targets are merged into one group, they become spatially enclosed with each other, which may cause the track switching referred in [22]. To penalize the tracking switching and comprehensively evaluate the trajectory estimation performance for group target tracking, the linear programming (LP) metric  $d(\cdot, \cdot)$  for sets of trajectories with parameters:  $p = 2, c = 10, \gamma = 1$  is used here. The root mean square(RMS) LP error at the given time is defined as

$$d(k) = \sqrt{\frac{1}{N_{mc}k} \sum_{i=1}^{N_{mc}} d^2(\mathbf{X}_k, \hat{\mathbf{X}}_k^i)} \quad (46)$$

where,  $\mathbf{X}_k$  is the true set of trajectories and  $\hat{\mathbf{X}}_k^i$  is its estimation at time  $k$  in the  $i$ -th MC run.

The trajectory estimation errors against time for all trajectories in terms of the LP trajectory metric are presented in Fig. 3. For all filters, the trajectory estimation error increase after 30s, in which two targets appear and the rest of the targets are maneuvering to merge into a new group. The estimation error also fluctuates at 90s due to the disappearance of one target. The GTPMB filter is the most accurate filter to estimate the trajectories of group target with coordinated motion. Meanwhile the second best performing filter in general is the TPMB filter which is considerably better than the GTPMBM and the PMBM

filter. The GTPMB and TPMB have similar estimation performance when targets move independently before 30s. However, when targets are merged into one group after 30s, the performance of the GTPMB filter which uses VLFM as kinematic model is considerably better than the TPMB filter. The same phenomenon occurs between the GTPMBM filter and the PMBM filter which proves that filter incorporating a group motion model can provide a better performance in estimating group trajectories.

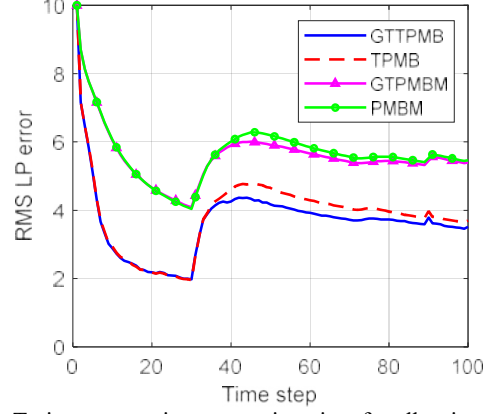


Fig. 3. Trajectory metric error against time for all trajectories

In addition, the LP trajectory metric can be decomposed into the square costs of localization estimation error, false targets, missed targets and track switches. Fig. 4. illustrates that filters based on group motion model have a lower error of localization estimation and smaller cost of false targets and track switches. Meanwhile, error for missed targets is considerably lower for all filters based on sets of trajectories.

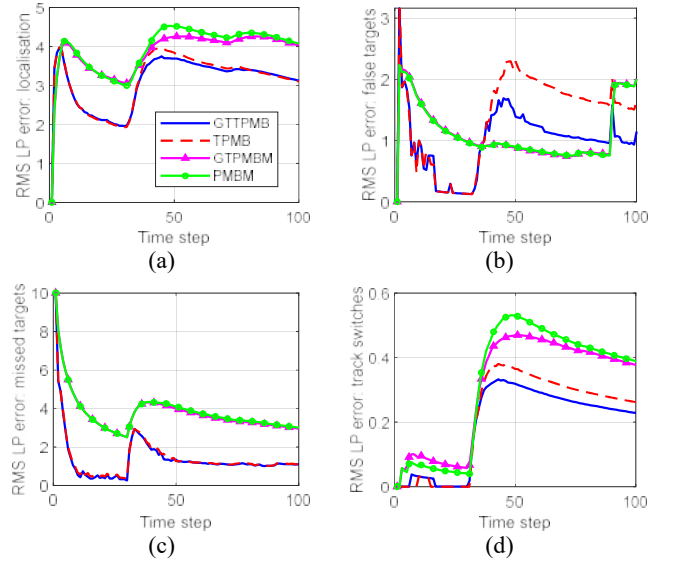


Fig. 4. Decomposition of the trajectory metric error against time for all trajectories. (a) localization estimation error, (b) false targets error, (c) missed targets error, (d) track switches error

We also proceed to analyze the performance of the four filters for different values of the  $L$ -scan window, detection probability and clutter intensity. In Table II, we show the resulting RMS LP error considering all time steps. The error is reduced by increasing  $L$  for the trajectory filters, mainly due to the improved localization of past states. The performance of all filters decreases as expected with an increase in clutter intensity. Conversely, higher probability of detection leads to improved performance. In general, the best performing filter is the GTPMB, followed by TPMB.



TABLE II  
TRAJECTORY METRIC ERRORS (RMS LP ERROR)

	GTPMB			TPMB			GTPMBM	PMBM
$L$	1	5	10	1	5	10	-	-
No change	4.9914	3.8199	3.7980	5.1346	4.0285	4.0284	5.6580	5.7548
$p_D = 0.8$	5.7206	4.4495	4.4020	5.8377	4.6309	4.5817	6.3439	6.4262
$p_D = 0.7$	6.7694	5.5022	5.4163	6.7646	5.5625	5.4735	7.1431	7.2189
$\lambda_C = 20$	5.2385	4.1209	4.0968	5.3525	4.2867	4.2791	6.1932	6.2930
$\lambda_C = 30$	5.4340	4.4475	4.4062	5.5165	4.5495	4.5037	6.9192	7.0153

Moreover, the average execution times of a single run (100 time steps) with Matlab implementation on the processor: Inter(R) Core(TM) i5-13600KF CPU @3.5GHz, are shown in Table III. All filters are implemented with parameters as follow:  $p_D = 0.9$ ,  $\lambda_C = 10$  and  $L = 5$  for trajectory set based filters. It shows that the filters based on PMB density are faster than the others as expect. Besides, the proposed GTPMB filter shares a similar computational complexity with the TPMB filter in our group tracking scenario.

TABLE III  
AVERAGE EXECUTION TIMES

	GTPMB	TPMB	GTPMBM	PMBM
Time	1.42s	1.40s	3.65s	3.49s

## V. CONCLUSION

In this paper, we proposed a group target trajectory estimation method based on the standard TPMB filter. Combined with the virtual leader-follower model, the standard TPMB is improved to the proposed GTPMB for group target tracking. Moreover, the Gaussian implementation and  $L$ -scan approximation for GTPMB filter are also provided in this paper. Finally, we build a simulation scenario with splitting and merging of groups and evaluate the proposed GTPMB filter in comparison with TPMB, GTPMBM and PMBM filter. The result shows that the proposed GTPMB filter has achieved a better performance in group target trajectories estimation than other filters. However, we only consider the VLFM as the group kinematic model and employ a clustering-based approach to construct group structure rather than estimate it in GTPMB recursion which are need to be improved in the future work.

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