Trajectory probability hypothesis density filter

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***Abstract*—This paper presents the probability hypothesis density (PHD) filter for sets of trajectories: the trajectory probability density (TPHD) filter. The TPHD filter is capable of estimating trajectories in a principled way without requiring to evaluate all measurement-to-target association hypotheses. The TPHD filter is based on recursively obtaining the best Poisson approximation to the multitrajectory filtering density in the sense of minimising the Kullback-Leibler divergence. We also propose a Gaussian mixture implementation of the TPHD recursion. Finally, we include simulation results to show the performance of the proposed algorithm.**

***Index Terms*—Random finite sets, multitarget tracking, sets of trajectories, PHD filter.**

I. Introduction

The probability hypothesis density (PHD) filter is a widely used algorithm for multitarget filtering, which aims to estimate the state of the targets at the current time, based on random finite sets (RFSs) [1]–[4]. The PHD filter fits into the assumed density filtering (ADF) framework and propagates a Poisson (multitarget) density on the current set of targets through the prediction and update steps by minimising the Kullback-Leibler divergence (KLD) [1], [5].

The main appealing characteristics of the PHD filter are its low computational burden and ease of implementation. It avoids the measurement-to-target association problem and we just need to calculate the PHD of the multitarget filtering density, which is defined over the single target space. It also has some drawbacks such as the spooky effect [1] or the fact that it does not build tracks. The corresponding smoother [6], [7] does not avoid these problems. Despite the inability of the PHD filter to provide tracks, track building procedures have been proposed for some implementations [8]–[11].

In this paper, we develop a PHD filter that estimates tracks from first principles: the trajectory PHD (TPHD) filter. The TPHD filter follows the same scheme as the PHD filter with a fundamental difference, instead of using a set of targets as the state, it uses a set of trajectories. The theory for performing multiple target tracking using sets of trajectories is explained in [12], [13]. A set of trajectories is a variable that encapsulates the number of trajectories, start times, lengths and sequence of target states for each trajectory. In the TPHD filter, we therefore propagate a Poisson (multitrajectory) density on the space of the set of trajectories through the prediction and update steps. We do not consider target spawning and assume Poisson target births so a KLD minimisation is only required after the update step [5]. A diagram of the resulting Bayesian recursion is given in Figure 1.

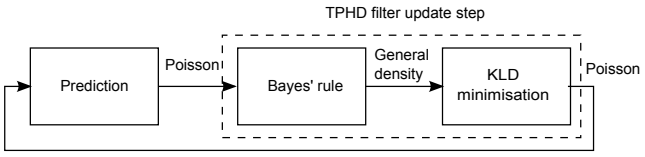

Figure 1: TPHD filter diagram. The TPHD filter assumes that the multitrajectory densities involved are Poisson (on the space of sets of trajectories). The output of Bayes' rule is not Poisson but the TPHD filter obtains the best Poisson approximation by minimising the KLD.

In this paper, we also propose an implementation of the TPHD filter based on Gaussian mixtures. The resulting Gaussian mixture TPHD (GMTPHD) filter builds trajectories without the use of labels under a Poisson approximation whose PHD is represented by a Gaussian mixture. Additionally, we propose a version of the GMTPHD filter with lower computational burden called the L-scan GMTPHD filter. This filter only updates the multitrajectory density of the trajectory states of the last L time instant leaving the rest unaltered, which yields an efficient implementation.

II. Background

This section describes some background material on sets of trajectories. More details can be found in [13].

A. Variables

A single target state $x \in \mathbb{R}^{n_x}$ contains information of interest about the target, e.g., its position and velocity. A set of single target states $\mathbf{x}$ belongs to $\mathcal{F}(\mathbb{R}^{n_x})$ where $\mathcal{F}(\mathbb{R}^{n_x})$ denotes the set of all finite subsets of $\mathbb{R}^{n_x}$. We are ultimately interested in estimating all target trajectories, where a trajectory consists of a sequence of target states that can start at any time step and end any time later on. Mathematically, a trajectory is represented as a variable $X = \left(t, x^{1:i}\right)$ where t is the initial time step of the trajectory, i is its length and $x^{1:i} = \left(x^1, ..., x^i\right)$ denotes a sequence of length i that contains the target states at consecutive time steps of the trajectory.

We consider trajectories up to the current time step k. As a trajectory $\left(t, x^{1:i}\right)$ exists from time step t to $t + i - 1$, variable (t, i) belongs to the set $I_{(k)} = \{(t, i) : 0 \leq t \leq k \text{ and } 1 \leq i \leq k - t + 1\}$. A single trajectory X up to time step k therefore belongs to the space $T_{(k)} = \uplus_{(t,i)\in I_{(k)}} \{t\} \times \mathbb{R}^{in_x}$, where $\uplus$ stands for disjoint union, which is used to highlight that the sets are disjoint. Similarly to the

set $\mathbf{x}$ of targets, we denote a set of trajectories up to time step k as $\mathbf{X} \in \mathcal{F}\left(T_{(k)}\right)$.

Given a trajectory $X = \left(t, x^{1:i}\right)$, the set $\tau^{k'}(X)$, which can be empty, denotes the corresponding target state at a time step k'. Given a set $\mathbf{X}$ of trajectories, the set $\tau^{k'}(\mathbf{X})$ of target states at time k' is $\tau^{k'}(\mathbf{X}) = \bigcup_{X \in \mathbf{X}} \tau^{k'}(X)$.

B. Set integral

Given a real-valued function $\pi(\cdot)$ on the single trajectory space $T_{(k)}$, its integral is

$$\int \pi(X)\, dX = \sum_{(t,i) \in I_{(k)}} \int \pi\left(t, x^{1:i}\right) dx^{1:i}. \tag{1}$$

This integral goes through all possible start times, lengths and target states of the trajectory. Given a real-valued function $\pi(\cdot)$ on the space $\mathcal{F}\left(T_{(k)}\right)$ of sets of trajectories, its set integral is

$$\int \pi(\mathbf{X})\, \delta\mathbf{X} = \sum_{n=0}^{\infty} \frac{1}{n!} \int \pi\left(\{X_1, ..., X_n\}\right) dX_{1:n} \tag{2}$$

where $X_{1:n} = (X_1, ..., X_n)$. Function $\pi(\cdot)$ is a multitrajectory density if $\pi(\cdot) \geq 0$ and its set integral is one.

