Calculating Some Exact MMOSPA Estimates for Particle Distributions

Marcus Baum*, Peter Willett†, and Uwe D. Hanebeck*

† University of Connecticut, USA

* Intelligent Sensor-Actuator-Systems Laboratory (ISAS), Institute for Anthropomatics,

Karlsruhe Institute of Technology (KIT), Germany.

Email: marcus.baum@kit.edu, willett@engr.uconn.edu, uwe.hanebeck@ieee.org

Abstract—In this work, we present some exact algorithms for calculating the minimum mean optimal sub-pattern assignment (MMOSPA) estimate for probability densities that are represented with particles. First, a polynomial-time algorithm for two targets is derived by reducing the problem to the enumeration of the cells of a hyperplane arrangement. Second, we present a linear-time algorithm for an arbitrary number of scalar target states, which is based on the insight that the MMOSPA estimate coincides with the mean of the order statistics.

NOTATION

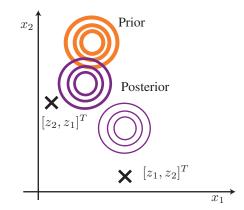|	
$\underline{x}$	Vectors are underlined
$(\underline{x})_i$	i-th component of $\underline{x}$
$\underline{\boldsymbol{x}}$	Random variables are printed in bold
$\langle \cdot, \cdot \rangle$	Scalar product
$\hat{\underline{x}}$	Point estimate
π	Permutation
$\mathcal{O}(\cdot)$	Big $\mathcal{O}$ notation
$\mathcal{Y}$	Measurements
S^d	Unit sphere in d-dimensional space
n	Number of targets
d	Dimension of a target state
N_p	Number of particles
$\gamma(\cdot)$	Sign vector for hyperplane arrangement

I. INTRODUCTION

In multi-object estimation cases – these could be "tracking" problems, although the concepts are best understood with the dynamic elements stripped out – measurement origin uncertainty (MOU) necessarily gives rise to uncertainty in target labeling. For example, consider two targets in one-dimensional space as depicted in Fig. 1a. If target 1 has a prior probability biased toward the left and likewise target 2 to the right, and if there are two (unlabeled) measurements, one close to target 1 and the other to target 2, then the posterior inference will likely cause the left/right bias to persist; but the event of a cross-over must be considered, meaning that the true posterior must be multimodal, see Fig. 1b. Consider estimation in such a case: the maximum a-posteriori (MAP) estimator must choose between modes (and, hence, ignore information about the lesser), while the minimum mean square error (MMSE) estimator can be between modes, and, hence, almost certainly nowhere near the jointly-specified "target" (see also [1], [2]).

(a) Two targets with states x_1 and x_2 from which two measurements z_1 and z_2 are received (with unknown origin).

(b) Joint density for two targets: The prior is as indicated, and comprises no uncertainty as to labeling. MOU in the measurements, however, does: the posterior is bimodal and, hence, the MMSE estimate is of little relevance.

Fig. 1: Notional figure describing a two-object scalar estimation problem.

An alternative is to eschew any pretense of estimating the (labeled) locations of target 1 and target 2, and simply to ask: "Where are there objects?" To seek an MMSE estimate makes no sense in this case, since MSE requires labels. However, we consider the path to the MMSE estimate: there is the squared-error (SE) metric, the criterion of interest is the mean square error (MSE) criterion; and the MMSE optimal estimator. As will be soon discussed, there has recently arisen a *label-free metric*, the optimal sub-pattern assignment (OSPA) metric [3], upon which the criterion MOSPA and optimal MMOSPA approach can be built [4].

The MMSE estimate has an explicit expression, the mean of the posterior; MMOSPA estimation is more complex. Earlier theory does provide an explicit expression, but unfortunately one that chases its own tail: it is the mean of a partic-

ular density, which depends on the MMOSPA estimate as part of its definition. How can one calculate the MMOSPA estimate? In fact it has earlier been shown that this "circular" definition can be obviated through iteration (that is: successively approximation to the MMOSPA) [4] and Monte Carlo integration. Additionally, an explicit expression was earlier derived for the two-object Gaussian case; and a decent approximation is available for Gaussian mixtures. In [5], [6], a greedy suboptimal algorithm for particles was introduced, which successively determines orderings. Furthermore, the problem was formulated as an S-D assignment problem in [5] and continuous quadratic semi-assignment formulations were given in [5], [7]. In [8], it was suggested to use importance sampling and [9] presented a closed-form approximation of the MOSPA integral for Gaussian Mixtures based on the Chernoff bound. Explicit solutions are currently available only for the scalar case [5], [10].

Contribution

In this paper – though a general solution remains to be found – we explore *exact* solutions for cases in which the probability densities are represented as "particles," meaning as mixtures of δ-functions. We present exact and reasonably efficient algorithms for two objects in arbitrary dimension with a runtime complexity that is polynomial in the number of particles. We also explore the relationship between MMOSPA and order statistics in one dimension: perhaps not surprisingly, an imposed ordering (sorting) considerably simplifies the estimation procedure and yields a linear-time algorithm.

