Abstract—This paper introduces a generalization of the multiple-hypothesis tracking (MHT) formalism for multi-target tracking (MTT). To our knowledge, MHT treatments in the literature do not consider undetected target birth events. Their inclusion leads to an interesting extension to the MHT recursion, and necessitates aggregation over indistinguishable global hypotheses. We show that the MHT recursion factors, enabling track-oriented MHT (TO-MHT), albeit with clusters of indistinguishable undetected births. The treatment requires a distinction between those targets that are eventually detected (we call these unnoticed targets) and those that are never detected (we call these ghost targets). The same number of relevant track hypotheses result as in the classical TO-MHT solution. In the time-invariant case, the solution simplifies further.

Key words—Multiple-hypothesis tracking (MHT), undetected target births, ghost targets.

NOTATION

\[ \Delta t \] Time interval from \( t_k \) to \( t_{k+1} \)
\[ \lambda \] Continuous-time target birth rate
\[ \lambda_d \] Continuous-time target death rate
\[ \lambda_b(k) \] Discrete-time target birth rate at time \( t_k \)
\[ Z_k \] Measurement set at time \( t_k \)
\[ Z^k \] Sequence of measurement sets up to time \( t_k \)
\[ X_k \] Multi-target state at time \( t_k \)
\[ X^k \] Multi-target state history up to time \( t_k \)
\[ Q_k \] Global hypothesis state at time \( t_k \)
\[ Q^k \] Global hypothesis up to time \( t_k \)
\[ Q^k(i) \] Local (track) hypothesis up to time \( t_k \) associated with measurement \( Z_{k,j} \)
\[ f_b(\cdot) \] Target birth prob. dist. in measurement space
\[ \hat{f}_b(\cdot) \] Target birth prob. dist. in state space
\[ p_d(k) \] Sensor detection probability at time \( t_k \)
\[ \lambda_{fa} \] False alarm rate
\[ \hat{f}_{fa}(\cdot) \] False alarm probability distribution in measurement space

I. INTRODUCTION

Multiple-hypothesis tracking (MHT) is well-established as a paradigm for the multi-target tracking (MTT) problem [1-2]. The fundamental approach includes many variants. Hypothesis-oriented MHT (HO-MHT) was first formalized by Reid [3]. The initial integer-programming formulation of the problem is due to Morefield [4]. The hybrid-state decomposition that allows for computationally efficient track-oriented MHT (TO-MHT) may be found in Kurien [5]. An efficient solution to the optimization problem required for hypothesis pruning via Lagrangian relaxation may be found in Poore and Rijavec [6] and Deb et al [7]. A simple linear-programming based relaxation approach was studied independently by Storms and Spieksma [8] and by Coraluppi and Carthel [9]. Recent computational advances are discussed in Papageorgiou [10]. In many settings, distributed MHT provides robustness and performance benefits [11].

In this paper, we revisit the derivation of the MHT recursion, allowing for targets that are undetected at birth. We will show that the problem, while more complex than the classical MHT recursion, includes significant structure that enables a tractable TO-MHT solution. We show that there is additional structure that simplifies the solution in
We consider a multi-target realization based on the Integrated Ornstein-Uhlenbeck (IOU) process [13]. Our undetected-birth solution approach involves aggregation over indistinguishable hypotheses. A similar approach can be employed fruitfully when measurements are indistinguishable, for the so-called cardinality-tracking problem [14]. An early treatment of the undetected-birth MHT problem, but without hypothesis aggregation, may be found in [15].

This paper is organized as follows. Section II summarizes the MTT problem. Sections III and IV address the enhanced MHT solution for the MTT problem, allowing for undetected target births. The time-invariant case is in Section V. Conclusions are in Section VI.

II. THE MULTI-TARGET TRACKING PROBLEM

We start with the general multi-target tracking (MTT) problem of interest. We are given a continuous-time birth and death process, with birth inter-arrival times exponentially distributed with rate $\lambda_b$ and object life exponentially distributed with rate $\lambda_x$. We consider a discrete-time sequence $(t_0,t_1,t_2,...)$ with inter-sampling times defined by $\Delta t_k := t_{k+1} - t_k$, $k \geq 0$. Correspondingly, the number of births in the interval $\Delta t_k$ is Poisson distributed with mean given by eqn. (1). The probability of target death in the interval $\Delta t_k$ is given by eqn. (2).

