Abstract—The cardinalized probability hypothesis density (CPHD) filter is a recursive Bayesian algorithm for estimating multiple target states with varying target number in clutter. In the present work, it is shown that a missed detection in one part of the field of view has a significant effect on the probability hypothesis density (PHD) arbitrarily far apart from the missed detection. In the case of zero false alarm rate, this effect is particularly pronounced and can be calculated by solving the CPHD filter equations analytically.

While the CPHD filter update of the total cardinality distribution is exact, the local target number estimate close to the missed detection is artificially strongly reduced. A first ad-hoc approach towards a “locally” cardinalized PHD filter for reducing this deficiency is presented and discussed.

Keywords: Probability hypothesis density filter, PHD, multi-target tracking, cardinalized probability hypothesis density filter, CPHD, missed detection problem.

I. INTRODUCTION

The probability hypothesis density (PHD) filter [1], [2] is an efficient Bayesian filter algorithm for tracking multiple targets in clutter. It is linear in the number of targets and avoids the explicit enumeration of all possible multi target–multi detection assignments leading to the so-called combinatorial disaster.

A disadvantage of the PHD filter, however, is due to the Poisson assumption for the target number (cardinality) distribution that leads to an exaggerating effect of missed detections on the target number estimator, the so-called missed detection problem [3]. This problem has been cured, recently, by the so-called cardinalized probability hypothesis density (CPHD) filter [2], [4], [5]. A not as rigorous yet more intuitive “physical state” derivation of both the PHD and the CPHD filter equations has been presented in [6] where some expanded discussion of this approach for the PHD filter can be found in [2, pp. 599–609]. For linear Gaussian systems, Gaussian mixture variants have been derived for both PHD [7] and CPHD [8] filters.

While the overall behavior of the target number estimator in the CPHD filter is greatly improved when compared to the PHD filter, we observe that local target number estimators exhibit a peculiar, counter-intuitive behavior: upon a missed detection, PHD weight is shifted from the undetected part of the PHD to the detected part, no matter how far apart the parts are. The amount of the shifted weight and, hence, the remaining weight of the undetected part both depend on the total target number. The phenomenon is particularly distinct and analytically traceable in the case of zero false alarm rate.

In the following, we will first analyze the problems arising in the CPHD filter in case of missed detections. Afterwards, a first general ad-hoc approach is presented that is expected to reduce these problems significantly in target tracking applications.

II. THE PROBLEM

In this section, we will show analytically how the CPHD filter equations induce their own kinds of missed detection problems. We will assume zero false alarm rate and, for the sake of simplicity, a finite and constant probability of target detection $P_d$ with $0 < P_d < 1$. We consider the probability hypothesis density (PHD) $v(x)$ and the cardinality distribution $p(n)$. We concentrate on the update part, i.e., the transition from $v_{k|k-1}(x)$ to $v_{k|k}(x)$ and $p_{k|k-1}(n)$ to $p_{k|k}(n)$ based on $m$ measurements only, since the prediction of both the PHD and the cardinality is irrelevant in the present context. According to [6], the update equations for the actual joint measurement $Z$ can be written in terms of likelihood ratios:

$$v_{k|k}(x) = \left(1 - P_d\right) \frac{\mathcal{L}(Z|\neg D)}{\mathcal{L}(Z)} + P_d \frac{\mathcal{L}(Z|D)}{\mathcal{L}(Z)} v_{k|k-1}(x)$$

(1)

$$p_{k|k}(n) = \frac{\mathcal{L}(Z|n)}{\mathcal{L}(Z)} p_{k|k-1}(n)$$

(2)

where we have omitted the scan index $k$ in the likelihood ratios $\mathcal{L}$ for the sake of convenience and “$\neg D$” and “$D$” symbolize the cases “target detected” and “target not detected”, respectively. For zero false alarm rate, the likelihood ratios take on the simple forms

$$\mathcal{L}(Z|\neg D) = \frac{1}{\langle n \rangle} \alpha^{(n+1)}$$

(3)

$$\mathcal{L}(Z|D) = \frac{1}{\langle n \rangle} \alpha^{(n)} \sum_{s=1}^{m} \frac{l(z^{(s)}|x)}{L^{(s)}}$$