II. PROBLEM DESCRIPTION

We consider Bayesian multi-object estimation problems in which the state of multiple targets is modeled as a random vector[1]

$$\boldsymbol{x} = \left[\boldsymbol{x}_1^T, \ldots, \boldsymbol{x}_n^T\right]^T ,$$

where $\boldsymbol{x}_i \in \mathbb{R}^n$ denotes the state vector of target i (with $1 \leq i \leq N$). Bayesian tracking algorithms maintain a probability density function for $\boldsymbol{x}$ conditioned on the available measurements $\mathcal{Y}$

$$p\left(\underline{x}|\mathcal{Y}\right) . \tag{1}$$

Typically, only an approximation of the true density is available, e.g., the *Joint Probabilistic Data Association Filter (JPDAF)* [11] uses a Gaussian approximation and the *Multiple Hypotheses Tracker (MHT)* [12] maintains a Gaussian mixture. In this work, we focus on particle filter methods [13], [14] that represent (1) with particles.

Although the posterior probability density (1) contains all available information about the target states, one is usually interested in a point estimate for the target states, i.e., a single deterministic value that summarizes the information encoded in the posterior density. For example, a point estimate is required for displaying the tracks [5].

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1 The time index is omitted here.

In general, a point estimate minimizes a specific risk function such as the widely-used mean square error (MSE), which yields the so-called minimum mean square error (MMSE) estimate [15]

$$\hat{\underline{x}}^{\mathrm{MMSE}} := \arg\min_{\hat{\underline{x}}} \mathrm{E}\big\{||\hat{\underline{x}} - \underline{x}||^2 |\mathcal{Y}\big\} .$$

It is well known that the MMSE estimate is given by the conditional mean $\hat{\underline{x}}^{\mathrm{MMSE}} = \mathrm{E}\{\underline{x}|\mathcal{Y}\}$.

The MSE is a standard risk function in Bayesian estimation theory. However, it may be unsuitable for multi-object estimation as described in the introduction. In order to overcome this problem, it was suggested in [4], [16], [17] to abandon the target labels by using a different risk function than the MSE, namely the mean optimal sub-pattern assignment (MOSPA). This risk function is based on the OSPA metric [3], which is a widely-used measure for evaluating multi-target tracking algorithms. The OSPA metric is quite general. In this work, we only need a special version of the OSPA metric for a known number of targets as defined in the following.

Definition 1 (OSPA). The *optimal sub-pattern assignment (OSPA)* [3] distance between the two vectors $\underline{x} = [\underline{x}_1^T, \ldots, \underline{x}_n^T]^T$ and $\underline{y} = [\underline{y}_1^T, \ldots, \underline{y}_n^T]^T$, which consist of n target state vectors of dimension d, is defined as

$$d^{\mathrm{OSPA}}(\underline{x}, \underline{y}) := \frac{1}{n} \min_{\pi \in \Pi_n} \sum_i ||\underline{x}_i - \underline{y}_{\pi(i)}||^2 , \tag{2}$$

where Π_n denotes all permutations of the set $\{1, \ldots, n\}$.

Remark 1. We also write

$$d^{\mathrm{OSPA}}(\underline{x}, \underline{y}) = \frac{1}{n} \min_{\pi \in \Pi_n} ||\underline{x}_i - P_\pi(\underline{y})||^2 ,$$

where $P_\pi(\underline{y})$ permutes the single target states in $\underline{y}$ according to π, i.e., $P_\pi(\underline{y}) = [\underline{y}_{\pi(1)}^T, \ldots, \underline{y}_{\pi(n)}^T]^T$. Furthermore, a permutation π can be written in vector notation $\big(\pi(1) \quad \pi(2) \quad \ldots \quad \pi(n)\big)$.

Remark 2. The minimizing permutation in (2) is denoted with π_{opt}.

In analogy to MMSE estimation, the MOSPA and MMOSPA estimate can be defined [4] as follows.

