Approximate Calculation of Marginal Association Probabilities using a Hybrid Data Association Model

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ABSTRACT

The calculation of marginal association probabilities is the major computational bottleneck in the Joint Probabilistic Data Association Filter (JPDAF). In this paper, we investigate approximations for the marginal associations that simplify the (computational complex) original association model in order to obtain efficient algorithms. In this context, we first discuss the Bakhtiar-Alavi algorithm and the Linear Multitarget Integrated Probabilistic Data Association (LMIPDA) algorithm. Second, we propose a fast novel approximation that exploits systematic combinations of the JPDAF measurement model with the Probabilistic Multi-Hypothesis Tracker (PMHT) measurement model. The discussed methods are evaluated by means of a tracking scenario with a high number of closely-spaced targets.

Keywords: Joint Probabilistic Data Association Filter (JPDAF), marginal association probabilities, Probabilistic Multi-Hypothesis Tracker (PMHT).

1. INTRODUCTION

The Joint Probabilistic Data Association Filter (JPDAF) [3, 4] is an algorithm for tracking multiple targets based on measurements that are unlabeled, i.e., the measurement-to-target association is unknown. The JPDAF updates the tracks based on a weighted sum constructed from the measurements. In order to calculate the weights, it is required to calculate the probabilities of all feasible measurement-to-target associations. As the number of feasible joint measurement-to-target associations grows exponentially with the number of targets, the exact calculation of marginal association probabilities is computationally tractable only for a small number of targets. In this context, a variety of fast approximate methods have been proposed, ranging from simple ad-hoc formulas [7] and sophisticated randomized algorithms [11] to algorithms that avoid track coalescence [13]. Recently, [12] showed that the so-called Bakhtiar-Alavi algorithm [2] gives the most precise approximation among several state-of-the-art methods.

In this paper, we focus on approaches that intentionally employ a different association model for efficiently approximating the marginal association probabilities. In this context, we discuss a simplified version of the Linear Multitarget Integrated Probabilistic Data Association (LMIPDA) [10] algorithm that can be derived from the assignment model used in the Probabilistic Multi-Hypothesis Tracker (PMHT) filter [15, 16], and the Bakhtiar-Alavi algorithm, which can be derived based on a PMHT measurement model with switched measurement and target roles. Subsequently, we propose a novel fast approximation that exploits systematic combinations of the JPDAF measurement model with the PMHT measurement model in order get closer to the original JPDAF measurement model (with the cost of a slightly increased runtime).

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(a) Two targets $\boldsymbol{x}_1$ and $\boldsymbol{x}_2$, and three measurements $\boldsymbol{y}_1$, $\boldsymbol{y}_2$, and $\boldsymbol{y}_3$.

(b) Marginal association probability for fixed association measurement 1 to target 2.

Figure 1: Problem illustration: Marginal association probabilities.

2. PROBLEM FORMULATION

In this work, we consider the problem of approximating the marginal association probabilities in the Joint Probabilistic Data Association Filter (JPDAF) [3,4]. In order to simplify the discussion, we restrict ourselves to a specific point in time and strip out the dynamic components of the JPDAF. There are N targets with state vectors $\boldsymbol{x}_t$ with $t \in \mathcal{T} = \{1, \ldots, N\}$. For each target, a Gaussian probability density

$$p(\boldsymbol{x}_t) = \mathcal{N}(\boldsymbol{x}_t - \hat{\boldsymbol{x}}_t, \mathbf{C}_t) \tag{1}$$

is available, where $\hat{\boldsymbol{x}}_t$ is the mean and $\mathbf{C}_t$ is the covariance matrix. Furthermore, a set of M measurements

$$\mathcal{Y} = \{\boldsymbol{y}_m\}_{m \in \mathcal{M}} \ ,$$

where $m \in \mathcal{M} = \{1, \ldots, M\}$, is given. The measurements are related to the states according to the measurement equation

$$\boldsymbol{y}_m = \mathbf{H}_t \boldsymbol{x}_{\boldsymbol{a}(m)} + \boldsymbol{v}_m \qquad \text{if } \boldsymbol{a}(m) \neq 0 \ , \tag{2}$$