C. Probability hypothesis density

The PHD [1] of a multitrajectory density $\pi(\cdot)$ is

$$D_\pi(X) = \int \pi\left(\{X\} \cup \mathbf{X}\right) \delta\mathbf{X}. \tag{3}$$

As in the PHD for RFS of targets, integrating the PHD in a region $A \subseteq T_{(k)}$ gives us the expected number of trajectories in this region [1, Eq. (4.76)]:

$$\begin{aligned} \hat{N}_A &= \int_A D_\pi(X) dX \\ &= \sum_{(t,i) \in I_{(k)}} \int 1_A\left(t, x^{1:i}\right) D_\pi(t, x^{1:i}) dx^{1:i} \end{aligned} \tag{4}$$

where $1_A(\cdot)$ is the indicator function of a subset A [1, App. A.3]. Therefore, the expected number of trajectories (in total) is given by substituting $A = T_{(k)}$ into (4).

Example 1. We consider a multitrajectory density $\nu(\cdot)$ with

$$D_\nu\left(1, x^1\right) = \mathcal{N}\left(x^1; 10, 1\right) + \mathcal{N}\left(x^1; 1000, 1\right) \tag{5}$$

$$D_\nu\left(1, x^{1:2}\right) = \mathcal{N}\left(x^{1:2}; (10, 10.1), \begin{bmatrix} 1 & 1 \\ 1 & 2 \end{bmatrix}\right), \tag{6}$$

where $\mathcal{N}(\cdot; m, P)$ is a Gaussian density with mean m and covariance matrix P, and zero otherwise. The expected number of trajectories that start at time one with length 1 is given by substituting $A = \{1\} \times \mathbb{R}^{n_x}$ into (4) so

$$\hat{N}_A = \int D_\nu\left(1, x^1\right) dx^1 = 2.$$

The expected number of trajectories is $\hat{N}_{T_{(k)}} = 3$. □

III. Poisson RFS of trajectories

In this section, we introduce the Poisson RFS on the trajectory space and some of its properties.

A. Probability density function

In the Poisson RFS, the cardinality of the set is Poisson distributed and its elements are independent and identically distributed (IID). A Poisson multitrajectory density $\nu(\cdot)$ has the form

$$\nu\left(\{X_1, ..., X_n\}\right) = e^{-\lambda_\nu} \lambda_\nu^n \prod_{j=1}^{n} \breve{\nu}(X_j) \tag{7}$$

where $\breve{\nu}(\cdot)$ is a single trajectory density, which implies

$$\int \breve{\nu}(X)\, dX = 1,$$

and $\lambda_\nu \geq 0$. A Poisson multitrajectory density is characterised by either its PHD $D_\nu(X) = \lambda_\nu \breve{\nu}(X)$ or by λ_ν and $\breve{\nu}(\cdot)$ [1]. As a result, using (4), the expected number of trajectories is $\hat{N}_{T_{(k)}} = \lambda_\nu$. Further, its cardinality distribution is given by [13]

$$\rho_\nu(n) = \frac{1}{n!} \int \nu\left(\{X_1, ..., X_n\}\right) dX_{1:n} = \frac{1}{n!} e^{-\lambda_\nu} \lambda_\nu^n \tag{8}$$

Example 2. We consider a Poisson RFS with the PHD of Example 1. Using (8), its cardinality distribution is Poisson with $\lambda_\nu = 3$ and, therefore, its single trajectory density is $\breve{\nu}(X) = D_\nu(X)/3$. □

We proceed to explain how to draw samples from $\nu(\cdot)$. The probability that a trajectory generated from $\nu(\cdot)$ starts at time t and has duration i is

$$P_{\breve{\nu}}(t, i) = \int \breve{\nu}\left(t, x^{1:i}\right) dx^{1:i}. \tag{9}$$

That is, we integrate over all possible trajectories with start time t and duration i. Given the start time t and duration i, the density of the states is

$$\breve{\nu}\left(x^{1:i} | t, i\right) = \breve{\nu}\left(t, x^{1:i}\right) / P_{\breve{\nu}}(t, i). \tag{10}$$

Therefore, the procedure to draw samples from a Poisson multitrajectory density $\nu(\cdot)$ is shown in Algorithm 1.

Algorithm 1 Sampling from a Poisson multitrajectory density

Input: Poisson multitrajectory density $\nu(\cdot)$.
Output: Sample $X \sim \nu(\cdot)$.
- Set $X = \emptyset$ and sample $n \sim \rho_\nu(\cdot)$, see (8).
for $j = 1$ to n **do**
- Sample $(t, i) \sim P_{\breve{\nu}}(\cdot)$ and $x^{1:i} \sim \breve{\nu}(\cdot | t, i)$, see (9) and (10).
- Set $X \leftarrow X \cup \left\{\left(t, x^{1:i}\right)\right\}$.
end for

B. Marginalisation for Poisson multitrajectory densities

Given a Poisson multitrajectory density $\nu(\cdot)$, the multitarget density $\nu_\tau^{k'}(\cdot)$ of the targets at a time k', with $1 \leq k' \leq k$, is Poisson with PHD

$$D_{\nu_\tau^{k'}}(y) = \sum_{t=1}^{k'} \sum_{j=0}^{k-k'} \int \int D_\nu\left(t, x^{1:k'-t}, y, z^{1:j}\right) dx^{1:k-t} dz^{1:j} \tag{11}$$

where $\left(t, x^{1:k-t}, y, z^{1:j}\right)$ denotes a trajectory that starts at time t with states $\left(x^{1:k-t}, y, z^{1:j}\right)$ so it has a duration $k-t+1+j$.

This result is obtained from the basic properties of Poisson processes [14, Chap. 2].

Example 3. We consider the Poisson multitrajectory density of Example 1. Using (11), the set of targets at time 1 is Poisson distributed with PHD

$$D_{\nu_\tau^1}(y) = 2\mathcal{N}(y;10,1) + \mathcal{N}(y;1000,1).$$

The expected number of targets at time 1 is 3. □

C. KLD minimisation

Using FISST [1], the KLD from $\pi(\cdot)$ to $\nu(\cdot)$ is given by

$$\mathrm{D}(\pi\|\nu) = \int \pi(\mathbf{X}) \log \frac{\pi(\mathbf{X})}{\nu(\mathbf{X})} \delta\mathbf{X}. \tag{12}$$

In Appendix A, we prove the following theorem.

Theorem 4. *Given a multitrajectory density $\pi(\cdot)$, the PHD that characterises the Poisson multitrajectory density $\nu(\cdot)$ that minimises the KLD $\mathrm{D}(\pi\|\nu)$ satisfies $D_\nu(\cdot) = D_\pi(\cdot)$.*

IV. Trajectory PHD filter

In this section, we derive the TPHD filter. In Section IV-A, we present the Bayesian filtering recursion for sets of trajectories. The prediction and update steps of the TPHD filter are given in Sections IV-B and IV-C, respectively.