Definition 2 (MOSPA). The *mean optimal sub-pattern assignment (MOSPA)* error [4] for the joint target state vector $\boldsymbol{x} = [\boldsymbol{x}_1^T, \ldots, \boldsymbol{x}_n^T]^T$ with posterior probability density $p(\underline{x}|\mathcal{Y})$ and a point estimate $\hat{\underline{x}}$ is defined as

$$\mathrm{MOSPA}(p(\underline{x}|\mathcal{Y}), \hat{\underline{x}}) := \mathrm{E}\big\{d^{\mathrm{OSPA}}(\boldsymbol{x}, \hat{\underline{x}})\big\}_{p(\underline{x}|\mathcal{Y})} .$$

Definition 3 (MMOSPA). The *minimum mean optimal sub-pattern assignment (MMOSPA)* [4] for $\boldsymbol{x} = [\boldsymbol{x}_1^T, \ldots, \boldsymbol{x}_n^T]^T$ with posterior probability density $p(\underline{x}|\mathcal{Y})$ is defined as

$$\hat{\underline{x}}^{\mathrm{MMOSPA}} := \arg\min_{\hat{\underline{x}}} \mathrm{E}\big\{d^{\mathrm{OSPA}}(\boldsymbol{x}, \hat{\underline{x}})\big\}_{p(\underline{x}|\mathcal{Y})} .$$

Remark 3. Note that there are $n!$ MMOSPA estimates, because each permutation of $\hat{\underline{x}}^{\mathrm{MMOSPA}}$ is also a MMOSPA estimate.

Remark 4. The MMOSPA estimate $\hat{\underline{x}}^{\text{MMOSPA}}$ can be written as $\hat{\underline{x}}^{\text{MMOSPA}} = \text{E}\left\{ P_{\pi_{opt}^{\text{MMOSPA},\boldsymbol{x}}}(\boldsymbol{x})|\mathcal{Y} \right\}$, where $\pi_{opt}^{\text{MMOSPA},\boldsymbol{x}} := \arg\min_{\pi \in \Pi_n} \frac{1}{n}||\hat{\underline{x}}^{\text{MMOSPA}} - P_\pi(\underline{x})||^2$ denotes the optimal permutation with respect to the MMOSPA estimate.

Note that an unlabeled covariance matrix can be defined in order to describe the uncertainty of the MMOSPA estimate. The unlabeled covariance matrix can easily be computed when the MMOSPA estimate is given (see [6]). Furthermore, although the MMOSPA estimate ignores the target labels, it is possible to extract labeling information [6].

All multi-target tracking algorithms have to perform approximations. Usually, these approximations are performed with regards to the MSE. However, when the MOSPA is used instead of the MSE, the approximation techniques can be tailored to the MOSPA. For example, the *Set JPDAF* [16], [17] and *Set MHT* [6] are MOSPA variants of *JPDAF* [11] and *MHT* [12].

III. Two Targets in d-Dimensional Space

In this section, we derive polynomial-time algorithms for computing the exact MMOSPA estimate for two targets when the probability distribution is represented with particles. The algorithms exploit the fact that it is sufficient to optimize over all direction vectors in order to find the MMOSPA estimate (see Section III-A). It can be shown that there is only a polynomial number of feasible directions (see Section III-B) for densities represented with particles. By this means, the problem is reduced to enumerating the cells of a hyperplane arrangement, which is a well-known problem in geometry and combinatorics [18]. This problem can be interpreted as *cake-cutting*: Determine the pieces into which a cake can be sectioned with a particular number of cuts.

In general, the worst-case complexity for d-dimensional target states is $\mathcal{O}(N_p^d)$, where N_p is the number of particles. We give concrete (simple) algorithms for

- 2D states with complexity $\mathcal{O}(N_p \log N_p)$, and for
- 3D states with complexity $\mathcal{O}(N_p^3)$.

A. Optimization over Directions

The following theorem states that the optimal permutation for computing the OSPA distance between two state vectors for two targets is fully determined by two direction vectors (see Fig. 2a).

Theorem 1. *The OSPA metric for* $\underline{x} = [\underline{x}_1^T, \underline{x}_2^T]^T$ *and* $\underline{y} = [\underline{y}_1^T, \underline{y}_2^T]^T$ *(two d-dimensional target states) is given by*

$$d^{OSPA}(\underline{x}, \underline{y}) = \frac{1}{n}||\underline{y} - P_{\pi_{opt}}(\underline{x})||^2 \ , \qquad (3)$$

where the optimal permutation π_{opt} *is given by*

$$\pi_{opt} = \left\{ \begin{array}{ll} \begin{pmatrix} 1 & 2 \end{pmatrix} & \text{if } \underline{a}^T\underline{b} \geq 0 \\ \begin{pmatrix} 2 & 1 \end{pmatrix} & \text{otherwise} \end{array} \right. ,$$

with $\underline{a} := \frac{\underline{y}_1 - \underline{y}_2}{||\underline{y}_1 - \underline{y}_2||}$ *and* $\underline{b} := \frac{\underline{x}_1 - \underline{x}_2}{||\underline{x}_1 - \underline{x}_2||}$. *Hence, the target states in* $\underline{x}$ *are switched if the direction vectors* $\underline{a}$ *and* $\underline{b}$ *point in opposite directions.*[2]