(4)
as well as
\[
\mathcal{L}(\mathbf{Z}) = \alpha^{(m)}(\mathbf{Z}) = \sum_{n=m}^{\infty} \frac{n!}{(n-m)!} P(n)(1-P_d)^{n-m}
\]
\[
\mathcal{L}(\mathbf{Z}|n) = \begin{cases} 
\frac{n!}{(n-m)!} (1 - P_d)^{n-m} & \text{for } n \geq m \\
0 & \text{for } n < m
\end{cases}
\]

Herein, we have denoted the predicted target number \(n_{k|k-1}\) by the symbol \(\langle n \rangle\). Note that the expressions used here in fact are identical to those in [6], [9] only up to a common factor that cancels in the update equations (1) and (2). The coefficients \(\alpha\), above, are given by
\[
\alpha^{(j)} \equiv \sum_{n=j}^{\infty} \frac{n!}{(n-j)!} P(n)(1-P_d)^{n-j}
\]
where we have used \(P(n)\) to abbreviate the predicted cardinality distribution \(p_{k|k-1}(n)\). Furthermore, there holds
\[
L^{(s)} = \frac{1}{\langle n \rangle} \int p(x) l(z^{(s)}|x) \, dx
\]
with \(l(z^{(s)}|x)\) denoting the single detection likelihood function.

From now on, we consider the case of \(n\) targets, tracked with a high probability \(P(n)\), and \(P(n' > n) = 0\), i.e., we assume the knowledge that the number of targets cannot exceed \(n\). For one missed detection out of \(n\) targets, i.e., \(m = n - 1\), the coefficients \(\alpha^{(j)}\) in (7) simplify to
\[
\alpha^{(m+1)} = \alpha^{(n)} = n! P(n)
\]
\[
\alpha^{(m)} = \alpha^{(n-1)} = (n-1)! P(n-1) + n! P(n)(1-P_d)
\]
\[
= n! \left[ \frac{P(n-1)}{n} + P(n)(1-P_d) \right]
\]

First, we confirm that the total cardinality distribution is correctly updated by the CPHD filter: With the insertion of \(m = n - 1\) into (6) and of (10) into (5), the update equation for the cardinality distribution (2) becomes
\[
P(n|m = n - 1) = \frac{\mathcal{L}(\mathbf{Z}|n)}{\mathcal{L}(\mathbf{Z})} P(n)
\]
\[
= \frac{P(n-1)}{n} + P(n)(1-P_d) P(n)
\]
and
\[
P(n-1|m = n - 1) = \frac{\mathcal{L}(\mathbf{Z}|n-1)}{\mathcal{L}(\mathbf{Z})} P(n-1)
\]
\[
= \frac{1}{P(n-1) + P(n)(1-P_d) \frac{n}{n}}
\]
with
\[
P(n|m = n - 1) + P(n-1|m = n - 1) = 1
\]
while the Bayesian result reads
\[
P(n|m = n - 1) = \frac{P(m = n - 1|n) P(n)}{P(m = n - 1)}
\]
\[
= 1 - P(n-1|m = n - 1)
\]
and
\[
P(m = n - 1) = P(m = n - 1|n) P(n)
\]
\[
+ P(m = n - 1|n-1) P(n-1)
\]
with
\[
P(m = n - 1|n) = n P_d n^m (1-P_d)
\]
and
\[
P(m = n - 1|n-1) = P_d n^m
\]

Further terms \(P(m = n - 1|n-2)\) etc. vanish in the absence of false alarms. Insertion of (16) and (17) into (14) and (15) indeed recovers the update equation (11). This is the generalization of the known fact that the CPHD filter recovers the Bayesian result for \(n = 1\)
\[
P(n = 1|m = 0) = \frac{1-P_d}{1-P_d} P(1)
\]

Now, we investigate the update of the PHD according to (1). Inserting (9) and (10) into (3) and (5), we find the update factor for the missed detection part of the PHD to be
\[
(1-P_d) \frac{\mathcal{L}(\mathbf{Z}|n)}{\mathcal{L}(\mathbf{Z})} = \frac{1}{\langle n \rangle} \frac{P(n)-1-P_d}{P(n)(1-P_d)}
\]
While this part is homogeneous in the field of view, the detection part (4) is concentrated around the actual detections. In total, this results in a strong decrease of PHD weight in regions without detections on the one hand and a missed detection induced enhancement of PHD weight close to the detections on the other.