A. Bayesian filtering recursion

The objective is to calculate the multitrajectory filtering density $\pi^k(\cdot)$ at time k, which is the multitrajectory density of the set of trajectories up to time step k conditioned on the measurements up to time step k. We assume that the set of trajectories at time k evolves with a transition density $f^k(\cdot|\cdot)$. In addition, given the targets at time k, the set $\mathbf{z}^k$ of measurements at time k has a density $\ell^k\left(\cdot|\tau^k(\mathbf{X})\right)$. We can calculate $\pi^k(\cdot)$ via the prediction and update steps [13]:

$$\omega^k(\mathbf{X}) = \int f^k(\mathbf{X}|\mathbf{Y})\,\pi^{k-1}(\mathbf{Y})\,\delta\mathbf{Y} \tag{13}$$

$$\pi^k(\mathbf{X}) = \frac{\ell^k\left(\mathbf{z}^k|\tau^k(\mathbf{X})\right)\omega^k(\mathbf{X})}{\ell^k(\mathbf{z}^k)} \tag{14}$$

where $\omega^k(\cdot)$ is the predicted multitrajectory density at time k, which denotes the density of the set of trajectories up to time step k given the measurements up to time step $k-1$. The density of the measurements is

$$\ell^k\left(\mathbf{z}^k\right) = \int \ell^k\left(\mathbf{z}^k|\tau^k(\mathbf{X})\right)\omega^k(\mathbf{X})\,\delta\mathbf{X}.$$

B. Prediction

We make the following assumptions in the prediction step:

- P1 Given the current multitarget state $\mathbf{x}$, each target $x \in \mathbf{x}$ survives with probability $p_S(x)$ and moves to a new state with a transition density $g(\cdot|x)$, or dies with probability $1-p_S(x)$.
- P2 The multitarget state at the next time step is the union of the surviving targets and new targets, which are born independently with a Poisson multitarget density $\beta_\tau(\cdot)$.
- P3 The multitrajectory density $\pi^{k-1}(\cdot)$ is Poisson.

Let $\mathbb{N}_k = \{1,...,k\}$. Then, the relation between predicted PHD at time k and the PHD of the posterior at time $k-1$ is given by the following theorem, which is proved in Appendix B.

Theorem 5 (Prediction)**.** *Under Assumptions P1-P3, the predicted PHD $D_{\omega^k}(\cdot)$ at time k is*

$$D_{\omega^k}(X) = D_{\xi^k}(X) + D_{\beta^k}(X)$$

where

$$D_{\beta^k}\left(t,x^{1:i}\right) = D_{\beta_\tau}\left(x^1\right)1_{\{k\}}(t)\,1_{\{1\}}(i)$$

$$\begin{aligned} &D_{\xi^k}\left(t,x^{1:i}\right) \\ &= D_{\pi^{k-1}}\left(t,x^{1:i}\right)1_{\mathbb{N}_{k-2}}(t+i-1) + \left(1-p_S\left(x^i\right)\right) \\ &\quad\times D_{\pi^{k-1}}\left(t,x^{1:i}\right)1_{\{k-1\}}(t+i-1) + p_S\left(x^{i-1}\right) \\ &\quad\times g\left(x^i\left|x^{i-1}\right.\right)D_{\pi_{k-1}}\left(t,x^{1:i-1}\right)1_{\{k\}}(t+i-1). \end{aligned}$$

The predicted PHD is the sum of the PHD $D_{\beta^k}(\cdot)$ of the trajectories born at time step k and the PHD $D_{\xi^k}(\cdot)$ of the trajectories present at previous time steps. The end time of trajectory $\left(t,x^{1:i}\right)$ is $t+i-1$. Therefore, the three terms of $D_{\xi^k}(\cdot)$ have clear interpretations in terms of trajectory end times. The prediction step does not change the PHD for the trajectories that ended before time step $k-1$. The PHD of the trajectories that end at time step $k-1$ is multiplied by $1-p_S\left(x^i\right)$, which represents the probability of not surviving. For the surviving trajectories, we multiply the PHD by the transition density and the survival probability.

C. Update

We make the following assumptions in the update step [5]:

- U1 For a given multi-target state $\mathbf{x}$ at time k, each target state $x \in \mathbf{x}$ is either detected with probability $p_D(x)$ and generates one measurement with density $l(\cdot|x)$, or missed with probability $1-p_D(x)$.
- U2 The measurement $\mathbf{z}^k$ is the union of the target-generated measurements and Poisson clutter with density $c(\cdot)$.
- U3 The multitrajectory density $\omega^k(\cdot)$ is Poisson.

Let Ξ_{n,n_z} denote the set that contains all the vectors $\sigma = (\sigma_1,...,\sigma_n)$ that indicate associations of n_z measurements to n targets, which can be either detected or undetected. If $\sigma \in \Xi_{n,n_z}$, $\sigma_i = j \in \{1,...,n_z\}$ indicates measurement j is associated with target i and $\sigma_i = 0$ indicates that target i has not been detected. Under Assumptions U1 and U2, which define the standard measurement model, the density of the measurement given the state is [1, Eq. (7.21)]

$$\begin{aligned} &\ell^k\left(\{z_1,...,z_{n_z}\}|\{x_1,...,x_n\}\right) \\ &\quad= e^{-\lambda_c}\left[\prod_{i=1}^{n_z}\lambda_c\breve{c}(z_i)\right]\left[\prod_{i=1}^{n}\left(1-p_D(x_i)\right)\right] \\ &\qquad\times\sum_{\sigma\in\Xi_{n,n_z}}\prod_{i:\sigma_i>0}\frac{p_D(x_i)\,l\left(z_{\sigma_i}|x_i\right)}{\left(1-p_D(x_i)\right)\lambda_c\breve{c}\left(z_{\sigma_i}\right)}. \end{aligned} \tag{15}$$

where λ_c and $\breve{c}(\cdot)$ characterise $c(\cdot)$, see (7).

Let $L_{\mathbf{z}^k}(\cdot)$ denote the PHD filter pseudolikelihood function, which is given by [1, Sec. 8.4.3]

$$L_{\mathbf{z}^k}(x) = 1 - p_D(x) + p_D(x) \times \sum_{z\in\mathbf{z}^k} \frac{l(z|x)}{\lambda_c \breve{c}(z) + \int p_D(y)\, l(z|y)\, D_{\omega_\tau^k}(y)\, dy}$$

with $D_{\omega_\tau^k}(\cdot)$ representing the PHD of the targets at time k of density $\omega^k(\cdot)$, see (11):

$$D_{\omega_\tau^k}(y) = \sum_{t=1}^{k} \int D_{\omega^k}\left(t, x^{1:k-t}, y\right) dx^{1:k-t}.$$

Then, we prove in Appendix C the TPHD filter update step:

Theorem 6 (Update)**.** *Under Assumptions U1-U3, the updated PHD $D_{\pi^k}(\cdot)$ at time k is*

$$D_{\pi^k}\left(t, x^{1:i}\right) = D_{\omega^k}\left(t, x^{1:i}\right)\left[1_{\mathbb{N}_{k-1}}(t+i-1) + 1_{\{k\}}(t+i-1)\, L_{\mathbf{z}^k}\left(x^i\right)\right]$$

if $t+i-1 \leq k$ or zero otherwise.