PROOF. The optimal permutation π_{opt} of $\underline{x}$ is $\begin{pmatrix} 1 & 2 \end{pmatrix}$ iff

$$\begin{array}{rcl} ||\underline{x}_1 - \underline{y}_1||^2 + ||\underline{x}_2 - \underline{y}_2||^2 & \leq & ||\underline{x}_1 - \underline{y}_2||^2 + ||\underline{x}_2 - \underline{y}_1||^2 \\ & \Updownarrow & \\ -2\langle \underline{x}_1, \underline{y}_1 \rangle - 2\langle \underline{x}_2, \underline{y}_2 \rangle & \leq & -2\langle \underline{x}_1, \underline{y}_2 \rangle - 2\langle \underline{x}_2, \underline{y}_1 \rangle \\ & \Updownarrow & \\ \langle \underline{x}_2 - \underline{x}_1, \underline{y}_1 \rangle & \leq & \langle \underline{x}_2 - \underline{x}_1, \underline{y}_2 \rangle \\ & \Updownarrow & \\ 0 & \leq & \langle \underline{x}_2 - \underline{x}_1, \underline{y}_2 - \underline{y}_1 \rangle \\ & \Updownarrow & \\ 0 & \leq & \langle \frac{\underline{x}_2 - \underline{x}_1}{||\underline{x}_2 - \underline{x}_1||}, \frac{\underline{y}_2 - \underline{y}_1}{||\underline{y}_2 - \underline{y}_1||} \rangle \end{array}$$

$\square$

The above theorem can be used to show that it is sufficient to know the direction vector specified by the MMOSPA estimate in order to determine the corresponding permutations of $p(\underline{x}|\mathcal{Y})$.

Remark 5. We define the operation

$$\text{sort}_{\underline{a}}(\underline{x}) = \left\{ \begin{array}{ll} [\underline{x}_1^T, \underline{x}_2^T]^T & \text{if } \underline{a}^T\underline{x} \geq 0 \\ [\underline{x}_2^T, \underline{x}_1^T]^T & \text{otherwise} \end{array} \right. ,$$

where $\underline{a}$ is a direction vector.

Theorem 2. *For a random vector* $\boldsymbol{x} = [\boldsymbol{x}_1^T, \boldsymbol{x}_2^T]^T$, *which consists of two d-dimensional single target states and a corresponding posterior density* $p(\underline{x}|\mathcal{Y})$, *the MMOSPA estimate* $\hat{\underline{x}}^{\text{MMOSPA}}$ *is given by*

$$\hat{\underline{x}}^{\text{MMOSPA}} = \text{E}\{\text{sort}_a(\boldsymbol{x})|\mathcal{Y}\} \ ,$$

where $\underline{a} := \frac{\hat{\underline{x}}_2^{\text{MMOSPA}} - \hat{\underline{x}}_1^{\text{MMOSPA}}}{||\hat{\underline{x}}_2^{\text{MMOSPA}} - \hat{\underline{x}}_1^{\text{MMOSPA}}||}$.

PROOF. The MMOSPA estimate is given by

$$\begin{array}{rcl} \hat{\underline{x}}^{\text{MMOSPA}} & = & \text{E}\left\{ P_{\pi_{opt}^{\text{MMOSPA},\boldsymbol{x}}}(\boldsymbol{x})|\mathcal{Y} \right\} \\ & = & \text{E}\{\text{sort}_a(\boldsymbol{x})|\mathcal{Y}\} \ , \end{array}$$
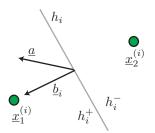
where $\pi_{opt}^{\text{MMOSPA},\boldsymbol{x}}$ denotes the optimal permutation of $\underline{x}$ with respect to the MMOSPA estimate. $\square$

A consequence of this theorem is that finding the MMOSPA estimate for two targets in d-dimensional space is a $(d-1)$-dimensional optimization problem over all possible direction vectors $\underline{a} \in S^d$, where the set of all direction vectors is denoted with $S^d := \{\underline{x} \in \mathbb{R}^d \mid ||\underline{x}|| = 1\}$. In other words: the direction vector that yields the minimum MOSPA error has to be found.

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2   W.l.o.g., we assume that $\underline{y}_1 \neq \underline{y}_2$ and $\underline{x}_1 \neq \underline{x}_2$.

(a) Illustration of Theorem 1. Both vectors $\underline{a}$ and $\underline{b}$ point to the same direction, i.e., $\langle \underline{a}, \underline{b} \rangle > 0$. Hence, no switching is performed.

(b) Illustration of Theorem 3. For all $\underline{a} \in h_i^+$ no switching of $\underline{x}_1^{(i)}$ and $\underline{x}_2^{(i)}$ is performed and for all $\underline{a} \in h_i^-$, the target states are switched.

Fig. 2: Optimization over directions.