$$\boldsymbol{y}_m = \boldsymbol{c}_m \qquad \text{if } \boldsymbol{a}(m) = 0 \ , \tag{3}$$

where

- $\boldsymbol{a}(m) \in \mathcal{T}_0 := \mathcal{T} \cup \{0\}$ denotes the the origin of measurement $\boldsymbol{y}_m$ ($\boldsymbol{a}(m) = 0$ indicates clutter),
- $\mathbf{H}_t$ is the measurement matrix,
- $\boldsymbol{v}_m$ is white Gaussian noise with mean covariance matrix $\mathbf{P}_m$, and
- $\boldsymbol{c}_m$ models clutter, which is typically uniformly distributed in the surveillance area.

The JPDAF [4] assumes that each target gives rise to at most one measurement (per time). In the following, we will call this association model *1-2-1 model.* Furthermore, we make the simplifying assumption that the probability of detection is one, which is often made by fast approximation techniques for the marginal probabilities. As a consequence, there are $\binom{M}{N}N!$ feasible assignments for M measurements to N targets. If each assignment is a priori equally probable, the prior association probability is

$$p(\boldsymbol{a}) = \tfrac{1}{\binom{M}{N}N!} \tag{4}$$

for a valid assignment $\boldsymbol{a}$ and otherwise $p(\boldsymbol{a}) = 0$. The posterior association probability results from Bayes' theorem as

$$p(\boldsymbol{a}|\mathcal{Y}) = c_1 \cdot \prod_m p(\boldsymbol{y}_m \,|\, \boldsymbol{a}(m)) \cdot p(\boldsymbol{a}) \ , \tag{5}$$

where

$$
\begin{aligned}
p(\boldsymbol{y}_m \,|\, \boldsymbol{a}_m = t) &= \mathcal{N}(\boldsymbol{y}_m - \mathbf{H}\hat{\boldsymbol{x}}_t, \mathbf{P}_{\mathbf{m}} + \mathbf{C}_t) && (6)\\
&=: G_{m,t} && (7)
\end{aligned}
$$

denotes the likelihood that measurement m comes from target t and c_1 is a normalization constant (in the remainder we will always use c with an index to denote normalization constants).

For the update step of the JPDAF, it is necessary to calculate the marginal association probabilities $\beta_{i,j}$ that measurement $i \in \mathcal{M}$ originates from target (or clutter) $i \in \mathcal{T}_0$ according to

$$
\begin{aligned}
\beta_{i,j} &= p(\boldsymbol{a}(i) = j \,|\, \mathcal{Y}) && (8)\\
&= \sum_{\boldsymbol{a} \text{ with } \boldsymbol{a}(i)=j} p(\boldsymbol{a} \,|\, \mathcal{Y}) && (9)\\
&= c_1 \cdot \sum_{\boldsymbol{a} \text{ with } \boldsymbol{a}(i)=j} p(\boldsymbol{a}) \prod_m G_{m,a(m)} \quad . && (10)
\end{aligned}
$$

The exact calculation of (10) requires the enumeration of an exponential number of association hypotheses, which becomes computationally challenging already for few targets. In the remainder of this paper, we will discuss efficient approximate algorithms for the marginal association probabilities.

3. KEY IDEA

In order to illustrate the key idea, we first factor out the term $G_{m,t}$ in (10) as it occurs in each summand, which leads to

$$
\beta_{i,j} = c_1 \cdot G_{i,j} \sum_{\boldsymbol{a} \text{ with } \boldsymbol{a}(i)=j} p(\boldsymbol{a}) \prod_{m \in \mathcal{M}^i} G_{m,\boldsymbol{a}(m)} \quad , \tag{11}
$$

where $\mathcal{M}^i := \mathcal{M} \setminus \{i\}$ and $\mathcal{T}^j := \mathcal{T} \setminus \{j\}$ denote the measurement and target indices without i and j respectively.