As in the prediction step, the update step does not change the PHD for the trajectories that have died before time step k. It should be noted that Bayes update (14) uses a likelihood (15) which involves a summation over all target to measurements associations in the multitarget space. In contrast, the TPHD filter update is similar to the PHD filter update in the sense that it uses a pseudolikelihood function $L_{\mathbf{z}^k}(\cdot)$, which is defined on the single target space and only involves associations between a single target and the measurements.

It can be checked that if we perform marginalisation at time step k, see (11), and apply the (target) PHD prediction and update, we obtain the same result as if we apply the (trajectory) PHD prediction and update and then apply marginalisation. Consequently, the information regarding the set of targets at the current time step is the same for the PHD and TPHD filters. For example, the estimated cardinality of alive trajectories/targets is the same for both filters.

V. Gaussian mixture TPHD filter

In this section, we propose a Gaussian mixture implementation of the TPHD filter. The prediction and update steps are provided in Section V-A. We motivate why the GMTPHD should only be used to track alive trajectories in Section V-B. The L-scan GMTPHD, which is a computationally efficient implementation, is described in Section V-C. An estimation procedure for the GMTPHD filter is given in Section V-D.

A. Prediction and update

The recursion of the GMTPHD filter is quite similar to the GMPHD filter [3]. We use the notation

$$\mathcal{N}\left(t, x^{1:i}; t^k, m^k, P^k\right) = \mathcal{N}\left(x^{1:i}; m^k, P^k\right) \quad \text{if } i = i^k, t = t^k \tag{16}$$

or zero otherwise, where $i^k = \dim\left(m^k\right)/n_x$. Equation (16) represents a single trajectory Gaussian density with start time t^k, duration i^k, mean $m^k \in \mathbb{R}^{i^k n_x}$ and covariance matrix $P^k \in \mathbb{R}^{i^k n_x \times i^k n_x}$ evaluated at $\left(t, x^{1:i}\right)$. We use $\otimes$ to indicate Kronecker product and $0_{m,n}$ is the $m \times n$ zero matrix.

We make the additional assumptions

- A1 The probabilities p_S and p_D are constants.
- A2 $g\left(x^i \left| x^{i-1}\right.\right) = \mathcal{N}\left(x^i; Fx^{i-1}, Q\right)$.
- A3 $l(z|x) = \mathcal{N}(z; Hx, R)$.
- A4 The PHD of the birth density $\beta^k(\cdot)$ is

$$D_{\beta^k}(X) = \sum_{j=1}^{J_\beta^k} w_{\beta,j}^k \mathcal{N}\left(X; k, m_{\beta,j}^k, P_{\beta,j}^k\right) \tag{17}$$

where $J_\beta^k \in \mathbb{N}$ is the number of components, $m_{\beta,j}^k \in \mathbb{R}^{n_x}$ and $P_{\beta,j}^k \in \mathbb{R}^{n_x \times n_x}$.

It should be noted that the models provided by A1-A4 could be time varying but omit time for notational convenience. Under Assumptions A1-A4, P1-P3 and U1-U3, we can calculate the TPHD filter in closed form giving rise to the GMTPHD filter, whose prediction and update steps are provided in the following.

Proposition 7 (Prediction)**.** *We denote the PHD of $\pi^k(\cdot)$ by*

$$D_{\pi^k}(X) = D_{\pi_\star^k}(X) + D_{\pi_\circ^k}(X)$$

where

$$D_{\pi_\star^k}(X) = \sum_{j=1}^{J^k} w_j^k \mathcal{N}\left(X; t_j^k, m_j^k, P_j^k\right)$$

$$D_{\pi_\circ^k}(X) = \sum_{j=1}^{J_\circ^k} w_{\circ,j}^k \mathcal{N}\left(X; t_{\circ,j}^k, m_{\circ,j}^k, P_{\circ,j}^k\right)$$

represent the PHD of alive and dead trajectories, i.e., $t_j^k + i_j^k - 1 = k$ and $t_{\circ,j}^k + i_{\circ,j}^k - 1 < k$ with $i_j^k = \dim\left(m_j^k\right)/n_x$ and $i_{\circ,j}^k = \dim\left(m_{\circ,j}^k\right)/n_x$. Then, the PHD of $\omega^{k+1}(\cdot)$ is

$$D_{\omega^{k+1}}(X) = (1-p_S) D_{\pi_\star^k}(X) + D_{\pi_\circ^k}(X) + D_{\beta^{k+1}}(X) + p_S \sum_{j=1}^{J^k} w_j^k \mathcal{N}\left(X; t_j^k, m_{\omega,j}^{k+1}, P_{\omega,j}^{k+1}\right) \tag{18}$$

where

$$m_{\omega,j}^{k+1} = \left[\left(m_j^k\right)^T, \left(\dot{F}_j m_j^k\right)^T\right]^T$$

$$P_{\omega,j}^{k+1} = \begin{bmatrix} P_j^k & P_j^k \dot{F}_j^T \\ \dot{F}_j P_j^k & \dot{F}_j P_j^k \dot{F}_j^T + Q \end{bmatrix}$$

$$\dot{F}_j = \left[0_{1,i_j^k-1}, 1\right] \otimes F.$$

Proposition 7 can be proved using Theorem 5. The GMTPHD filter prediction is similar to the GMPHD filter prediction with the main differences that previous states are not integrated out, as in [15], and there is information about dead trajectories.