B. Exact Algorithm: Particles for Two Targets

Based on Theorem 2, we derive an exact algorithm for the case that the posterior density (1) is specified by a mixture of δ-functions

$$p(\underline{x}|\mathcal{Y}) = \sum_{i=1}^{N_p} w_i \cdot \delta(\underline{x} - \underline{x}^{(i)}) \qquad (4)$$

and $\underline{x} = [x_1^T, x_2^T]^T$ consists of two d-dimensional target states. The MOSPA of (4) is given by [10]

$$\text{MOSPA}(p(\underline{x}|\mathcal{Y}), \hat{\underline{x}}) := \frac{1}{n} \sum_{i=1}^{N_p} w_i \cdot \min_{\pi_i} ||\hat{\underline{x}} - P_{\pi_i}(\underline{x}^{(i)})||^2,$$

where π_i denotes the permutation of the i-th particle. The naïve approach for computing MMOSPA estimates for particles is to check all possible permutations π_i, i.e., 2^{N_p} possibilities for two targets. We will show in the following that it is possible to significantly reduce the number of feasible permutations.

According to Theorem 2, the MMOSPA estimate can be found by calculating the MOSPA error for all direction vectors. The next theorem shows that it is only necessary to try a polynomial number of directions in case of particles.

Theorem 3. *Suppose we are given the random vector $\underline{x} = [\underline{x}_1^T, \underline{x}_2^T]^T$, which consists of two d-dimensional single target states and a corresponding posterior density*

$$p(\underline{x}|\mathcal{Y}) = \sum_{i=1}^{N_p} w_i \cdot \delta(\underline{x} - \underline{x}^{(i)}) \ .$$

Then there is a set of N_a direction vectors $A = \{\underline{a}_1, \ldots, \underline{a}_{N_a}\}$ such that

$$\{ \, \mathrm{E}\{\text{sort}_a(\underline{x})|\mathcal{Y}\} \mid \underline{a} \in S^d \, \} = \{ \, \mathrm{E}\{\text{sort}_a(\underline{x})|\mathcal{Y}\} \mid \underline{a} \in A \, \}$$

and the number of direction vectors N_a can be bounded by a polynomial depending on the number of particles N_p, i.e.,

$$N_a \in \mathcal{O}((N_p)^{d-1}) \ .$$

PROOF. Each particle $\underline{x}^{(i)} \in \mathbb{R}^{2d}$ defines a hyperplane in $\mathbb{R}^d$

$$h_i := \{a \in \mathbb{R}^d \mid \underline{b}_i^T a = 0\} \ , \qquad (5)$$

where

$$\underline{b}_i := \frac{\underline{x}_1^{(i)} - \underline{x}_2^{(i)}}{||\underline{x}_1^{(i)} - \underline{x}_2^{(i)}||}$$

is the unit vector that connects the two target states, see Fig. 2b for a visualization. Each hyperplane partitions $\mathbb{R}^d$ into three sets

$$
\begin{aligned}
h_i^+ &= \{\underline{a} \in \mathbb{R}^d \mid \underline{b}_i^T \underline{a} > 0\} \ , \\
h_i^0 &= \{\underline{a} \in \mathbb{R}^d \mid \underline{b}_i^T \underline{a} = 0\} \ , \\
h_i^- &= \{\underline{a} \in \mathbb{R}^d \mid \underline{b}_i^T \underline{a} < 0\} \ .
\end{aligned}
$$

The set of all hyperplanes

$$\mathcal{A} = \{h_i \mid i = 1, \ldots, N_p\}$$

is called the *central arrangement of hyperplanes* (see [18]) since all hyperplanes pass through the origin. The arrangement is composed of unbounded d-dimensional regions we shall call *cells*. Each point $\underline{a} \in \mathbb{R}^d$ can be labeled with a sign vector $\gamma(\underline{a}) \in \{-, 0, +\}^{N_p}$, whose i-th component is defined as

$$(\gamma(\underline{a}))_i := \begin{cases} - & \text{if } \underline{a} \in h_i^- \\ 0 & \text{if } \underline{a} \in h_i^0 \\ + & \text{if } \underline{a} \in h_i^+ \end{cases} \ .$$

Each cell of an arrangement can be uniquely represented by a sign vector $\underline{s} \in \{-, +\}^{N_p}$. The key observation is that $\text{sort}_a(\underline{x}^{(i)})$ is the same for all direction vectors $\underline{a}$ in a particular half-space h_i^+ and h_i^- according to Theorem 1. Hence, for all $\underline{a}_1, \underline{a}_2 \in S^d$ the following holds:

$$
\begin{aligned}
\gamma(\underline{a}_1) = \gamma(\underline{a}_2) \quad &\Rightarrow \quad \text{For all } i \in \{1, \ldots, N_p\} : \\
&\qquad \text{sort}_{a_1}(\underline{x}^{(i)}) = \text{sort}_{a_2}(\underline{x}^{(i)}) \\
&\Rightarrow \quad \mathrm{E}\{\text{sort}_{a_1}(\underline{x})|\mathcal{Y}\} = \mathrm{E}\{\text{sort}_{a_2}(\underline{x})|\mathcal{Y}\} \ .
\end{aligned}
$$