To further illustrate the problem, we consider two well-separated tracks with weight \(Q\) each, hence a predicted PHD of the form
\[
v_{k|k-1}(x) = Q \left( v_{k|k-1}^{(1)}(x) + v_{k|k-1}^{(2)}(x) \right)
\]
with normalized densities \(v_{j|k-1}^{(j)}(x)\) (\(j = 1, 2\)). In case of a single detection close to track 1, far away from track 2, and no false alarms, a Bayesian analysis (assuming independence between the tracks and with \(Q\) representing the individual probability of existence) in view of (18) yields
\[
v_{k|k}(x) = v_{k|k}^{(1)}(x) + \frac{1-P_d}{1-QP_d} Q v_{k|k-1}^{(2)}(x),
\]
which is identical to what one would get when applying the CPHD filter update equation to the individual tracks separately. But, with \(P(2) = Q^2\) and \(P(1) = 2Q(1-Q)\) implying \(n = 2Q^2 + 2Q(1-Q) = 2Q\), the application of (19) and insertion into (1) yields a different result (where the fact that the two results differ constitutes the first problem):
\[
v_{k|k}(x) = \frac{1}{2} \frac{1}{1-QP_d} Q v_{k|k-1}^{(1)}(x) + \frac{1}{2} Q v_{k|k-1}^{(2)}(x)
\]
We observe that the undetected track has lost 50\% of its correctly updated weight, and the lost weight has been transferred
towards the detected track where the occurrence of this effect is independent on how far apart the tracks are. This counter-intuitive shift of weight (constituting the second problem) becomes particularly obvious in the case of a Gaussian mixture PHD with well-separated components. Before we discuss this case in more detail, we note that the (uncardinalized) PHD filter exhibits a similar “non-locality” where the missed detection update factor (19) in (22) is replaced by $1 - P_{d}$. Depending on the target number and the value of $P_{d}$, the effect can be more or less pronounced. As the expression $1 - P_{d}$ depends neither on the actual nor on the estimated number of targets, the results of the PHD filter upon a missed detection when applied globally to separated independent tracks do not differ from what would be obtained when applying the PHD filter to the tracks individually. In contrast to the CPHD filter, however, the update of the total target number estimate is not correct in the PHD filter.

Now, we consider a Gaussian mixture PHD with $j$ components, defined by the following weighted sum over normal distributions [8]:

$$v(x) = \sum_{j=1}^{J} w^{(j)} N(x; m^{(j)}, P^{(j)})$$

(23)

For well-separated components, each weight $w^{(j)}$ determines the expected number of targets covered by this component or, briefly, a local target number estimate. In the updating step of the (C)PHD filter, from each component $m + 1$ new components are derived; one for each detection and one for the missed detection hypothesis. In the CPHD filter, the updated weight of the component $j$ associated to detection $s$ is given by

$$w^{(j,s)} = w^{(j)} \frac{P_{d}^{(j)}}{\langle n \rangle} \frac{N(z^{(s)}; z^{(j)}, S^{(j,s)})}{L^{(s)}}$$

(24)

with the innovation likelihood $N(z^{(s)}; z^{(j)}, S^{(j,s)})$ and the averaged single detection likelihood from eq. (8)

$$L^{(s)} = \frac{1}{\langle n \rangle} \sum_{j=1}^{J} P_{d}^{(j)} w^{(j)} N(z^{(s)}; z^{(j)}, S^{(j,s)})$$

(25)

The (common) scaling factor for the weights of the missed detection components has been determined above and is given by (19).

