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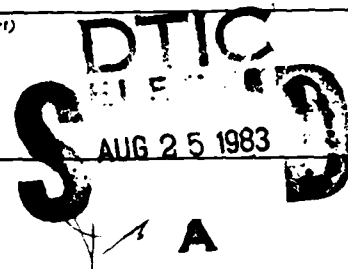
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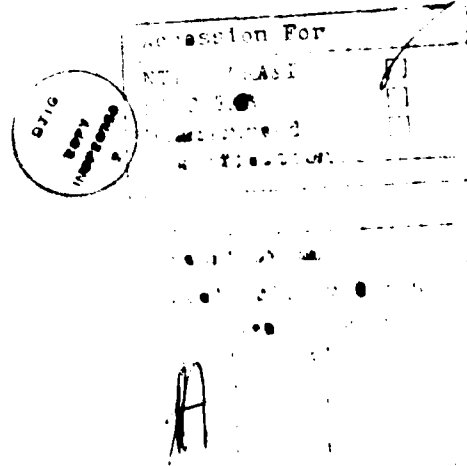
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ABSTRACT

This report describes the development of an advanced multitarget tracking algorithm for surveillance radars. The approach is based on the development of mathematical models relating targets, the environment, and radar parameters to the measurements supplied to the tracking algorithm. The fundamentals of the surveillance and tracking algorithm are based on adaptive hypothesis testing techniques, and specifically, on the multiple model adaptive estimation approach. The algorithm was developed, computer-programmed, and exercised on several hypothetical but realistic surveillance/tracking scenarios.

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SECTION 1

OVERVIEW

This report is concerned with the development and evaluation of an advanced tracking algorithm for surveillance radars. Similar algorithms have been studied for many years. Recent advances in computer technology make a re-examination of current tracking algorithms timely, since it will be possible to implement more sophisticated algorithms in the near future. The most promising algorithms are based on statistical estimation theoretic concepts, specifically on adaptive hypothesis testing techniques. Most of the individual issues that arise in the design of tracking algorithms (false and missing returns, target maneuvers, data association, etc.) have been previously addressed within this framework, but research is needed to handle all of these issues simultaneously.

The algorithm developed in the present research effort provides the capability to incorporate most of the subjective conditions associated with a realistic surveillance/tracking scenario. At present, the algorithm can handle a multitarget tracking situation, it can identify targets' "births" or "deaths" (i.e., appearance or disappearance) and distinguish these from a detection or a missed detection. In the future, the algorithm might be augmented with additional features. It could detect and estimate the occurrence and magnitude of target maneuvers, and it could have the capability of identifying target formations, missile launches, etc.

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The development of the tracking algorithm is firmly grounded in statistical estimation theory; it is an example of the multiple model adaptive estimation approach. In its optimal form, the algorithm cannot be implemented due to data storage and processing requirements which grow without bound. But starting from the complete optimal algorithm, we developed rules for limiting these requirements without significantly compromising tracking performance and implemented the resulting algorithm. Using a selection of simple but realistic scenarios the power of the tracking algorithm and its resiliency in the face of stressing environments has been demonstrated. The implementation is quite general and flexible, providing an excellent example of how to organize a multitarget algorithm for stressing radar surveillance environments.

This report begins with the development of a mathematical model of the target state equations and of the radar measurements (including such environmental factors as clutter and multipath). It should be emphasized that this model is not intended to be a so-called "truth model" capable of faithfully replicating the precise details of radar returns, but rather a "design model" used to ensure that all of the environmental issues are reflected in the tracking algorithm. Subsequently, we develop the so-called algorithmic or simulation model. This model describes the target/radar relationship in a manner suitable for synthetic radar measurement generation which are needed to exercise the surveillance/tracking algorithm. These models are developed and described in detail in Section 2.

Once the radar environment models are established, they are incorporated in the surveillance and tracking algorithm. The optimal version of the tracking algorithm is developed in Section 3; it constitutes a member of the so-called adaptive estimation algorithms family. Section 3 begins with a

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description of the most basic technique for adaptive estimation, the multiple model estimation algorithm. The optimal algorithms are next presented for the three cases of environment phenomena. These cases have the following formulation:

1. one target with measurement errors, missed detections, and false detections, but no maneuvers;
2. one target with measurement errors, missed detections, false detections, appearance and disappearance, but no maneuvers; and
3. an unknown number of targets with measurement errors, missed detections, false detections, appearance and disappearance, but no maneuvers.

Each algorithm is more complex than the preceding, but the progression through the cases aids understanding of the algorithms. Section 3 finishes with a useful reformulation of the algorithm for the most complex case; it is the formulation which is used in implementing the algorithm.

At this point it will have become apparent that implementing the optimal full-blown tracking algorithm is infeasible. This is evident from the exponentially growing number of data association hypotheses with each additional scan. Clearly, practicality dictates that the number of hypotheses actually generated and tested by a tracking algorithm be bounded by some value dependent on the host computer. Consequently, we develop in Section 4 methods that relax the optimal algorithm. The relaxation rules include several approaches such as ignoring unlikely hypotheses (e.g., a "birth" immediately followed by a "death"), gating of data associations (this rule "gates-out" returns from consecutive scans which are unreasonably separated, thus implying impossible target measurement errors), and pruning (i.e., only a fixed number of the most likely hypotheses is allowed).