Note that there are birth-death events between sampling times that are not reflected in the discrete-time model.

$$
\mu_b(k+1) = \int_{t_k}^{t_{k+1}} \lambda_b \exp(-\lambda_x(t_{k+1}-t))\,dt
= \lambda_b \left(1 - \exp(-\lambda_x \Delta t_k)\right), k \geq 0,
$$

$$
p_x(k+1) = 1 - \exp(-\lambda_x \Delta t_k), k \geq 0.
$$

We assume there are no targets at time $t_0$. When the inter-sampling time is constant we may omit the time index for simplicity and write $\mu_b$ and $p_x$.

For each target, we assume the initial state is characterized by a (time-invariant) probability density function (pdf) defined over target state space. Correspondingly, let $f_b(.)$ denote the pdf of target birth observations in measurement space. We assume that the target state evolves according to a time-invariant continuous-time kinematic model. Further, we assume a known discrete-time measurement model at times $t^k = (t_1, t_2, ..., t_k)$.

While the linear-Gaussian kinematic and measurement model is common, it is not required. Let $f_s(.)$ denote the probability density for the sensor measurement on a target at time $t_k$ given a preceding sequence of measurements.

We must be careful in using $f_s(.)$ as the distribution of target births in measurement space that are observed in discrete time. Strictly speaking, due to probability diffusion effects, $f_b(.)$ applies at target birth time, not at the discretization times $t^k = (t_1, t_2, ...)$. However, we will assume stationary stochastic dynamics, so that $f_b(.)$ is an exact characterization of the discrete-time birth probability distribution [12].

Let $p_d(k)$ denote the target detection probability at time $t_k$, and let $\Lambda$ be the mean of the Poisson-distributed number of false alarms at each scan time. False alarms are distributed in measurement space according to $f_{fa}(.)$.

Let $X^k$ denote a multi-target realization based on the birth-death statistics and target kinematic evolution discussed above. That is, $X^k$ is a set of target trajectories defined on $(t_1, t_2, ...)$. The set $X^k$ is not to be confused with $X^k$, the latter being the usual notation for a single-target trajectory given by $X^k = (X_1, ..., X_k)$. Each element of $X^k$ is a distinct target with a birth time, a state trajectory, and (possibly) a death time. Based on the sensor modeling discussed above, we observe a sequence of sets of contacts $Z^k = (Z_1, ..., Z_k)$ at a sequence of times $t^k$. We denote the contacts in each set with a double subscript as follows: $Z_i = \{z_{i1}, ..., z_{ii} | x_i \}$. 

Arguably, a solution to the multi-target tracking problem is given by the probability distribution $p(X^k | Z^k)$ over all sets of target trajectories conditioned on the sequence of sets of measurements. This solution is problematic for at least two reasons. First, even for small problems, $p(X^k | Z^k)$ is extremely challenging to compute. A second difficulty is that, generally, one is interested in a specific tracking solution (i.e. a specified set of tracks) rather than a probability distribution over tracking solutions. Indeed, most tracking paradigms documented in the literature seek an estimate $\hat{X}^k$ that is close to $X^k$, according to some set of metrics.

Since $\hat{X}^k$ and $X^k$ are complex objects, the issue of what are appropriate tracking metrics is a topic of interest and research in its own right. Generally, we find that several
metrics are required to quantify the quality of a tracking solution [1-2]. A recent and useful contribution to this regard relies on scan-based track-truth assignment, and a figure of merit that is a metric in the classical (mathematical) sense [16].

We proceed with the assumption that the maximum a posteriori (MAP) tracking solution is a reasonable one. That is, we seek the following:

\[ \hat{X}^k = \arg \max p(X^k \mid Z^k). \]  

(3)

Of course, even if one could compute \( \hat{X}^k \) precisely, there is no guarantee that this solution performs well with respect to metrics of interest.\(^1\)

III. MULTIPLE-HYPOTHESIS TRACKING

The estimate \( \hat{X}^k \) given by (3) is difficult to compute. Thus, we proceed with a hybrid-state formulation that will aid us in determining an approximation to \( \hat{X}^k \). Our approach expands upon the framework presented in [5] by including undetected target birth hypotheses.