In the case of well-separated single target tracks and no false alarms, each detection $s$ belongs to one component $j_{s}$ per definition, because for all alternative associations, the innovation likelihood vanishes. Therefore, the averaged single detection likelihood (25) is reduced to:

$$L^{(s)} = \frac{P_{d}^{(j_{s})}}{\langle n \rangle} w^{(j_{s})} N(z^{(s)}; z^{(j_{s})}, S^{(j_{s},s)})$$

(26)

Starting with $n$ components and inserting the above into (24), the new component weights are exactly equal to one regardless of what they have been before. We thus have $m = n - 1$ updated detection components with weight one each. On the other hand, there are $n$ missed detection components being scaled by a common factor. For large target numbers or in the limiting case of certain knowledge about the target number ($P(n) = 1$), (19) simplifies to

$$(1 - P_{d}) \frac{\mathcal{L}(Z|\neg D)}{\mathcal{L}(Z)} = \frac{1}{\langle n \rangle}$$

(27)

and the respective weights of the missed detection components are $w^{(j)}/\langle n \rangle$ thus adding up to one (as weights $w^{(j)}$ have added up to $\langle n \rangle$). This means that, in these cases, the track where detection has been missed gets an updated weight $w^{(j)}/\langle n \rangle$ while each other one, being supported by both its detection and its missed detection component—those two components will then merge into a single new component as long as predicted and updated target state do not differ too much—has a total weight of $1 + w^{(j)}/\langle n \rangle$. A similar behavior can also be observed for more realistic situations with low clutter and highly peaked cardinality distributions. Herein, the assumption $P(n' > n) = 0$ is not required to hold.

Overall, we thus make the following peculiar observations:

1. A missed detection of one track $j$ has an influence on the weights of the other ones. The latter tracks in general even gain weight. The lower the estimated number of targets in the surveillance volume, the higher the gain becomes.

2. The updated weight of the track having suffered from the missed detection depends on the total number of targets in the surveillance volume (as well). The higher the estimated number of targets in the surveillance volume, the lower the weight becomes.

To summarize, the CPHD filter update of the overall cardinality distribution for a single missed detection without false alarms is exact. However, in the situation of well-separated target tracks, the CPHD filter suffers from an artificially correlated and thus non-physical behavior of the local PHD in different regions of phase space. In practical applications, the exaggerated reduction of weight on a track with a missed detection in particular might lead to problems as such a track could be lost due to a weight threshold. While there exist heuristic track-management based approaches to handle such problems somehow, in general separated target tracks should not be treated globally within a CPHD filter in order to avoid abrupt changes in local target number estimates. A first step towards a locally cardinalized PHD filter will be briefly discussed next. There, we only consider the Gaussian mixture case.

III. AN AD-HOC APPROACH

One possible approach to reducing the remote interaction problem of the CPHD encompasses the division of the surveillance volume into separate regions and a subsequent application of the CPHD to each of the regions individually. Clearly, this approach would require an appropriate handling of the boundaries between the individual regions as targets may cross those boundaries. Hence, we propose rather to dynamically select the respective regions driven by the existing tracks in order to get to some kind of a locally cardinalized
PHD filter. To this end, an appropriate clustering of tracks may be used, where tracks belonging to a cluster can be identified by, e.g., having common plots in gates. These clusters then inherently define the dynamically changing individual regions the CPHD filter equations will be applied to.

Now, clustering of course is a common approach to reducing computational load in many assignment strategies. But, for the CPHD filter, we must assign a cardinality distribution to each of the clusters—the (small) contribution a Gaussian component of one cluster has on the PHD of the remaining clusters is neglected here—and we thus have to track more than one cardinality distribution at a time. This induces the need for some special measures when clusters are formed dynamically over time. However, the maximum number of targets that must be specified when using the Gaussian mixture CPHD filter [8], [9] now is the maximum number of targets in each individual cluster and thus can take on a smaller value.