If we now introduce a new association function $b : \mathcal{M}^i \to \mathcal{T}^j$ that coincides with the function $\boldsymbol{a}(\cdot)$ except for measurement i, we can write

$$
\beta_{i,j} = c_1 \cdot G_{i,j} \cdot \sum_{\boldsymbol{b}} p(\boldsymbol{b}) \prod_{m \in \mathcal{M}^i} G_{m,\boldsymbol{b}(t)} \quad , \tag{12}
$$

which is the same as

$$
\beta_{i,j} = c_1 \cdot G_{i,j} \cdot \sum_{\boldsymbol{b}} p(\mathcal{Y}^i \,|\, \boldsymbol{b}) \cdot p(\boldsymbol{b}) = c_1 \cdot \underbrace{G_{i,j}}_{(*)} \cdot \underbrace{\sum_{\boldsymbol{b}} p(\boldsymbol{b} \,|\, \mathcal{Y}^i)}_{(**)} \quad , \tag{13}
$$

where $\mathcal{Y}^i := \mathcal{Y} \setminus \{\boldsymbol{y}_i\}$. Note that this reformulation is exact, if $p(\boldsymbol{b}) = p(\boldsymbol{a})$ for all $\boldsymbol{a}(\cdot)$ with $\boldsymbol{a}(i) = j$. Hence, in order to calculate the marginal probability $\beta_{i,j}$ we have to calculate

(*) the probability that measurement i comes from target j, and

(**) the probability that all other measurements come from all other targets.

The second part is the computationally challenging part for which a huge variety of fast approximate methods have been proposed.

The underlying key idea to this paper is the following: *In order to calculate (2), we change the (computationally intractable) 1-2-1 association model to a different association model that, however, results in a non-exponential runtime.*

The association model is only modified for the associations to be marginalized out. Hence, altogether one obtains a model that is a mix between the JPDAF association model and the “fast” model. In particular, we will discuss the use of a

- many-2-1 association model as used in *Probabilistic Multi-Hypothesis Tracker (PMHT)* (Section 4). The resulting algorithm for the marginal association probabilities then basically corresponds to the LMIPDA algorithm [10],
- 1-2-many association model that results in the Bakhtiar-Alavi algorithm [2] in Section 5, and a
- hybrid model [5] in Section 6, which has not yet been used for the approximate calculation of marginal association probabilities.

4. MANY-2-1 MODEL: LMIPDAF

An alternative to the computationally complex (but physically correct) 1-2-1 association model used within the JPDAF, is the so-called many-2-1 model [1, 15], which assumes that the association variable specifying the origin of a given measurement is independent of all other measurements. A consequence of this independence assumption is that the resulting likelihood function can be efficiently evaluated as a product of sums. For example, the *Probabilistic Multi-Hypothesis Tracker (PMHT)* [15] and several multi-target particle filters [8, 9] are based on a many-2-1 model. Imposing the many-2-1 model for the marginal associations results in the same method as used within the LMIPDA [6, 10]. However, note that the LMIPDA [10] framework is more general than discussed here, e.g., it incorporates detection probabilities and unknown target existence.

For the marginal associations in (13), the a priori assignment probability under the many-2-1 model can be written as

$$p^{\mathrm{M21}}(\boldsymbol{b}) = \prod_{m \in \mathcal{M}^i} p^{\mathrm{M21}}(\boldsymbol{b}(m)) \ . \tag{14}$$

Due to the independence assumption, several measurements may be associated to one target. However, it also allows us to write

$$\begin{aligned} \sum_{\boldsymbol{b}} p(\boldsymbol{b}|\mathcal{Y}^i) \cdot p^{\mathrm{M21}}(\boldsymbol{b}) &= \sum_{\boldsymbol{b}} p^{\mathrm{M21}}(\boldsymbol{b}) \prod_{m \in \mathcal{M}^i} G_{m,\boldsymbol{b}(t)} & (15) \\ &= \prod_{m \in \mathcal{M}^i} \sum_{t \in \mathcal{T}_0^j} G_{m,t} \cdot \pi_t & (16) \end{aligned}$$

with

$$\pi_t := p^{\mathrm{M21}}(\boldsymbol{b}(m) = t) \ ,$$

which can be evaluated in linear time $O(NM)$ depending on the number of measurements and targets.