We start by introducing the discrete state variable \( Q^k \); this variable identifies all birth, death and measurement-association events up to time \( t_k \). Conditioned on \( Q^k \), the general tracking problem simplifies to a set of nonlinear filtering problems. In principle, one could recover the original tracking formulation by a weighed combination over all discrete-state realizations, as stated with eqn. (4). Rather, under the MHT paradigm, we seek the MAP estimate for \( Q^k \), given by eqn. (5). Next, we rely on the approximation given by eqn. (6) to replace eqn. (3) by the much simpler eqn. (7).

\[ p(X^k \mid Z^k) = \sum_{Q^k} p(X^k \mid Z^k, Q^k) p(Q^k \mid Z^k). \]  

(4)

\[ \hat{Q}^k = \arg \max p(Q^k \mid Z^k). \]  

(5)

\[ p(X^k \mid Z^k) \approx p(X^k \mid Z^k, \hat{Q}^k). \]  

(6)

\[ \hat{X}^k = \arg \max p(X^k \mid Z^k, \hat{Q}^k). \]  

(7)

To conclude, since solving eqn. (3) is intractable, the MHT approach can be understood as the selection of a single high-probability global hypothesis, followed by the determination of the corresponding tracking solution.

In order for the MHT approach to be both computationally viable and utilizable in real-time, we seek a recursive implementation for the (batch) estimation problem given by eqn. (5).

Proceeding in a straightforward manner with Bayes’ theorem, we have:

\[ p(Q^k \mid Z^k) = \frac{f(Z_k \mid Z^{k-1}, Q^k)}{c_k} p(Q^k \mid Z^{k-1}) = \frac{f(Z_k \mid Z^{k-1}, Q^k)}{c_k} p(Q_k \mid Z^{k-1}, Q^k) p(Q^{k-1} \mid Z^{k-1}) \]  

(8)

\[ c_k = p(Z_k \mid Z^{k-1}) = \sum_{Q^k} f(Z_k \mid Z^{k-1}, Q^k) p(Q^k \mid Z^{k-1}). \]  

(9)

For notational simplicity, we have omitted time indices in eqn. (8). Also, for notational simplicity in the sequel we omit the time dependence of the detection probability \( p_d \), the death probability \( p_d \), and the birth rate \( \lambda_b \). There are two factors in the numerator of eqn. (8) required for a recursive expression: \( f(Z_k \mid Z^{k-1}, Q^k) \) and \( p(Q_k \mid Z^{k-1}, Q^k) \). Let us consider these in turn.

Under \( Q_k \), each measurement in the set \( Z_k \) has a defined provenance. Let us denote by \( J_k(Q_k) \) the set of indices for the track update measurements in \( Z_k \). That is, \( i \in J_k(Q_k) \) implies that \( Z_{k,i} \) is a track update under hypothesis \( Q_k \). Similarly, let \( J_k(Q_k) \) denote the set of indices for the track birth measurements in \( Z_k \). Finally, let \( J_{fa}(Q_k) \) denote the set of indices for the false alarm measurements in \( Z_k \).

With this notation, we can express \( f(Z_k \mid Z^{k-1}, Q^k) \) as follows:

\[ f(Z_k \mid Z^{k-1}, Q^k) = \prod_{i \in J_k(Q_k)} f(Z_{k,i} \mid Z^{k-1}, Q^k(i)) \cdot \prod_{j \in J_{fa}(Q_k)} f_j(Z_{k,j}) \cdot \prod_{j \in J_{fa}(Q_k)} f_j(Z_{k,j}). \]  

(10)

We now consider \( p(Q_k \mid Z^{k-1}, Q^k) \). Assume that, given \( Q^{k-1} \), there are \( T \) track hypotheses (i.e. assumed number of existing targets) at time \( t_{k-1} \). We will distinguish two types of target births in the absence of a detection: unnoticed target births are those for which the target is eventually detected prior to termination; ghost target births are those for which the target is never detected. Further, it is helpful to introduce the auxiliary variable \( \psi_k \), which identifies at time \( t_k \) the number of detections of existing targets (\( d \)), the number of detected target births (\( b \)), the number of unnoticed target births (\( u \)), the number of target births (\( g \)), the number of target