As long as there is no transition of tracks from one cluster to another (e.g., by a split off of one or more tracks resulting in one or more new clusters) and clusters remain well-separated, no special action has to be taken and processing within each cluster follows the standard CPHD filter equations. All other cases in particular require an appropriate handling of the individual cardinality distributions. At least, the cases of merging several regions into one and splitting one region into more than one must be considered. In the former case, one cardinality distribution has to be computed from several given ones, in the latter case the task is just the converse.

The computation of one cardinality distribution from several given ones is easy under the assumption that the individual given distributions are independent (which is true whenever the clusters to merge have always been well-separated before). In this case, the distribution of the merged cluster is merely the convolution of the individual ones and can be computed by appropriate methods.

But, the case of splitting one region into several ones is far more involved. In order to keep things simple, let us consider the case of splitting one region into two (disjoint) regions $a$ and $b$. Now, the question is: given the cardinality distribution $p(n)$ of the complete region with mean $\mu$ and variance $\sigma^2$, what do we know about the distributions $p_a(n_a)$ and $p_b(n_b)$ of the cardinality in the two regions $a$ and $b$? Herein, all information we can use in addition to $p(n)$ is in the weights of the components that now are assigned to either region. In order to be consistent, the expected target number in each region (in the following denoted as $\mu_a$ and $\mu_b$, respectively) must coincide with the sum of the weights of the respective Gaussian components. No more information can immediately be extracted from the given PHD. But, with this information alone, the distributions $p_a(n_a)$ and $p_b(n_b)$ are by no means uniquely determined. In particular, we cannot use the assumption of $p_a(n_a)$ and $p_b(n_b)$ being independent (from which we would, in addition to $\mu_a + \mu_b = \mu$, obtain $\sigma^2_a + \sigma^2_b = \sigma^2$). This becomes immediately apparent when considering the special case $p(n) = 1$ for some integer $(n)$, which implies $\sigma^2 = 0$ (and thus would also yield $\sigma^2_a = \sigma^2_b = 0$). This would mean that, when we know for sure that there are $n$ targets in the complete region, we would also know the target number in the both regions without error. Obviously, this cannot be true. But we do know in this extreme case that $\sigma^2_a = \sigma^2_b$ must hold.

In order to illustrate the complexity of the problem stemming from the fact that the two distributions are not independent, we investigate the problem for the special case of having two targets at most, i.e.,

$$p(0) = p_0, \quad p(1) = p_1, \quad p(2) = p_2 = 1 - p_0 - p_1, \quad (28)$$

which, with $\mu = p_1 + 2p_2$ and $\sigma^2 = p_1 + 4p_2 - \mu^2$, in particular implies

$$\max\{\mu(1-\mu), (\mu-1)(2-\mu)\} \leq \sigma^2 \leq \mu(2-\mu) \quad (29)$$

Now, denoting with $p_{ij}$ the joint probability $P[n_a = i, n_b = j]$, we seek the values of these $p_{ij}$ for a given $p(n)$ as in (28) and given $\mu_a \geq 0$ and $\mu_b = \mu - \mu_a \geq 0$ under the constraints $p_{00} \geq 0$ and $\sum p_{ij} = 1$. Once these values are found, the marginal distributions $p_a(n_a)$ and $p_b(n_b)$ are easily computed. A detailed analysis shows that each admissible solution of this set of relations can be written as

$$p_{00} = p_0 \quad (30)$$
$$p_{01} = -\mu_a + p_1 + p_2 - p_{20} - p_{02} \quad (31)$$
$$p_{10} = \mu_a - p_2 - p_{12} - p_{10} - p_{02} \quad (32)$$
$$p_{11} = p_2 - p_{12} - p_{02} \quad (33)$$

with

$$\max\{0, \mu_a - p_1 - p_2\} \leq p_{20} \leq \min\{\mu_a/2, p_2\} \quad (34)$$
$$\max\{p_2 - \mu_a + p_{20}\} \leq p_{02} \quad (35)$$

and all other $p_{ij}$ being zero. Herein,

$$\sigma^2_a + \sigma^2_b = \sigma^2 + 2p_a\mu_b - 2p_{11} \quad (36)$$
$$\sigma^2_a - \sigma^2_b = \mu_b(1-\mu_b) - \mu_a(1-\mu_a) + 2(p_{02} - p_{20}) \quad (37)$$

holds, which determines the admissible ranges of values for the variances $\sigma^2_a$ and $\sigma^2_b$. Note that these ranges are coupled. Furthermore, the corresponding bounds are in general tighter than those one can deduce from the marginal distributions $p_a(n_a)$ and $p_b(n_b)$ alone in analogy to (29).