Altogether, the marginal association probability (9) then can be approximated with

$$\beta_{i,j} \approx c_2 \cdot G_{i,j} \prod_{m \in \mathcal{M}^i} \sum_{t \in \mathcal{T}_0^j} G_{m,t} \cdot \pi_t \ . \tag{17}$$

Using the shorthand notations

$$\begin{aligned} F_m &:= \sum_{j \in \mathcal{T}_0} G_{m,t} \cdot \pi_t \ , & (18) \\ H_t &:= \prod_{m \in \mathcal{M}} (F_m - G_{m,t} \cdot \pi_{m,t}) \ , & (19) \end{aligned}$$

(17) can be written as

$$\beta_{i,j} \approx c_2 \cdot G_{i,j} \cdot \frac{H_j}{F_i - G_{i,j} \cdot \pi_j} \ ,$$

which becomes

$$\beta_{i,j} \approx c_3(j) \cdot G_{i,j} \cdot \frac{1}{F_i - G_{i,j} \cdot \pi_j} \tag{20}$$

after incorporating factors independent of the measurements in the normalization constant. The overall runtime complexity is $O(NM)$ in order to calculate (20) for all targets $t \in \mathcal{T}_0$ and measurement $m \in \mathcal{M}$.

(a) Valid assignment. (b) Non-valid assignment.

Figure 2: Hybrid measurement model for given $t_1 = 1$ (left) and $t_2 = 3$ (right). Exactly one measurement has to be assigned to target t_1 (note that we assume detection probability of 1) [5].

$t_1 = 1$	meas 1	1	1	1	1	2	2	3	3	2	2	3	3
	meas 2	2	2	3	3	1	1	1	1	2	3	2	3
	meas 3	2	3	2	3	2	3	2	3	1	1	1	1
$t_1 = 2$	meas 1	2	2	2	2	1	1	3	3	1	1	3	3
	meas 2	1	1	3	3	2	2	2	2	1	3	1	3
	meas 3	1	3	1	3	1	3	1	3	2	2	2	2
$t_3 = 3$	meas 1	3	3	3	3	1	1	2	2	1	1	2	2
	meas 2	1	1	2	2	3	3	3	3	1	2	1	2
	meas 3	1	2	1	2	1	2	1	2	3	3	3	3

Table 1: Example [5] for hybrid assignments for the case of 3 targets and measurements. The top table indicates the targets to which the measurements are assigned for $t_1 = 1$, middle for $t_1 = 2$, and lower for $t_1 = 3$. For example, the assignment $[1, 2, 3]^T$ is enumerated three times (because of three unique targets), while $[2, 2, 1]^T$ is enumerated only once (because of one unique targets).

5. 1-2-MANY MODEL: BAKHTIAR-ALAVI

The many-2-1 approximation (17) looks quite similar to the Bakhtiar-Alavi algorithm [2] given by

$$\beta_{i,j} \approx c_4 \cdot G_{i,j} \prod_{t \in \mathcal{T}^j} \sum_{m \in \mathcal{M}^i \cup \{0\}} \left(G_{m,t} + G_{0,t}\delta(i) \right) \quad , \tag{21}$$

where $\delta(i)$ is the Kronecker delta function. However, there is a significant difference: The Bakhtiar-Alavi formula (21) is a product over all targets and a sum over all measurements. According to this finding, one could say that the Bakhtiar-Alavi formula (21) employs a *1-2-many assignment model*, which allows multiple targets to be assigned to the same measurement, i.e., it is a many-2-1 model with switched measurement and target roles.

Although not mentioned in the original work [2], the Bakhtiar-Alavi formula can be simplified in the same manner as the LMIPDA (17) in the previous section in order get an algorithm that calculates all weights in linear time.