Proposition 8 (Update)**.** *We denote the PHD of $\omega^k(\cdot)$ by*

$$D_{\omega^k}(X) = D_{\omega_\star^k}(X) + D_{\omega_\circ^k}(X)$$

where

$$D_{\omega_\star^k}(X) = \sum_{j=1}^{J_\omega^k} w_{\omega,j}^k \mathcal{N}\left(X; t_{\omega,j}^k, m_{\omega,j}^k, P_{\omega,j}^k\right)$$

$$D_{\omega_{\circ}^k}(X) = \sum_{j=1}^{J_{\circ}^k} w_{\circ,j}^k \mathcal{N}\left(X; t_{\circ,j}^k, m_{\circ,j}^k, P_{\circ,j}^k\right)$$

represent the PHD of alive and dead trajectories. Then, the PHD of $\pi^k(\cdot)$ *is*

$$D_{\pi^k}(X) = D_{\omega_{\circ}^k}(X) + (1-p_D) D_{\omega_{\star}^k}(X) + \sum_{z\in\mathbf{z}^k}\sum_{j=1}^{J^k} w_j(z)\mathcal{N}\left(X; t_{\omega,j}^k, m_j^k(z), P_j^k\right) \quad (19)$$

where

$$\begin{aligned} w_j(z) &= \frac{p_D w_{\omega,j}^k \mathcal{N}(z; \overline{z}_j, S_j)}{\lambda_c \breve{c}(z) + p_D \sum_{l=1}^{J_{\omega}^k} w_{\omega,l}^k \mathcal{N}(z; \overline{z}_l, S_l)} \\ \overline{z}_j &= \dot{H} m_{\omega,j}^k, \quad S_j = \dot{H} P_{\omega,j}^k \dot{H}^T + R \\ \dot{H}_j &= \left[0_{1, i_{\omega,j}^k - 1}, 1\right] \otimes H \\ m_j^k(z) &= m_{\omega,j}^k + P_{\omega,j}^k \dot{H}^T S_j^{-1}(z - \overline{z}_j) \\ P_j^k &= P_{\omega,j}^k - P_{\omega,j}^k \dot{H}^T S_j^{-1} \dot{H} P_{\omega,j}^k. \end{aligned}$$

where $i_{\omega,j}^k = \dim\left(m_{\omega,j}^k\right)/n_x$

Proposition 8 can be proved using Theorem 6. As $D_{\omega_{\star}^k}(\cdot)$ and $D_{\omega_{\circ}^k}(\cdot)$ represent the alive and dead trajectories, respectively, it is met that $t_{\omega,j}^k + i_{\omega,j}^k - 1 = k$ and $t_{\circ,j}^k + i_{\circ,j}^k - 1 < k$. Also, the GMTPHD filter update is similar to the GMPHD filter update. The main differences is that we keep the PHD that represents dead trajectories and we update the whole trajectories. The updated weights of the alive components are the same as in the GMPHD filter because the likelihood only depends on the the current set of targets.

B. Tracking of only alive trajectories

In this section, we motivate why practical GMTPHD implementations should not attempt to track the dead trajectories. As in the PHD filter, the Poisson approximation for the multitarget density of the current set of targets, is a strong approximation but yields acceptable results in many situations [1]. The Poisson approximation for the multitrajectory density is even stronger as we proceed to explain. First, the number of total trajectories is, in most cases, greater than the number of current targets and, therefore, the Poisson approximation for the number of trajectories is usually worse (the variance of a Poisson distribution is equal to its mean). Second, in practice, we argue that the Poisson approximation is only useful to obtain information about the present trajectories at the current time step. The reason is that, in the prediction step, the weight of the components of trajectories that die at the current time step is multiplied by $(1-p_S)$, see the first term in (18). Then, the weights of the components of dead trajectories are never modified at future time steps, see $D_{\pi_{\circ}^k}(X)$ and $D_{\omega_{\circ}^k}(X)$ in Propositions 7 and 8. The probability p_S of survival is usually close to one so these components have very low weights. As a result, all components that represent dead trajectories have very low weight even if they were very likely in the past.

The conclusion is that the Poisson approximation to the full multitrajectory filtering density is not an accurate representation of the knowledge over all trajectories that have existed up to the current time. Nevertheless, the TPHD filter is useful to approximate the posterior of the alive trajectories. In practice, this implies setting $D_{\pi_{\circ}^k}(X) = 0$ and removing the term $(1-p_S) D_{\pi_{\star}^k}(X)$ in (18) and setting $D_{\omega_{\circ}^k}(X) = 0$ in (19).

C. L-scan GMTPHD

In this section, we propose a computationally efficient implementation of the GMTPHD filter: the L-scan GMTPHD filter. The GMTPHD filter has an increasing number of components as time progresses so we need to bound the number of components in practice. The simplest technique is to prune the components whose weight is below a threshold Γ_p and set a maximum number J_{max} of components [3]. In addition, if two components have a very similar current state, based on a Mahalanobis distance criterion, future measurements will affect both component weights and future states in a similar way. Therefore, we can remove components that are close to another component with higher weight. We account for this decrease in the number of components by increasing the weight of the component that has not been removed by the weights of the removed components. We refer to as this technique as absorption. The steps of the pruning and absorption algorithms for the GMTPHD are given in Algorithm 2, where we use the notation $\Phi_j^k = \left(w_j^k, t_j^k, m_j^k, P_j^k\right)$.

Algorithm 2 Pruning and absorption for the GMTPHD filter

Input: Posterior parameters $\left\{\Phi_j^k\right\}_{j=1}^{J^k}$, pruning threshold Γ_p, absorption threshold Γ_a, maximum number of terms J_{max}.
Output: Pruned posterior parameters $\left\{\Phi_{o,j}^k\right\}_{j=1}^{\hat{J}^k}$

- Set $l = 0$ and $I = \left\{j \in \left\{1, ..., J^k\right\} : w_j^k > \Gamma_p\right\}$.
while $I \neq \emptyset$ **do**
- Set $l \leftarrow l + 1$.
- $j = \arg\max_{i\in I} w_i^k$.
- $L = \left\{i \in I : \left(\hat{m}_i^k - \hat{m}_j^k\right)^T \left(\hat{P}_j^k\right)^{-1} \left(\hat{m}_i^k - \hat{m}_j^k\right) \leq \Gamma_a\right\}$

with $\hat{m}_j^k \in \mathbb{R}^{n_x}$ and $\hat{P}_j^k \in \mathbb{R}^{n_x \times n_x}$ denoting the mean and covariance matrix of the state at the current time step.
- $\Phi_{o,l}^k = \Phi_j^k$ with weight $w_{o,l}^k = \sum_{i\in L} w_i^k$.
- $I \leftarrow I \setminus L$.
end while
- If $l > J_{max}$, only keep the J_{max} components with highest weight

In addition, as time progresses, the lengths of the trajectories increase so, eventually, the direct implementation of the GMTPHD is not computationally feasible. Fortunately, in practice, measurements at the current time step only have a significant impact on the trajectory state estimates for recent time steps. Based on this insight combined with the ADF framework and KLD minimisation, we propose a computationally efficient, single trajectory L-scan filter in Appendix D. The density that this filter propagates is composed by the joint density of the states of the last L time steps and independent densities for the previous states. We apply this filter to each mixture component of the GMTPHD posterior and the resulting algorithm is referred to as L-scan GMTPHD.