The previous elaborations have shown that we cannot expect to find a general decomposition of one cardinality distribution into several ones that is both rigorous and easy to handle at the same time. For now, we recommend using the following ad-hoc scheme for finding applicable (marginalized) cardinality distributions for the split clusters $c$ instead:

1) Determine each expected value $\mu_a$ as the sum of weights of the relevant Gaussian mixture components.

2) Determine some variances $\sigma^2_a$ from $\sigma^2$, honoring the fact that the split process increases uncertainty of the cardinality estimates.
3) Using the $\mu_a$ and $\sigma^2_a$, select the cardinality distribution $p_{n_a}(n_c)$ from some suitable class of distributions that can be parameterized by those two parameters.

In the last one of the steps above, the class of Panjer’s distributions [10] may be used use for example, which is defined by the recursion—we omit the subscript $c$ from now on—

$$p(n+1) = \left( a + \frac{b}{n+1} \right) p(n) \quad (38)$$

with $a + b \geq 0$ and $a < 1$ where $p(0)$ is specified by the constraint $\sum p(n) = 1$. With this, one has

$$\mu = \frac{a + b}{1 - a}, \quad \sigma^2 = \frac{a + b}{(1 - a)^2} \quad (39)$$

or, equivalently,

$$a = 1 - \frac{\mu}{\sigma^2}, \quad b = \frac{\mu^2}{\sigma^2} - a \quad (40)$$

This class encompasses three special cases that, at the same time, are the only distributions of this form [11]. For $a < 0 \iff \sigma^2 < \mu$, Panjer’s distribution boils down to a binomial distribution. For $a = 0 \iff \sigma^2 = \mu$, it is Poisson’s distribution. Finally, it becomes a negative binomial distribution for $a > 0 \iff \sigma^2 > \mu$. Thus, this class is general enough to cover the case $\sigma^2 = \mu$ and the case $\sigma^2 > \mu$ with arbitrary $\mu$ and $\sigma^2$ as well as the case $\sigma^2 < \mu$, where it is then required that $b$ be an integer multiple of $-a$. By fulfilling the latter restriction and thus getting a distribution with finite support, the bounds for $\sigma^2$ that we have observed above to be inherent in the marginal distribution are automatically honored.

Clearly, the steps described here are, at various points, rather ad-hoc and thus leave much room for further investigation. On the other hand, the proposed approach is expected to effectively reduce the problem of remote interaction via missed detections in the CPHD filter. In our approach, a track without any detection in its gates will, by definition, fall into an isolated cluster and thus does not interfere with the weights of the other tracks. Nevertheless, some careful fine-tuning of the clustering process is necessary in order to avoid frequent successive merge and split operations on clusters where we combine cardinality distributions via convolution under the independence assumption (until more sophisticated solutions are found) while distributing it as outlined above. Both operations increase uncertainty in the distributions and thus dilute parts of the already gained knowledge about the (local or total) cardinality in the surveillance volume. And of course, the problem of remote interaction via missed detections itself is not eliminated from the CPHD filter equations.