As a consequence, we can enumerate the cells $\mathcal{C}_1, \ldots, \mathcal{C}_{N_a}$ and pick $\underline{a}_i \in \mathcal{C}_i$. Furthermore, the number of cells of a central arrangement of N_p hyperplanes is known to be bounded by (see [18])

$$N_a < 2 \sum_{k=0}^{d-1} \binom{N_p - 1}{k} \in \mathcal{O}((N_p)^{d-1}) \ .$$

$\square$

Based on Theorem 2 and Theorem 3, the MMOSPA estimate can be computed by enumerating the cells of a hyperplane arrangement. Note that it is not necessary to explicitly compute the set A, because a sign vector $\underline{s} \in \{-,+\}^{N_p}$ is sufficient to determine the permutation of the particles, i.e.,

$$\pi_i^{\underline{s}} := \begin{cases} (1 \quad 2) & \text{if } (\underline{s})_i = + \\ (2 \quad 1) & \text{if } (\underline{s})_i = - \end{cases}$$

for all $i \in \{1, \ldots, N_p\}$. Furthermore, the sign vectors of a central arrangement of hyperplanes are symmetric, i.e., $\underline{s} \in \delta(\mathbb{R}^d) \Rightarrow -\underline{s} \in \delta(\mathbb{R}^d)$. Hence, we actually only have to enumerate half of the cells, because the resulting MMOSPA estimates are the same for $\underline{s}$ and $-\underline{s}$.

Algorithms for enumerating the cells of a d-dimensional hyperplane arrangement are described in [18], [19]. There are algorithms that are optimal in the sense that they enumerate each cell exactly once. For each of these cells, the MOSPA error has to be computed in order to find the cell with the minimum MMOSPA error. Hence, the *exact* MMOSPA estimate for two arbitrary dimensional target states can be computed with an overall runtime complexity of $\mathcal{O}(N_p^d)$.

As cell enumeration algorithms [18], [19] for arbitrary dimensional arrangements are in general rather complicated, we propose two simple algorithms for the 2D and 3D case.

C. Two-dimensional States

For 2D target states, a very simple algorithm for enumerating the cells can be found, because hyperplanes in 2D can be ordered according to their orientation. This observation is used in Algorithm 1 to compute the MMOSPA estimate for two 2D target states.

Remark 6. In order to avoid case distinctions in Algorithm 1, we assume that there are no duplicate hyperplanes h_i and no hyperplane coincides with the x-axis.

The complexity for sorting the hyperplanes is $\mathcal{O}(N_p \log N_p)$. For each cell, the MOSPA error has to be computed (Line 8 in Algorithm 1). Hence, the overall complexity of Algorithm 1 is $\mathcal{O}(N_p^2)$ with a naïve implementation of line 8.

Due to the ordering of the hyperplanes, the MMOSPA error does not have to be computed from scratch for each $\underline{s} \in S$ and line 8 can be implemented in linear time. As a consequence, the overall complexity becomes $\mathcal{O}(N_p \log N_p)$.

D. Three-dimensional States

In order to compute the MMOSPA estimate for two 3D target states, it is necessary to enumerate the cells of a 3D central hyperplane arrangement. A 3D central arrangement of hyperplanes can be considered as 2D non-central hyperplane arrangement by means of intersection with the 3D unit sphere S^3 (see Fig. 3b). The basic idea is to calculate all vertices in the arrangement and enumerate the adjacent cells [19] as described in Algorithm 2. For a so-called *non-degenerate* [19] arrangement there are always four adjacent cells. Otherwise the algorithm for 2D central arrangements can be used for enumerating adjacent cells. Again, for each cell, the MOSPA
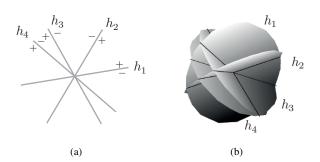

Fig. 3: Central arrangements of hyperplanes in 2D (a) and 3D (b).

Algorithm 1 Two 2D targets:
MMOSPA estimate for $p(\underline{x}|\mathcal{Y}) = \sum_{i=1}^{N_p} w_i \cdot \delta(\underline{x} - \underline{x}^{(i)})$

1: **Assumption:** $\underline{x}^{(i)}$ are sorted such that $\beta_1 \leq \ldots \leq \beta_{N_p}$, where $\beta_i \in (0, \pi)$ is the angle between the x-axis and hyperplane $\underline{h}_i$ (as defined in (5)).
2: $\underline{s} = \gamma([1,0]^T)$ // Sign vector of first cell
3: $\mathcal{S} = \{\underline{s}\}$
4: **for** $i = 1, \ldots, N_p - 1$ **do**
5:    $(\underline{s})_i := -(\underline{s})_i$ // Sign vector of next cell
6:    $\mathcal{S} = \mathcal{S} \cup \{\underline{s}\}$
7: **end for**
8: $\underline{s}_{min} = \arg\min_{\underline{s} \in S}\{\text{MOSPA}(p(\underline{x}|\mathcal{Y}), \hat{\underline{x}}^{\underline{s}})\}$, where $\hat{\underline{x}}^{\underline{s}} := \sum_{i=1}^{N_P} w_i \cdot P_{\pi^s}(\underline{x}^{(i)})$
9: **return** $\hat{\underline{x}}^{\underline{s}_{min}}$