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In Section 5 the computer implementation of the algorithm is discussed. In Section 6 the computer program is exercised on four hypothetical (but realistic) scenarios involving two and three crossing targets. It is then demonstrated that the (theoretically) suboptimal algorithm (i.e., relaxed by the rules developed in Section 4) performs as accurately as the optimal version. Finally, conclusions drawn from this research effort are summarized in Section 7.

SECTION 2

MODELING OF TARGETS AND OF THE RADAR ENVIRONMENT

Research into tracking theory for airborne surveillance radars requires two sorts of radar environment models. One sort is mathematical and describes the relationship of the radar returns to target variables (position, velocity, etc.) as a function of the radar environment (thermal noise, clutter, etc.) in a manner suitable for tracking algorithm design. The other sort of model is algorithmic and describes the same relationship in a manner suitable for synthetic radar measurement generation. Synthetic radar measurements are needed to exercise any tracking algorithm and to determine its performance and robustness. In this section, we first present our algorithm design model. Then we briefly present the very simple radar measurement generation model used to produce the algorithm performance reported in Section 6. Finally, we sketch a design for a more sophisticated radar model which, if implemented, would allow more thorough testing of airborne surveillance radar tracking algorithms.

2.1 ALGORITHM DESIGN MODEL

Several target-relative phenomena should be modeled: the number of targets (aircraft and missiles) within radar coverage can vary from scan to scan as aircraft land, take off, crash, are shot down, or fly into or out of coverage; in effect targets are "mortal," being "born" and "dying." Targets can move on essentially constant headings with essentially constant velocities or

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they can maneuver (within reasonable limits). An aircraft can launch a missile, i.e., one target splits into two, or be hit by one, i.e., two targets merge into one. In addition, several radar-related phenomena should be modeled: each target can produce only one detection per scan, but may produce none because of thermal noise, clutter, scintillation, etc. False detections may be caused by thermal noise, clutter, jamming, etc. Errors occur in measuring target locations due to thermal noise, clutter jamming, glint, etc. Targets flying in formation may be unresolvable.

Each phenomena included requires a model. Some models can be quite simple, as in the measurement errors which can be treated as white Gaussian noise of known covariance. Others can be relatively complex, as in target maneuvers. And many possible models are plausible for some phenomena, such as target "mortality," i.e., appearance and disappearance. The intuitive model of target "mortality" is simple; but a formal model is needed specifying the probabilities of various numbers of targets being "born" per scan, the probability density function of target states at "birth," the probabilities of targets "dying" on a given scan, etc.

Our model development effort has proceeded by considering just a few phenomena (without trivializing the problem), then adding additional phenomena one step at a time. The cases we have formulated are:

1. one target (known) with measurement errors, missed detections, and false detections, but no maneuvers or other complex phenomena;
2. one target (known) with measurement errors, missed detections, false detections, "mortality," but no maneuvers, etc.; and
3. an unknown number of targets with measurement errors, missed detections, false detections, "mortality," but no maneuvers, etc.

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Complete models for these three cases have been developed and are described in the succeeding three subsections. Presentation of the models in this manner makes the third (and most complex) far more comprehensible than it would be if it were presented in isolation.

2.1.1 Case 1

The first requirement is for a model of the target's dynamic state. We use

$$x(t) = Ax(t-1) + w(t-1) \quad \text{for all } t \quad (2-1)$$

where $w(t)$ is Gaussian distributed with mean 0 and variance W . We can further assume that the components of the dynamic state vector are target position North and East of some arbitrary point and the North and East target velocities. Then we would have

$$x(t) = [P_E(t) \quad P_N(t) \quad \dot{P}_E(t) \quad \dot{P}_N(t)]^T$$

and

$$A = \left[\begin{array}{c|c} I_2 & I_2 T_s \\ \hline 0 & I_2 \end{array} \right] \quad (2-2a)$$

$$W = \left[\begin{array}{c|c} 0 & 0 \\ \hline 0 & W_a T_s^2 \end{array} \right] \quad (2-2b)$$

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where I_2 is the 2x2 identity matrix, T_s is the scan time, and W_a is the covariance of the East and North target accelerations produced by wind, etc. Note that it is possible to define the algorithm without reference to the dimension or content of the dynamic state vector or of the covariance of the state driving noise.

The dynamic state of the target is not its complete state. At any given moment, the one target may or may not be detected; if detected, it may be any one of the detections. We define the target's detection state as $d(t)$, which consists of two components:

$$d(t) = [b(t), i(t)]^T \quad (2-3)$$

where

$$b(t) \in \{D, \bar{D}\} \quad (2-4)$$

and

$$i(t) \in \{1, \dots, L(t)\} \quad (2-5)$$

where $b(t)$ equals D if the target is detected at t and $\bar{D}$ otherwise, where $i(t)$ equals the index of the target detection if the target is detected at t , and where $L(t)$ is the number of detections at t .