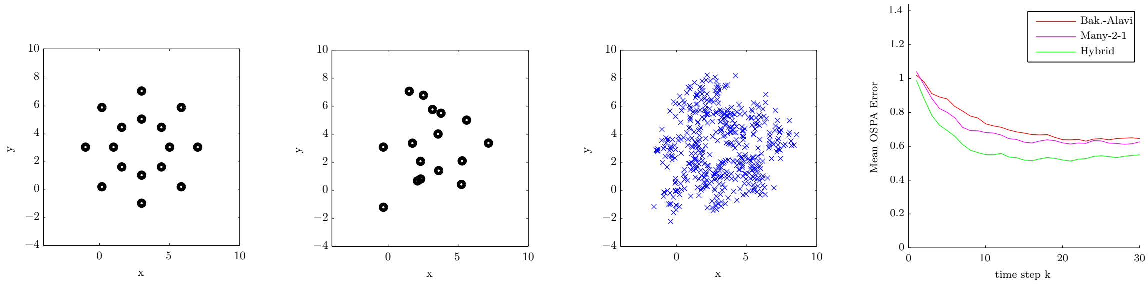
6. HYBRID MODEL: A NOVEL FORMULA

The recently introduced hybrid data association model [5] is closer to the 1-2-1 model of the JPDAF than the many-2-1 model but still has a polynomial runtime complexity. In the following, we employ a variant of the hybrid model that results in a quadratic runtime.

In order to motivate the hybrid model, we first restrict ourselves to the case where no false measurements may occur, i.e., $N = M$. The goal is to obtain the following prior association probabilities

$$p^{\text{hybrid}}(\boldsymbol{b}) = c_5 \cdot u(\boldsymbol{b}) \quad , \tag{22}$$

where u($\boldsymbol{b}$) denotes the number of targets in $\boldsymbol{b}$ that are assigned to exactly one measurement. For example, for the association $[\boldsymbol{b}(1), \boldsymbol{b}(2), \boldsymbol{b}(3)]^T = [2, 1, 1]^T$, we have $u(\boldsymbol{b}) = 1$ as only target 2 is associated with exactly one measurement.



(a) Initial target locations.

(b) Target locations (time step 30).

(c) All Measurements.

(d) Mean OSPA Error (over 30 runs).

Figure 3: Tracking results.

It is clear that the prior association probabilities (22) are "closer" to the 1-2-1 model than the many-2-1 model in the sense that they are biased towards associations with more unique assignments. Note that in case of equal weights, i.e., $\pi_t = \frac{1}{N}$, all assignments in the many-2-1 model are equally likely, i.e., $p^{\text{M21}}(\boldsymbol{b}) = \frac{1}{N^M}$.

The prior association probability (22) can be achieved by enforcing that the 1-2-1 model holds for one target (say t_1), where this target is selected uniformly from the set of targets, i.e., $p(t_1) = \frac{1}{N}$. For the remaining targets, the many-2-1 model is imposed, i.e., multiple assignments are allowed (see Fig. 2 and Tab. 1).

Technically, we then obtain in (13)

$$\sum_{\boldsymbol{b}} p(\boldsymbol{b} \,|\, \mathcal{Y}^i) \cdot p^{\text{hybrid}}(\boldsymbol{b}) \quad = \quad c_6 \cdot \sum_{m_1 \in \mathcal{M}^i} \sum_{t_1 \in \mathcal{T}^j} G_{m_1,t_1} \prod_{m_2 \in \mathcal{M}^{i,m_1}} \sum_{t_2 \in \mathcal{T}_0^{j,t_1}} G_{m_2,t_2} \tag{23}$$

with $\mathcal{M}^{i,m_1} := \mathcal{M} \backslash \{i, m_1\}$ and $\mathcal{T}^{j,t_1} := \mathcal{T} \backslash \{j, t_1\}$, which sums over all targets t_1 and measurements m_1, enforces the 1-2-1 mapping G_{m_1,t_1}, and uses the many-2-1 model for all other targets and measurements. Based on this approximation, we obtain the approximate marginal association probability

$$\beta_{i,j} \approx c_7 \cdot G_{i,j} \cdot \sum_{m_1 \in \mathcal{M}^i} \sum_{t_1 \in \mathcal{T}_0^j} G_{m_1,t_1} \prod_{m_2 \in \mathcal{M}^{i,m_1}} \sum_{t_2 \in \mathcal{T}_0^{j,t_1}} G_{m_2,t_2} \ . \tag{24}$$