**IV. A SIMULATION EXAMPLE**

In order to demonstrate the various effects discussed above, we have simulated two targets moving in the $(x, y)$ plane with constant speeds $v = 180 \text{ m/s}$ both with crossing trajectories as depicted in Fig. 1. Herein, the sensor was centered at the origin $(0, 0)$ and supplied polar measurements with a scan time $T = 5 \text{ s}$ and $\sigma_{\text{range}} = 20 \text{ m}$ as well as $\sigma_{\text{az}} = 0.005 \text{ rad}$. There was (moderate) clutter with some inhomogeneous spatial distribution, i.e., the intensity decreased with increasing distance from the sensor. Four detections were missed as indicated (the last two in consecutive scans). Tracking of the Gaussian mixture components in the (locally) cardinalized PHD filters was performed by Kalman filters having states position and velocity in both spatial dimensions with assumed (almost) constant velocity, a process noise of about $0.3 \text{ g}$, and using converted Cartesian pseudo-measurements. The CPHD filters in particular assumed $P_d = 0.98$ and used the clutter density $\lambda$ within the correct order of magnitude (assuming homogeneous clutter in the surveillance volume). Mixture components were merged using moment matching where a merge was initiated based on the statistic distance between the individual state estimates. A track was considered to be established when the weights of the corresponding Gaussian mixture component exceeded 0.2 after the pruning process (but components were continuously tracked until their weight fell below $10^{-5}$).

Fig. 2 shows the behavior of the CPHD filter with respect to the estimate for the total number of targets as well as the corresponding estimates for the individual tracks. There was one established track representing both targets in the time interval from 245 to 300 s, and two separated tracks existed in the remaining times.

Overall, the algorithm proves to be robust against the deviation between assumed and actual spatial clutter density. Yet the predicted remote interaction between the two individual target number estimates due to missed detections is clearly visible. In addition to that, we see another kind of interaction (at $t \approx 240 \text{ s}$). Here, targets are fairly close, yet still tracked with two separated tracks. But a more detailed inspection shows that one of the tracks gets updated with one plot, the other one with two. Thus, both tracks share...
Fig. 2. Target numbers estimated by the CPHD filter. Missed detections occurred at the time instances marked by dashed lines.

Fig. 3. Numbers of established tracks and clusters formed by the locally cardinalized PHD filter.

a common plot they are individually updated with. We thus note that, although it has been shown that the CPHD filter equations are identical to the update equations of a MHT (multi hypotheses tracker) with inherent sequential probability ratio test in case of single target tracking [9], this equivalence does not hold in the multi target case. While in a full-blown multi target MHT, each measurement (finally) is associated to one track at most, the CPHD on this behalf resembles a joint probabilistic data association (JPDA) technique where the fact that one observation stems from one target at most is honored when deriving the update equations without leading to a final association decision.

Figs. 3 and 4 display the results of a locally cardinalized PHD filter as proposed above. In Fig. 3, we see the number of clusters formed (by gating) and the number of tracks within one of the clusters. We see that, for this specific scenario, the two individual tracks fall into a common cluster well before being merged (with three scans’ delay) into a single track then representing both targets. On the other hand, splitting into two clusters here closely follows the separation of the Gaussian mixtures into two well-separated tracks (with one scan delay). We note from Fig. 4 that our proposed locally cardinalized PHD filter is indeed able to remove the remote interaction between the individual target number estimates due to missed detections when targets fall into separated clusters. But it is no surprise that problems inherent in the CPHD framework still prevail for targets falling into common clusters.

V. CONCLUSION

We have shown that the cardinalized probability hypothesis density filter for multiple target tracking exhibits spurious remote interactions between arbitrarily distinct parts of the phase space. The reason lies in the fact that the CPHD filter provides the cardinality distribution for the total target number as well as local target number estimates, but no information whatsoever on the variance of the local estimates, and thus the weight of the missed detection part of the PHD is always assumed homogeneous in the field of view. Therefore, we conclude that the CPHD filter in its present
shape requires additional measures when used for tracking several independent targets. We have discussed an ad hoc approach for the Gaussian mixture CPHD filter that divides portions of the phase space by clustering the tracks. Each individual cluster may be tracked by its own CPHD filter. Without having a rigorous scheme for the splitting of a cluster into two (or more), we have proposed a heuristic method for the decomposition of a cardinality distribution. Further research is necessary at this point.

Acknowledgment: We thank Ron Mahler for fruitful discussions and for valuable suggestions that helped to improve the quality of the manuscript. His proposition of the two target example is especially gratefully acknowledged.

REFERENCES