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has to be computed in order to find the MMOSPA. If the number of adjacent cells is bounded, the overall complexity of this algorithm is $\mathcal{O}(N_p^3)$. Note that this is a very simple algorithm, there are more efficient (but more complicated) algorithms.

Algorithm 2 Two 3D targets:
MMOSPA estimate for $p(\underline{x}|\mathcal{Y}) = \sum_{i=1}^{N_p} w_i \cdot \delta(\underline{x} - \underline{x}^{(i)})$

1: $\mathcal{S} = \{\}$
2: **for** all vertexes $\underline{v}$ in $S^3 \cap \bigcap_i \underline{h}_i$ **do**
3:    $\underline{s} := \gamma(\underline{v})$
4:    $S := \mathcal{S} \cup \text{adjacentCells}(s)$
5: **end for**
6: $\underline{s}_{min} = \arg\min_{\underline{s} \in S}\{\text{MOSPA}(p(\underline{x}|\mathcal{Y}), \hat{\underline{x}}^{\underline{s}})\}$, where $\hat{\underline{x}}^{\underline{s}} := \sum_{i=1}^{N_P} w_i P_{\pi^s}(\underline{x}^{(i)})$
7: **return** $\hat{\underline{x}}^{\underline{s}_{min}}$

IV. MMOSPA ESTIMATES AND ORDER STATISTICS

In this section, we highlight an interesting connection between MMOSPA estimation and order statistics for the case of one-dimensional (1D) target states. First, we show that the OSPA distance for one-dimensional target states can be computed by sorting the state vectors. Then, we prove that

the MMOSPA estimate coincides with the mean of the order statistics.

Theorem 4. *The OSPA metric for two vectors $\underline{x} = [x_1, \ldots, x_n]^T$ and $\underline{y} = [y_1, \ldots, y_n]^T$ of n one-dimensional target states is given by*

$$d^{OSPA}(\underline{x}, \underline{y}) = \frac{1}{n} \| \operatorname{sort}(\underline{x}) - \operatorname{sort}(\underline{y}) \|^2 , \qquad (6)$$

where the operator $\operatorname{sort}(\cdot)$ *sorts the elements of a vector in ascending order.*

PROOF. For sorted $\underline{x} = [x_1, \ldots, x_n]^T$ and $\underline{y} = [y_1, \ldots, y_n]^T$, i.e., $x_1 \leq \ldots \leq x_n$ and $y_1 \leq \ldots \leq y_n$, we have to show that π_{opt} is given by

$$\pi_{opt}(i) = i \text{ for all } i \in \{1, \ldots, n\} .$$

Proof by induction over the number of targets n.

Induction Basis for $n = 2$: For $\underline{x} = [x_1, x_2]^T$ and $\underline{y} = [y_1, y_2]^T$, we have to show that

$$(x_1 - y_1)^2 + (x_2 - y_2)^2 \leq (x_1 - y_2)^2 + (x_2 - y_1)^2 .$$

With $x_2 = x_1 + e_x$ and $y_2 = y_1 + e_y$, where $e_x > 0$ and $e_y > 0$, we obtain

$$(x_1 - y_1)^2 + (x_1 + e_x - (y_1 + e_y))^2 \leq$$
$$(x_1 - (y_1 + e_y))^2 + (x_1 + e_y - y_1)^2 ,$$

which can be simplified to

$$e_x \cdot e_y > 0 .$$

Induction Step from n to $n+1$: The *Induction Hypothesis* is that (6) holds for n targets. We have to show that this also holds for $n + 1$ targets: For the optimal assignment, it must be $\pi_{opt}(n + 1) = n + 1$. If this were not the case, we would have $\pi_{opt}(n + 1) = l$ and $\pi_{opt}(k) = n + 1$ for some $l, k < n + 1$. However, in this case, a better assignment would be $\pi_{opt}(n+1) = n+1$ and $\pi_{opt}(k) = l$. Finally, we can conclude that also $\pi_{opt}(i) = i$ for $i < n + 1$, because of the induction hypothesis and the above argument. $\qquad \square$

Remark 7. A similar proof for the absolute distance (instead of the squared distance), i.e., $d_{\mathrm{abs}}^{\mathrm{OSPA}}(\underline{x}, \underline{y}) := \frac{1}{n} \min_{\pi \in \Pi_n} \sum_i |x_i - y_{\pi(i)}|$ can be found in [20].