\(^1\) As an illustration, consider a biased coin with \( p(\text{heads})=0.6 \). Toss the coin 100 times. Assume there is no measured data. What is the maximum a posteriori estimate for the unknown realization? The answer: 100 consecutive heads. Assume the metric of interest is the total number of heads. Based on the MAP estimate, we estimate 100 total heads. This is a poor estimate of the actual number of heads in the realization, which is close to 60.
deaths \((\chi)\), and the number of false alarms \((r - d - b)\). Let \(r\) be the number of measurements in the current scan, i.e. \(|Z_r| = r\).

Notice that, somewhat subtly, in defining \(\psi_k\) we are exploiting the future structure of the global hypothesis as it relates to undetected target births. In particular, we distinguish between unnoticed targets (i.e. undetected at birth, but eventually detected) and ghost targets (i.e. never detected). Nonetheless, the global hypothesis score will be computed recursively.

Having defined \(\psi_k\), we consider the following useful decomposition:

\[
p(Q_k | Z^{k-1}, Q^{k-1}) = \psi_k \left| Z^{k-1}, Q^{k-1} \right| p(Q_k | Z^{k-1}, Q^{k-1}, \psi_k).
\]

Now we consider in turn the factors in eqn. (11). The first factor is given by eqn. (12). This expression characterizes the probability that, given \(\tau\) track hypotheses, \(\chi\) deaths occur, \(d\) of the remaining \(\tau - \chi\) targets are detected, \(b\) detected births occur, \(u + g\) undetected births occur (both unnoticed targets and ghost targets), and \(r - d - b\) false alarms occur.

\[
p(\psi_k | Z^{k-1}, Q^{k-1}) = \left\{ \begin{array}{l} \tau \chi \prod_{i=1}^{n} g - \sum_{j=1}^{n-1} n_j \left| g \right| \\
\sum_{i=1}^{\tau - \chi} \frac{d}{d} (1 - p_d) (1 - p_d)^{r - X - d} \cdot \exp(-p_d h_i) \cdot \frac{p_d h_i}{b} \left( u + g \right) \left( r - d - b \right) \end{array} \right.
\]

(12)

The second factor in eqn. (11) is given by eqn. (13).

\[
p(Q_k | Z^{k-1}, Q^{k-1}, \psi_k) = \left\{ \begin{array}{l} \tau \chi \prod_{i=1}^{r} \left( \frac{r - d}{d} \right) \left( \frac{r - d}{b} \right) \end{array} \right.
\]

(13)

This expression characterizes the probability of a specific global hypothesis, among all those that are consistent with the counting (or auxiliary) variable \(\psi_k\). As such, we must consider the number of ways that \(\chi\) deaths can be chosen among \(\tau\) track hypotheses, the number of ways that \(d\) targets can be detected among \(\tau - \chi\) still-alive targets, the number of ways that \(r\) update measurements can be selected among \(r\) measurements (where order matters), and the number of ways that \(b\) birth measurements can be selected among \(r\) measurements (where order does not matter). This accounts for the denominator terms in eqn. (13).

However, there is also hypothesis aggregation to be considered. That is, there is a number of indistinguishable global hypotheses that we wish to identify with \(Q_k\). Specifically, there are a number of ways to specify which \(u\) undetected births are to be treated as track hypotheses (where order matters), a number of ways to specify which \(n_i\) ghost targets live for a scan, and, more generally, which \(n_j\) ghost targets of the remaining \(g = \sum_{j=1}^{a} n_j\) ghost targets live for \(i\) scans.

It may appear odd that order matters when selecting unnoticed births among all undetected births. This, in fact, is a crucial step that enables a factored form for the global hypothesis score. Unlike sensor measurements, unnoticed birth events are indistinguishable. Thus, there are many ways to select the undetected birth to which a sensor measurement is ultimately associated in a later scan. We account precisely for this multiplicity by selecting unnoticed births with order.