The L-scan GMTPHD is implemented as the GMTPHD with a minor modification in the prediction step, where we

discard the correlations of states that happened at least L time steps before the current time step. Given a predicted PHD $D_{\omega^k}(\cdot)$, see Proposition 7, its L-scan version is

$$D^{(L)}_{\omega^k}(X) = \sum_{j=1}^{J^k_\omega} w^k_{\omega,j} \mathcal{N}\left(X; t^k_{\omega,j}, m^k_{\omega,j}, P^{k(L)}_{\omega,j}\right) \tag{20}$$

where $P^{k(L)}_{\omega,j} = \text{diag}\left(\tilde{P}^{t^k_{\omega,j}}_j, \tilde{P}^{t^k_{\omega,j}+1}_j, ..., \tilde{P}^{k-L}_j, \tilde{P}^{k-L+1:k}_j\right)$. Matrix $\tilde{P}^{k-L+1:k}_j \in \mathbb{R}^{L\cdot n_x \times L\cdot n_x}$ represents the joint covariance of the L last time instants, obtained from $P^k_{\omega,j}$, and $\tilde{P}^k_j \in \mathbb{R}^{n_x \times n_x}$ represents the covariance matrix of the target state at time k, obtained from $P^k_{\omega,j}$. Therefore, we have independent Gaussian densities to represent the states outside the L-scan window and a joint Gaussian density for the states in the L-scan window. The steps of the L-scan GMTPHD filter are summarised in Algorithm 3.

It should be noted that the estimated number of alive trajectories and the target states at the current time are not affected by L. This implies that the estimated number of alive trajectories is equal to the number of targets of the GMPHD filter and the estimated targets at the current time using both the GMPHD or GMTPHD are alike.

Algorithm 3 L-scan GMTPHD filter steps

- Initialisation: $D_{\pi^0}(\cdot) = 0$: $J^0 = 0$.
for $k = 1$ to *final time step* **do**
  - Prediction using Proposition 7 with this modification:
    - After calculating $P^k_{\omega,j}$, represent it in the form of $P^{k(L)}_{\omega,j}$, see (20), by discarding correlations outside the L-scan window.
  - Update using Proposition 8.
  - Estimation of the alive trajectories, see Section V-D.
  - Pruning/absorption using Algorithm 2.
end for

D. Estimation

We adapt the estimator for the GMPHD filter described in [1, Sec. 9.5.4.4] for sets of trajectories. First, the number of trajectories is estimated as

$$\hat{N}^k = \text{round}\left(\sum_{j=1}^{J^k} w^k_j\right). \tag{21}$$

Then, the estimated set of trajectories corresponds to $\left\{\left(t^k_{l_1}, m^k_{l_1}\right), ..., \left(t^k_{l_{\hat{N}^k}}, m^k_{l_{\hat{N}^k}}\right)\right\}$ where $\left\{l_1, ..., l_{\hat{N}^k}\right\}$ are the indices of the components with highest weights.

There are several drawbacks with this sub-optimal estimator. First, J^k cannot be smaller than $\hat{N}^k$. Also, this estimator does not work well if there is a component with weight higher than two because there are at least two targets in that region but only one is reported. Nevertheless, this estimator is commonly used in the GMPHD filter and has a low computational complexity, so we suggest its use for the GMTPHD filter as well.

VI. Simulations

We proceed to assess the performance of the L-scan TPHD filter by simulations. We consider a target state $x = [p_x, \dot{p}_x, p_y, \dot{p}_y]^T$, which contains position and velocity. All the units of the quantities in this section are given in the international system. The parameters of the single-target dynamic process are

$$F = I_2 \otimes \begin{pmatrix} 1 & \tau \\ 0 & 1 \end{pmatrix}, \quad Q = qI_2 \otimes \begin{pmatrix} \tau^3/3 & \tau^2/2 \\ \tau^2/2 & \tau \end{pmatrix}$$

where $\tau = 0.5$ is the sampling time and $q = 3.24$ is a parameter. We also set $p_S = 0.99$. The parameters of the measurement model are

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

where $\sigma^2 = 16$, and $p_D = 0.9$. The clutter intensity is $D_c(z) = \lambda_c \cdot u_A(z)$ where $u_A(z)$ is a uniform density in region $A = [0, 2000] \times [0, 2000]$ and $\lambda_c = 50$ is the average number of clutter measurements per scan. The birth process parameters are $J^k_\beta = 3$, $w^k_{\beta,j} = 0.1$, $P^k_{\beta,j} = 100 I_4$ for $j \in \{1, 2, 3\}$ and $m^k_{\beta,1} = [85, 0, 140, 0]^T$, $m^k_{\beta,2} = [-5, 0, 220, 0]^T$ and $m^k_{\beta,3} = [7, 0, 50, 0]^T$.

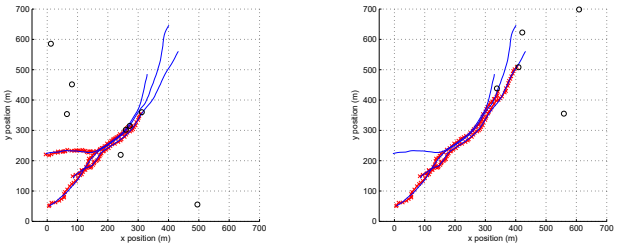

Figure 2: Exemplar outputs at time steps 50 (left) and 70 (right). The blue lines represent the true trajectories, which start at time steps $(1, 5, 10)$ and finish at $(80, 70, 95)$. The red lines with crosses represent the estimated alive trajectories. Black circles represent the current measurements. The TPHD filter is able to estimate the alive trajectories.

We have implemented the L-scan TPHD filter with $L \in \{1, 2, 5, 10\}$ in a scenario with 100 time steps. We use a pruning threshold $\Gamma_p = 10^{-4}$, absorption threshold $\Gamma_a = 4$ and limit the number of components to 30. Two exemplar outputs of the 10-scan TPHD filter and the considered ground truth are shown in Figure 2. At each time step, the TPHD provides an estimate of the set of present trajectories at the current time. The start and end times of an estimated trajectory do not depend on the choice of L so the output for any other L looks alike but with a different error.