Based on the above theorem, we can relate order statistics to MMOSPA estimation.

Theorem 5. *The MMOSPA estimate for a random $\underline{\boldsymbol{x}} = [\boldsymbol{x}_1, \ldots, \boldsymbol{x}_n]^T$ consisting of n one-dimensional targets and a corresponding posterior density $p(\underline{x}|\mathcal{Y})$ is given by the mean of the posterior order statistics of $\underline{\boldsymbol{x}}$*

$$\hat{x}^{MMOSPA} = \mathrm{E}\{\operatorname{sort}(\underline{\boldsymbol{x}})|\mathcal{Y}\} \qquad (7)$$

PROOF. W.l.o.g., let the MMOSPA estimate $\hat{x}^{MMOSPA}$ be sorted (there are $n!$ MMOSPA estimates and one of them is sorted). Then $\operatorname{sort}(\underline{\boldsymbol{x}})$ coincides with the optimal permutation $P_{\pi_{opt}^{MMOSPA, \underline{\boldsymbol{x}}}}(\underline{\boldsymbol{x}})$ according to Theorem 6. $\qquad \square$

Remark 8. The median of $p(\underline{z}|\mathcal{Y})$ yields the MMOSPA estimate for $d_{\mathrm{abs}}^{\mathrm{OSPA}}(\underline{x}, \underline{y}) := \frac{1}{n} \min_\pi \sum_i |x_i - y_{\pi(i)}|$.

According to the above theorem, the MMOSPA estimate for one-dimensional targets can be computed by means of a probabilistic forward mapping from $\underline{\boldsymbol{x}}$ to $\operatorname{sort}(\underline{\boldsymbol{x}})$. In case of a particle representation, this forward mapping can be computed by sorting the particles (see Algorithm 3). The runtime complexity of the algorithm is $\mathcal{O}(N_p \, n \log n)$, i.e., linear in the number of particles N_p.

Algorithm 3 n targets in 1D:
MMOSPA estimate for $p(\underline{x}|\mathcal{Y}) = \sum_{i=1}^{N_p} w_i \cdot \delta(\underline{x} - \underline{x}^{(i)})$

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   return $\sum_{i=1}^{N_P} w_i \cdot \operatorname{sort}(\underline{x}^{(i)})$

Remark 9. Note that the sort operation is a symmetric transformation, i.e., $\operatorname{sort}(\underline{\boldsymbol{x}}) = \operatorname{sort}(P_\pi(\underline{\boldsymbol{x}}))$ for all permutations π. Symmetric transformations in the context of point estimates have been treated in [21].

V. NUMERICAL EXAMPLES

In this section, we give two numerical examples of the proposed exact algorithm for calculating the MMOSPA estimate in two-dimensional space. The exact MMOSPA estimate is compared with the iterative algorithm [4] tailored to particles. The iteration is initialized with the mean of the density. Fig. 4 depicts two example densities plus the corresponding MMO-SPA estimates obtained by the exact and iterative algorithm. In Fig. 4a, a significant difference can be seen between the exact and iterative solution. However, in Fig. 4b both estimates coincide exactly. In general, we observed that the iterative algorithm often provides the exact solution.

VI. SUMMARY

This paper has investigated several ways to calculate MMO-SPA estimators, specifically for cases when distributions are described as "particles," and where there are two (unlabeled) objects. We also explore the relationship between sorting and MMOSPA: in the scalar case, MMOSPA estimation and MMSE estimation of an ordered set (no particles here) are equivalent.

We believe this is a significant progress toward a general MMOSPA estimator, although much work remains. Besides extending the presented results to exact algorithms for $n > 2$ targets in arbitrary-dimensional space and the derivation of even more efficient algorithms, the underlying ideas can be used for deriving approximate algorithms. For example, a more efficient but approximate algorithm for the two-target case is obtained when only some direction vectors are considered. Furthermore, the ordering ideas persist (at least approximately) in more general situations via projection onto "space-filling curves". Some of these, as well as further numerical results showing the application of the theory given in this manuscript, are presently in preparation.
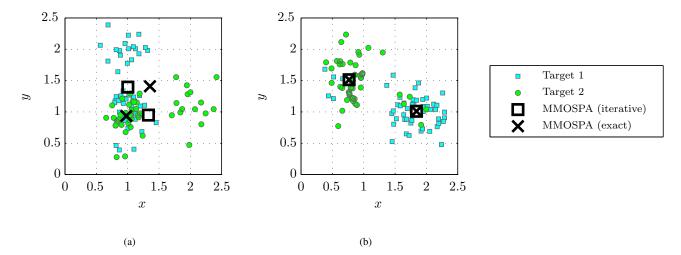
Fig. 4: Numerical examples for the exact MMOSPA estimate for two targets. The probability distribution is represented with (equally weighted) particles.

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