Note that, just as we exploited the distinction between unnoticed targets and ghost targets in defining \(\psi_k\), in defining eqn. (13) we have exploited the structure of ghost targets in terms of their future evolution, specifically their time of death. Nonetheless, as noted before, we will still achieve a valid recursive computation of the global hypothesis score.

Combining eqns. (12-13), it can be shown with some manipulation that eqn. (14) results. Finally, substituting eqns. (10, 14) into eqn. (8) leads to eqn. (15).

\[
p(Q_k | Z^{k-1}, Q^{k-1}) = \frac{\exp(-\mu_h - \Lambda)}{r!} \cdot \frac{(1 - p_d) \mu_h}{\Lambda} \cdot \prod_{j=1}^{g} n_j!
\]

(14)

Eqn. (15) is the fundamental recursion that enables TOMHT. In particular, we see that the global hypothesis can be factored with a normalizing constant that is the same for all global hypotheses and a number of local (track) hypothesis scores. These factors allow for systematic updates to local hypothesis scores; global hypotheses scores are obtained by identifying a set of local
hypotheses, with the restriction that each sensor measurement be selected at most once.

\[
p(Q^k \mid Z^k) = \frac{\exp(-\mu_b - \Lambda \chi)}{r!} \prod_{\kappa = \Lambda, \kappa \neq \chi} \frac{\prod_{j_k \in (Q_k)} p_{f_j}(Z_{k,j})}{\Lambda_{j_k} (Z_{k,j})} \]

\[
\prod_{\kappa = \Lambda, \kappa \neq \chi} \frac{\prod_{j_k \in (Q_k)} p_{f_j}(Z_{k,j})}{\Lambda_{j_k} (Z_{k,j})} \frac{[1 - (1 - p_d) \mu_b]^{\alpha}}{(1 - p_d) \mu_b} \prod_{i=1}^{\gamma} \frac{\mu_{\chi_{Q_i}}}{\Lambda_{\chi_{Q_i}} (Z_{\chi_{Q_i}})}
\]

Let us examine the factors in eqn. (15). There are factors that correspond to \( \chi \) terminated targets, \( \tau - \chi \) undetected (previously-born) targets, \( d \) updated targets, \( b \) detected births, and \( u \) unnoticed births. Additionally, there is a factor for each set of indistinguishable ghost targets that are born and that live for \( i \) scans. Note that eqn. (16) holds: under \( Q_k \), there are a total of \( g \) ghost targets born at time \( t_k \).

\[
\sum_{i=1}^{\infty} n_i = g
\]

**IV. Structure of the MAP Solution**

An immediate concern with the expanded MHT treatment introduced in this paper is that, given \( Z^k \), it appears that the number of feasible global hypotheses \( Q^k \) that we must consider is infinite. Indeed, targets may be born at an arbitrary time step prior to being first detected, if at all. In fact, there is no need to consider all such possibilities. Rather, there is significant structure that can be brought to bear on the problem.

As we are interested in the MAP global hypothesis, it is sufficient to consider the likeliest existence sequence prior to first detection in each local (track) hypothesis. This is true because the incremental contribution to the track probability from first detection to track termination is independent of the existence sequence prior to first detection. This follows immediately from our assumption of stationary stochastic dynamics. Mathematically, we can say that \( f_b(Z_{k,j}) = f_j(Z_{k,j} \mid Z^{k-1}, Q^k(i)) \) if there are no sensor measurements associated with track hypothesis \( Q^k(i) \) prior to \( Z_{k,j} \). It follows as well that the optimal track-birth structure is identical for all tracks whose first detection time is the same. The structure depends solely on the discrete-time birth-death statistics, i.e. \( \lambda_b(\cdot) \) and \( p_x(\cdot) \), and the detection probability sequence \( p_d(\cdot) \).

Likewise, it is sufficient to consider the likeliest existence sequence after the last detection in each local (track) hypothesis. This is true because the incremental contribution to the track probability after the last detection until track termination is independent of the track hypothesis. This, in fact, is true with or without the assumption of stationary stochastic dynamics. It follows also that the optimal track-termination structure is identical for all tracks whose last detection time is the same. Tracks with an earlier-still last-detection time also observe a consistent structure. The terminal structure depends solely on the discrete-time death probability \( p_x(\cdot) \) and the detection probability sequence \( p_d(\cdot) \).