In the following, we evaluate the performance of the L-scan TPHD filters by Monte Carlo simulation with 500 runs. At each time step k, we measure the distance between the set $\mathbf{X}^k_a$ of alive trajectories and its estimate $\hat{\mathbf{X}}^k_a$ using the metric $d(\cdot, \cdot)$ for sets of trajectories based on linear programming in [16], with parameters $p = 2$, $c = 10$ and $\gamma = 0.1$. We only use the position elements and normalise the metric by $\sqrt{k}$. The resulting mean errors for the L-scan TPHD filter are plotted in Figure 3. At the beginning, the filters have the same error but soon the differences start to appear. As expected, the error decreases as we increase L in the filter because we are considering a longer time window to update the trajectories. In addition, the running times of a non-optimised Matlab implementation on a Intel Core i7 laptop

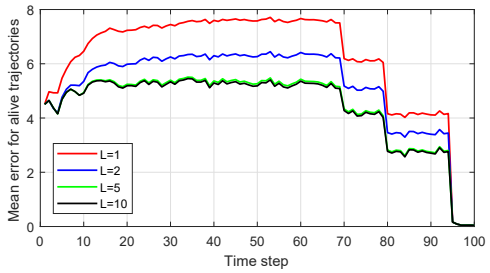

Figure 3: Error calculated with the sets of trajectories metric for the L-scan TPHD filter. Performance improves as we increase L.

Table I: Error in alive trajectories averaged over all time steps

Changed parameter	L=1	L=2	L=5	L=10
No change	6.20	5.18	4.46	4.41
$\sigma^2 = 25$	7.12	6.02	5.08	5.02
$\sigma^2 = 9$	5.20	4.32	3.82	3.79
$\lambda_c = 70$	6.25	5.24	4.52	4.47
$\lambda_c = 90$	6.30	5.30	4.60	4.55
$p_D = 0.99$	5.51	4.39	3.66	3.61
$p_D = 0.95$	5.82	4.74	4.03	3.98
$p_D = 0.85$	7.07	6.17	5.52	5.48

are basically the same for $L \in \{1, 2, 5, 10\}$: 7.7 seconds. In our implementation, the computational burden associated to operations resulting of using an L window of sizes between 1 and 10 is negligible compared to the computational burden of the rest of the filter. If we continue increasing L, the running time increases considerable, for example, 14.8 s for $L = 20$ and 28.0 s for $L = 30$.

We also show the error averaged over all time steps changing several parameters of the simulation in Table I. Logically, with lower measurement noise or clutter rate or higher probability of detection, performance increases.

VII. Conclusions

We have presented the trajectory PHD filter and a Gaussian mixture implementation. The trajectory PHD filter uses sets of trajectories as state variable to enable inference over the trajectories, without the need of evaluating all data association hypotheses. It is based on propagating a Poisson multitrajectory density through the filtering recursion and performing a KLD minimisation after each update step.

We have also presented the computationally efficient L-scan GMTPHD filter for linear/Gaussian models, which can be adapted for nonlinear/non-Gaussian models using nonlinear Gaussian filters.

Appendix A

In this appendix, we prove Theorem 4. A multitrajectory density $\pi(\cdot)$ can be written as

$$\pi(\{X_1, ..., X_n\}) = \rho_\pi(n)\, n! \pi_n(X_{1:n}) \tag{22}$$

where $\pi_n(\cdot)$ is a permutation invariant ordered density with

$$\int \pi_n(X_{1:n})\, dX_{1:n} = 1.$$

The marginal density of one trajectory of this density is

$$\tilde{\pi}_n(X) = \int \pi_n(X, X_{2:n})\, dX_{2:n}$$

Substituting (7) into (12), we have that

$$\begin{aligned} \mathrm{D}(\pi \| \nu) = &\sum_{n=0}^{\infty} \rho_\pi(n) \log \frac{\rho_\pi(n)}{e^{-\lambda_\nu} \lambda_\nu^n / n!} \\ &+ \sum_{n=0}^{\infty} \rho_\pi(n) \int \pi_n(X_{1:n}) \log \frac{\pi_n(X_{1:n})}{\prod_{j=1}^{n} \breve{\nu}(X_j)} dX_{1:n}. \end{aligned} \tag{23}$$

We want to find λ_ν and $\breve{\nu}(\cdot)$ that minimise (23). By derivating the first term w.r.t. λ_ν and equating it to zero, we obtain that the unique minimum is achieved by setting $\lambda_\nu = \sum_{n=0}^{\infty} n \rho_\pi(n)$. The minimisation over $\breve{\nu}(\cdot)$ can be done as in the target case [5] , which results in

$$\breve{\nu}(X) = \frac{D_\pi(X)}{\sum_{n=0}^{\infty} \rho_\pi(n)\, n}$$

or, equivalently, $D_\nu(\cdot) = D_\pi(\cdot)$.

Appendix B

In this appendix, we prove Theorem 5. A set of trajectories at time k can be decomposed as $\mathbf{W} \uplus \mathbf{X} \uplus \mathbf{Y} \uplus \mathbf{Z}$ where $\mathbf{W}$ denotes the set of new born trajectories at time k, $\mathbf{X}$ the set of trajectories present at times $k-1$ and k but not present at $k+1$, $\mathbf{Y}$ the set of trajectories present at time $k-1$ but not present at time k and $\mathbf{Z}$ the set of trajectories present at a time before $k-1$ but not at time k. We first clarify that if $(t, x^{1:i}) \in \mathbf{W}$, then, $t = k$, $i = 1$; if it belongs to $\mathbf{X}$, then $t < k$, $i = k-t+1$; if it belongs to $\mathbf{Y}$, then $t < k$, $i = k - t$; and finally, if it belongs to $\mathbf{Z}$, then, $t < k-1$, $i < k-t$. As $\mathbf{W}, \mathbf{X}, \mathbf{Y}$ and $\mathbf{Z}$ are independent and Poisson distributed due to Assumptions P2-P3 so we can obtain their predicted PHDs independently. The overall predicted PHD is then the sum of these predicted PHDs due to the superposition of Poisson processes [5].

We use Theorem 5 in [13]. For dead trajectories, the prediction step leaves the multitrajectory density unaltered and so its PHD. The PHD of new born trajectories is analogous to the PHD of new born targets by setting the time to k and duration to one. Using Theorem 5 in [13], we have that for $\mathbf{Y} = \left\{ \left(t_1, x_1^{1:i_1}\right), ..., \left(t_n, x_n^{1:i_n}\right) \right\}$,

$$\begin{aligned} \omega^k(\mathbf{Y}) = &\pi^{k-1}\left(\left\{ \left(t_1, x_1^{1:i_1}\right), ..., \left(t_n, x_n^{1:i_n}\right) \right\} \right) \\ &\times \prod_{j=1}^{n} \left(1 - p_S\left(x_j^{i_j}\right)\right). \end{aligned}$$

Using Assumption P3 and (7), we get that the predicted PHD, for $(t, x^{1:i}) \in \mathbf{Y}$, is

$$D_{\omega^k}\left(t, x^{1:i}\right) = \left(1 - p_S\left(x^i\right)\right) D_{\pi^{k-1}}\left(t, x^{1:i}\right).$$

Similarly, for $\mathbf{X} = \left\{ \left(t_1, x_1^{1:i_1}\right), ..., \left(t_n, x_n^{1:i_n}\right) \right\}$,

$$\begin{aligned} \omega^k(\mathbf{X}) = &\pi^{k-1}\left(\left\{ \left(t_1, x_1^{1:i_1-1}\right), ..., \left(t_n, x_n^{1:i_n-1}\right) \right\} \right) \\ &\times \prod_{j=1}^{n} \left(g\left(x_j^{i_j} \middle| x_j^{i_j-1}\right) p_S\left(x_j^{i_j-1}\right) \right) \end{aligned}$$

which implies that the predicted PHD for $\mathbf{X}$ is the one indicated in Theorem 5, which finishes the proof.