Similarly to the many-2-1 model in Section 4, we can simplify (24) by defining

$$F_m \quad := \quad \sum_{j \in \mathcal{T}_0} G_{m,t} \ , \ \text{and} \tag{25}$$

$$H_{t_1,t_2} \quad := \quad \prod_{m \in \mathcal{M}} (F_m - G_{m,t_1} - G_{m,t_2}) \ , \tag{26}$$

so that

$$\beta_{i,j} \approx c_7 \cdot G_{i,j} \sum_{m \in \mathcal{M}^i} \sum_{t \in \mathcal{T}_0^j} G_{m,t} \frac{H_{j,t}}{(F_i - G_{i,j} - G_{i,t}) \cdot (F_m - G_{m,j} - G_{m,t})} \ , \tag{27}$$

which yields a quadratic time complexity (in both number of targets and measurements) for computing all weights, i.e., $O(N^2 M^2)$.

Note that (27) contains a product of likelihoods that might be close to zero. In order to avoid numerical problems, it might be suitable to work with logarithms. Also, for the sake of numerical stability, it can be useful to pragmatically set $H_{j,t} = 1$ in (27).

7. EVALUATION

The performance of the discussed approximations for the marginal association probabilities is assessed in a tracking scenario with 16 closely-spaced targets that evolve according to a random walk model in two-dimensional Cartesian space, i.e., the dimension of the state vector is two and the system model is

$$\boldsymbol{x}_t(k+1) = \boldsymbol{x}_t(k) + \boldsymbol{w}_t(k) \ ,$$

where $\boldsymbol{w}_t(k)$ is zero-mean Gaussian noise with covariance matrix $0.02\,\mathbf{I}_2$ in which $\mathbf{I}_2$ is the two-dimensional identity matrix. We assume that two-dimensional position measurements of the targets are available, i.e., the measurement function is

$$\boldsymbol{y}_m(k) = \boldsymbol{x}_t(k) + \boldsymbol{v}_m(k) \ ,$$

where the covariance of $\boldsymbol{v}_m(k)$ is $0.3\,\mathbf{I}_2$. No false measurements are considered in this scenario.

The initial track estimates have a covariance $\Sigma_t^x = \mathbf{I}_2$ and the initial mean is sampled randomly from $\mathcal{N}(\tilde{\boldsymbol{x}}_t - \mathbf{0}, \Sigma_t^x)$, where $\tilde{\boldsymbol{x}}_t$ denotes the true initial target position.

The true targets locations are initially arranged as indicated in Fig. 3a and the final locations after 30 time steps are shown in Fig. 3b. The entire set of measurements received over this period of time are depicted in Fig. 3c. The performance of both filters is measured with the *Optimal Sub-Pattern Assignment (OSPA)* metric [14]. The averaged OSPA distance over 30 Monte Carlo runs is shown in Fig. 3d. It can be seen that the hybrid approximation outperforms the other approximations in this scenario. This is reasonable as the hybrid model is closer to the true model, however, it comes with the price of a slightly higher runtime. Also, it must be stressed that all methods are approximations so that a general statement about the quality is difficult – meaning in different scenarios the results may be different.

8. CONCLUSIONS

In this work, we considered efficient methods for approximating the marginal association probabilities in the JPDAF algorithm. The key idea pursued was to change the original association model to a “wrong” but computational feasible model. A reasonable choice for this association model is given by the so-called many-2-1 model used within the PMHT filter, which leads here to a simplified version of the LMIPDA filter. We have shown that further be improvements are possible with the price of a slightly higher computational complexity by means of imposing a hybrid approach that systematically combines 1-2-1 and many-2-1 associations. In general, the hybrid approach can be further improved by enforcing the 1-2-1 model for more than one target [5], however, the runtime complexity then further increases, too. Also note that the discussed methods are not coalescence avoiding [13].

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