These simplifications are perhaps best understood with a notional example. Consider the set of global hypotheses characterized by the set of hypothesis graphs in Figure 1. (Note that we do not call these hypothesis trees, as the structure includes merging in addition to branching.) The example is for \( |Z_1| = 0 \), \( |Z_2| = 2 \), \( |Z_3| = 1 \), and \( |Z_4| = 0 \). We assume no further scans all available; this notion is captured with \( t_5 \rightarrow \infty \). Correspondingly, \( p_x(5) = 1 \), so we need only consider target death hypotheses at time \( t_5 \).

\[\text{Figure 1. Set of hypothesis graphs for a simple example.}\]

First, let us describe the set of hypothesis graphs. Each of the measurements \( Z_{2,1} \) and \( Z_{2,2} \) at time \( t_2 \) may be target-originated. If so, either targets may have been born at time \( t_2 \), corresponding to the null state \( \emptyset \) at time \( t_1 \), or the targets may have been born at time \( t_1 \), corresponding to the existence state \( O \) at time \( t_1 \). The measurement \( Z_{3,1} \) at time \( t_3 \) may be target originated and, if so, it may have the same provenance as \( Z_{2,1} \) or \( Z_{2,2} \), or it may correspond to a distinct object. This latest possibility is the reason for the third hypothesis graph. In the event that \( Z_{3,1} \) is the first detection of an object, we see that there are several possibilities for when this object was born, corresponding to time \( t_1 \), \( t_2 \), or \( t_3 \). For all objects, we see a number of possibilities for time of death.

In Figure 1, we have highlighted some links in the set of
hypothesis graphs to illustrate relevant branches, for certain choices of \( \mu_b(\cdot) \), \( p_x(\cdot) \), and a detection probability sequence \( p_d(\cdot) \). There are several points to note: (1) for each hypothesis graph, there is only one relevant branch preceding the first detection; (2) for each hypothesis graph and for each possible final detection, there is only one relevant branch following the final detection; (3) relevant branches are consistent, in the sense that branches 1 and 4 match, branches 3 and 6 match, and branches 2, 5, and 8 match. Indeed, the likeliest sequences are data-independent. Finally, it was noted above that “tracks with an earlier still last-detection time observe a consistent structure as well”. By this we mean that, had branches 3 and 6 identified the target existence or “coast” hypothesis instead of the death hypothesis, branch 6 would necessarily be followed by yet another coast hypothesis, for consistency with branches 2 and 5.

The upshot of this discussion is that, based on offline analysis, one may simplify the hypothesis graph shown in Figure 1 with the one shown in Figure 2. The latter is a set of (more familiar) hypothesis trees. The crucial observation is that our enhanced MHT treatment has no impact on the number of relevant track hypotheses for detected targets; we need only identify the appropriate birth and death times for each track hypothesis.

Unfortunately, in general we can make no claims as to the structure of the ghost-target MAP solution. The number of ghost target births may vary with each scan, and the structure of the target lifetimes is variable as well. Nonetheless, we do know that the solution is data-independent and, as such, it can be computed offline with knowledge of discrete-time birth-death statistics and the detection probability sequence.

The classical TO-MHT solution for the example above is based on the track-hypothesis trees shown in Figure 3. The difference is a subtle one: here, some track hypotheses are born at \( t_2 \) rather than at \( t_1 \).

In order to emphasize the significance of the difference in Figures 2-3, first let us consider the track hypotheses in Figure 1. Referring to eqn. (15), we neglect the normalizing constant in braces and focus on the incremental contribution to the global hypothesis score by including track hypotheses in the solution set. For instance, the first track hypothesis has score:

\[
\bar{p}(T_1) = (1 - p_d(1))\mu_b(1) \frac{(1 - p_x(2))p_d(2)\Lambda_f(Z_{2,1})}{\Lambda_f(Z_{2,1})}.
\]

\[
(1 - p_x(3))p_d(2)f_5(Z_{3,2}|Z_{2,1}) \frac{(1 - p_x(4))}{(1 - p_d(4))}
\]

\[
(17)
\]

\[
(18)
\]

\[
(19)
\]

\[
(20)
\]