APPENDIX C

In this appendix, we prove Theorem 6. As with the PHD filter, we first compute the density of the measurement [5]. Using (11) and Assumption U3, the multitarget predicted density at time k is Poisson with PHD

$$D_{\omega_{\tau}^{k}}(y)=\sum_{t=1}^{k}\int D_{\omega^{k}}\left(t,x^{1:k-t},y\right)dx^{1:k-t} \tag{24}$$

where we have used that $\omega^{k}(\cdot)$ is zero for trajectories present later than time k. Due to the Poisson prior, the density of the measurement is Poisson with density [5]

$$\begin{aligned}\ell^{k}\left(\mathbf{z}^{k}\right)&=e^{-\int p_{D}(y)l(z|y)D_{\omega_{\tau}^{k}}(y)dy-\lambda_{c}}\\&\times\prod_{z\in\mathbf{z}^{k}}\left[\lambda_{c}\breve{c}(z)+p_{D}(y)\,l(z|y)\,D_{\omega_{\tau}^{k}}(y)\,dy\right].\end{aligned} \tag{25}$$

Using (3) and (14), we calculate the updated PHD

$$\begin{aligned}&D_{\pi^{k}}(X)\\&=\frac{1}{\ell^{k}\left(\mathbf{z}^{k}\right)}\int\ell^{k}\left(\mathbf{z}^{k}\left|\tau^{k}\left(\{X\}\cup\mathbf{X}\right)\right.\right)\omega^{k}\left(\{X\}\cup\mathbf{X}\right)\delta\mathbf{X}\\&=\frac{\lambda_{\omega^{k}}\breve{\omega}^{k}(X)}{\ell^{k}\left(\mathbf{z}^{k}\right)}\int\ell^{k}\left(\mathbf{z}^{k}\left|\tau^{k}(X)\cup\tau^{k}(\mathbf{X})\right.\right)\omega^{k}(\mathbf{X})\,\delta\mathbf{X}.\end{aligned}$$

We consider two cases: X is not present at time k and X is present at time k. For $\tau^{k}(X)=\emptyset$, we have

$$D_{\pi^{k}}(X)=\lambda_{\omega^{k}}\breve{\omega}^{k}(X)=D_{\omega^{k}}(X).$$

For $\tau^{k}(X)\neq\emptyset$, we have that [5, Eq. (14)]

$$\begin{aligned}&\ell^{k}\left(\mathbf{z}^{k}\left|\tau^{k}(X)\cup\tau^{k}(\mathbf{X})\right.\right)\\&=\left(1-p_{D}\left(\tau^{k}(X)\right)\right)\ell^{k}\left(\mathbf{z}^{k}\left|\tau^{k}(\mathbf{X})\right.\right)\\&+p_{D}\left(\tau^{k}(X)\right)\sum_{z\in\mathbf{z}^{k}}l\left(z|\tau^{k}(X)\right)\ell^{k}\left(\mathbf{z}^{k}\setminus\{z\}\left|\tau^{k}(\mathbf{X})\right.\right)\end{aligned}$$

where $B\setminus A=\{z\in B|\,z\notin A\}$. Using (25) and following the same steps as in (target) PHD filter derivation [5], we find

$$\begin{aligned}D_{\pi^{k}}(X)&=\left(1-p_{D}\left(\tau^{k}(X)\right)\right)\lambda_{\omega^{k}}\breve{\omega}^{k}(X)\\&+p_{D}\left(\tau^{k}(X)\right)\lambda_{\omega^{k}}\breve{\omega}^{k}(X)\\&\times\sum_{z\in\mathbf{z}^{k}}\frac{l\left(z|\tau^{k}(X)\right)}{\lambda_{c}\breve{c}(z)+\int p_{D}(y)\,l(z|y)\,D_{\omega_{T}^{k}}(y)\,dy},\end{aligned}$$

which finishes the proof of Theorem 6.

APPENDIX D

In this appendix, we derive an L-scan single trajectory filter that jointly updates the density over the last L time steps and leaves unaltered the density at previous time steps. We use the ADF so we assume the posterior at time k is of a certain form and then we perform KLD minimisations to continue with the filtering recursion. For the sake of notational simplicity, we assume the trajectory exists at all time steps so we represent a trajectory as $x^{1:k}$. Let the posterior at time k be

$$\pi^{k}\left(x^{1:k}\right)=p^{k}\left(x^{k-L+1:k}\right)\prod_{i=1}^{k-L}q^{i}\left(x^{i}\right) \tag{26}$$

where $q^{i}(\cdot)$ is a density for the state at time step $i<k-L$ and $p^{k}(\cdot)$ is the joint density for the last L time steps. That is, the states corresponding to the last L time steps are considered jointly and the previous states are independent.

After the prediction and update on (26), we obtain

$$\begin{aligned}\pi_{,}^{k+1}\left(x^{1:k+1}\right)&=r^{k+1}\left(x^{k-L+1:k+1}\right)\prod_{i=1}^{k-L}q^{i}\left(x^{i}\right)\\r^{k+1}\left(x^{k-L+1:k+1}\right)&\propto l\left(z^{k+1}|x^{k+1}\right)g\left(x^{k+1}\left|x^{k}\right.\right)\\&\times p^{k}\left(x^{k-L+1:k}\right)\end{aligned}$$

where $l\left(z^{k+1}|\cdot\right)$ and $g(\cdot\,|\cdot)$ represent the likelihood and the transition density, respectively. We obtain the density of the form (26) that minimises the KLD $D\left(\pi_{,}^{k+1}\left\|\pi^{k+1}\right.\right)$ with [17]

$$\begin{aligned}p^{k+1}\left(x^{k-L+2:k+1}\right)&=\int r^{k+1}\left(x^{k-L+1:k+1}\right)dx^{k-L+1}\\q^{k+1-L}\left(x^{k+1-L}\right)&=\int r^{k+1}\left(x^{k-L+1:k+1}\right)dx^{k-L+2:k+1}.\end{aligned}$$

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