Let us further assume that \( t_0 \to -\infty \), \( t_1 = t_2 = 0 \) sec, \( t_3 = 1 \) sec, \( t_4 = 1.1 \) sec, \( \lambda_b = 100 \) sec\(^{-1} \), \( \lambda_x = 1 \) sec\(^{-1} \), \( \lambda_f = 1 \), and \( p_d = 0.5 \). First, we validate the simplifications leading from Figure 1 to Figure 2:

\[
0 = \mu_b(2) < (1 - p_d)(1 - p_x(2))\mu_b(1) = 50,
\]

(accounting for branches 1, 4), (21)

\[
0.0832 = (1 - p_d)^2(1 - p_x(3))(1 - p_x(4)) < p_x(3) = 0.632,
\]

(accounting for branches 3, 6), (22)

\[
0.0952 = p_x(4) < (1 - p_d)(1 - p_x(4)) = 0.452,
\]

(accounting for branches 2, 5, 8). (23)

Next, using eqns. (18-20), we find that the track
hypothesis scores are given by: \( \tilde{p}(T_1) = 2.08 \), \( \tilde{p}(T_2) = \tilde{p}(T_4) = 15.80 \), \( \tilde{p}(T_3) = 15.80 \). Accordingly, the MAP global hypothesis is given by \( \hat{Q} = \{T_2, T_4, T_3\} \).

For the classical MHT approach corresponding to Figure 3, the track hypotheses and the corresponding scores are different. In particular, we have:

\[
\tilde{p}(T_1) = \frac{(1 - p_d) p_d^2 \mu_b (2)}{\Lambda^2} (1 - p_X (3))(1 - p_X (4)) ,
\]
\[
\tilde{p}(T_2) = \tilde{p}(T_4) = \frac{p_d \mu_b (2) p_d (3)}{\Lambda} ,
\]
\[
\tilde{p}(T_3) = \frac{(1 - p_d) p_d \mu_b (3)}{\Lambda} .
\]

Now we find \( \tilde{p}(T_1) = \tilde{p}(T_2) = \tilde{p}(T_4) = 0 \) and \( \tilde{p}(T_3) = 15.80 \). Thus, the solution under the classical MHT formulation is given by \( \bar{Q} = \{T_3\} \). This solution has much lower posterior probability than the MAP solution identified above. In particular, we have \( p(\hat{Q})/p(\bar{Q}) = \tilde{p}(T_1)\tilde{p}(T_2)\tilde{p}(T_4) \).

To summarize, in Sections III-IV we have derived a recursive expression (eqn. 15) that enables the systematic evaluation of relevant global hypotheses for the MTT problem. The MAP solution includes two types of undetected target births that we call unnoticed targets (those that are eventually detected) and ghost targets (those that are never detected). Though the formulation appears more complex than classical TO-MHT, it has shown that the number of relevant track hypotheses for the visible-target portion of the solution (i.e. ignoring ghost targets) is identical. Further, the optimal track-birth and track-death structure is data-independent and common across many target hypotheses, as described above. We have seen by a simple example that the performance gains that are achieved with the enhanced formulation are nontrivial in terms of posterior probability of the optimal global hypothesis.

V. THE TIME-INARIANT CASE

We now consider the time-invariant (TI) case, by which we mean that the time scans are uniformly spaced, i.e. \( \Delta t = \Delta t \), \( k \geq 0 \). In addition, we same detection statistics apply to each scan, i.e. we have constants \( p_d \) and \( \Lambda \).

It is immediately clear that, in the TI case, the MAP solution does not include any unnoticed target births for any scan, as noted in eqn. (27). Indeed, each missed detection that precedes the first detection for any track hypothesis introduces a factor less than one to the track hypothesis score, namely \( (1 - p_d)(1 - p_X) < 1 \).

\[
\mu = 0 .
\]

Similarly, the MAP solution does not include any track hypotheses with terminal missed detections prior to target death, as each such missed detection introduces the same factor to the track hypothesis score, \( (1 - p_d)(1 - p_X) < 1 \).

Thus, in the TI case the enhanced TO-MHT approaches corresponds precisely to the classical TO-MHT, so far as detected targets are concerned. However, recall that the enhanced TO-MHT solution includes as well ghost targets. Let us now proceed to examine the structure of the MAP ghost-target solution in the TI case.

The incremental contribution to the global hypothesis probability for the ghost targets born at any scan is the following, where \( g \) is the number ghost targets and \( n_i \) is the number of ghosts that live for \( i \) scans. For consistency, we have the relationship given by eqn. (16), which is repeated below as eqn. (29).

\[
\bar{p} = \frac{p_g ((1 - p_X)(1 - p_d)) \sum_{i=1}^{\infty} \frac{((1 - p_d) \mu_b)^i}{i!}}{\prod_{i=1}^{\infty} n_i!}.
\]

It is interesting to observe the structure of the MAP solution to eqns. (28-29), i.e. that solution that maximizes \( \bar{p} \). The first point to note is that ghosts do exist. The null solution, for which \( \bar{p} = 1 \), can be improved upon in the general case.

The next point to note is that, despite the penalty factor \( (1 - p_d)(1 - p_X) < 1 \) associated each additional scan of ghost life, the singleton solution \( n_i = g \), whereby all target ghosts live for a single scan, can be improved upon in the general case. The interpretation for this is that it is beneficial to have varying ghost targets lifetimes, as this corresponds to aggregation over a larger number of indistinguishable global hypotheses.

The penalty factor \( (1 - p_d)(1 - p_X) < 1 \) does have an impact on the structure of the optimal ghost solution. In particular, the optimal solution must obey the following:

\[
n^*_i \geq n^*_{i+1}, i \geq 1 ,
\]
\[
g^* = \sum_{i=1}^{g} n^*_i .
\]

In searching for the optimal ghost structure (30-31), it is sufficient to determine sequentially the optimal structure
for any number of ghosts $g \in \{0, 1, \ldots, g^* + 1\}$. Once we find that the inclusion of an additional ghost cannot lead to an improved solution with respect to maximization of $\mathcal{P}$, we may terminate the search; further ghosts are of no benefit.

Let us consider an example. Let $\mu_b = 70$, $p_X = 0.1$, and $p_d = 0.5$. The optimal singleton solution is given by $g = [(1 - p_d)\alpha_b p_x]$ = 3. More generally, the optimal solution is given by the following: $g^* = 4$ with $n_1^* = 3$, $n_2^* = 1$. This is displayed pictorially in Figure 4. It is easy to see that, under the MAP solution, the steady-state number of ghosts targets alive at any time after the first scan is given by $\mathcal{G}^* = 5$.

Figure 5. An example MAP ghost-target solution.

Ghost targets are not localized in target state space. More precisely, the state of ghost target is consistent with the probability distribution $f_b(\cdot)$ in measurement space. As before, we assume stationary stochastic dynamics so that this distribution applies at birth and subsequently.

VI. CONCLUSIONS

This paper has introduced a generalization of the MHT formalism for MTT. To our knowledge, MHT treatments in the literature do not consider undetected target birth events. Their inclusion leads to an interesting extension to the MHT recursion, and necessitates aggregation over indistinguishable global hypotheses. We show that the MHT recursion factors, enabling TO-MHT, albeit with clusters of indistinguishable undetected births. The treatment requires a distinction between those targets that are eventually detected (unnoticed targets) and those that are never detected (ghost targets).

While the enhanced formulation appears more complex, there is structure to the solution that can be exploited resulting in the same number of relevant track hypotheses for detected targets as in the classical TO-MHT solution. Crucially, as shown with a simple example in the paper, in general the enhanced formulation encompasses global hypotheses that outperform those of the classical formulation in terms of the MAP criterion.

In the time-invariant case, the solution simplifies further as we need not consider unnoticed targets and there is a fixed structure to the ghost-target solution that may be computed offline. This is illustrated with an example.

Efficient hypothesis management remains an important challenge in MHT implementations. In practice, sequential hypothesis pruning and track extraction are required [1-2]. Though this paper is not directly concerned with these aspects, existing algorithms are directly applicable to the enhanced hypothesis space as to the classical one. We emphasize again that the enhanced hypothesis space modifies the classical one but without increasing the number of track hypotheses.

Related work (not in an MHT setting) that introduces the notion of target perceivability may be found in [17].

REFERENCES