The detection state, like the dynamic state, is Markovian because we assume

$$\text{Prob}[d(t)|d(\tau) \text{ for } \tau < t] = \text{Prob}[d(t)] \text{ for all } t. \quad (2-6)$$

The basic property of conditional expectations allows us to write

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$$\text{Prob}[d(t)] = \text{Prob}[i(t)|b(t)]\text{Prob}[b(t)] \quad \text{for all } t, \quad (2-7)$$

and we model the two terms on the right-hand side of Eq. 2-7 as follows:

$$\begin{aligned} \text{Prob}[b(t)] = & 1 \quad \text{for } b(t)=\bar{D} \text{ and } L(t)=0 \\ & 1-P_D \quad \text{for } b(t)=\bar{D} \text{ and } L(t)>0 \\ & P_D \quad \text{for } b(t)=D \text{ and } L(t)>0 \\ & 0 \quad \text{otherwise,} \end{aligned} \quad (2-8)$$

and

$$\begin{aligned} \text{Prob}[i(t)|b(t)] = & 1/L(t) \quad \text{for } b(t)=D \text{ and } 1 \leq i(t) \leq L(t) \\ & 0 \quad \text{otherwise.} \end{aligned} \quad (2-9)$$

The complete state of the target is the hybrid of the continuous-valued dynamic state x and the discrete-valued detection state d . This hybrid is also Markovian because we assume the dynamic and detection states evolve independently.

The single target is assumed to cause at most one detection per scan, but any number of false detections may occur. We denote the number of false detections at t by $L_{FA}(t)$ and assume it to be Poisson distributed with parameter λ_{FA} . That is,

$$\begin{aligned} \text{Prob}[L_{FA}(t)] = & e^{-\lambda_{FA}} \lambda_{FA}^{L_{FA}(t)} / L_{FA}(t)! \quad \text{for } L_{FA}(t) \geq 0 \\ & 0 \quad \text{otherwise} \end{aligned} \quad (2-10)$$

Note that

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$$L(t) = L_{FA}(t) \quad \text{if } b(t) = \bar{D} \quad (2-11)$$

$$L(t) = L_{FA}(t) + 1 \quad \text{otherwise,}$$

so $L(t)$ is conditionally Poisson distributed. Also note that λ_{FA} is the expected number of false alarms per scan.

The above paragraphs describe the detection process for the 1 target in the presence of false alarms, but not the measurement process. We define $z(i,t)$ to be the measurement of the i -th detection at t and let

$$z(i(t),t) = Cx(t) + v(t) \quad \text{if } b(t) = D \quad (2-12a)$$

$$z(k,t) = v'(k,t) \quad \text{for } k \in \{1, \dots, L(t)\} - \{i(t)\} \quad \text{if } b(t) = D \quad (2-12b)$$

$$z(k,t) = v'(k,t) \quad \text{for } k \in \{1, \dots, L(t)\} \quad \text{if } b(t) \neq D \quad (2-12c)$$

where $v(t)$ is Gaussian distributed with mean 0 and covariance V while $v'(i,t)$ is uniformly distributed over the surveillance set Ξ . This surveillance set is a closed subset of the measurement space. We further assume that

$$C = [I_2 \quad 0] \quad (2-13)$$

and

$$\Xi = \{z \mid \|z\| < \text{maximum surveillance range}\} \quad (2-14)$$

Again, it is not necessary to be so restrictive in defining the algorithm; we have chosen this simple model for our initial development in order to avoid the obscuring of the key concepts to be developed.

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It will prove convenient to let $|\Xi|$ symbolize the area or volume of the surveillance set. Then

$$\begin{aligned} \text{Prob}[v'(i,t)] &= |\Xi|^{-1} \quad \text{if } v'(i,t) \in \Xi \\ &0 \quad \text{otherwise} \end{aligned} \quad (2-15)$$

where $\text{Prob}[v'(i,t)]$ is shorthand for the probability density function of $v'(i,t)$. It will also prove convenient to define a constant, ρ_{FA} , such that

$$\rho_{FA} = \lambda_{FA} / |\Xi| \quad . \quad (2-16)$$

This constant is the expected number of false detections per scan and per unit area or volume and will be referred to as the false alarm density; it is proportional to the radar false alarm rate.

2.1.2 Case 2

Taking into account target "mortality," we must model the "birth" and "death" of the single target. We do so by expanding the definitions of $d(t)$ and $b(t)$ in the previous case. As before

$$d(t) = [b(t), i(t)]^T \quad (2-17)$$

but in this case,

$$b(t) \in \{\bar{B}, D, \bar{D}, X\} \quad (2-18)$$

where $b(t)$ equals $\bar{B}$ if the target has never been detected on or before t (i.e., it is "unborn"), equals D if the target is detected, equals $\bar{D}$ if the target is undetected but has been detected and will be again (i.e., it is

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still "alive"), and X if the target will never be detected again (i.e., it is "dead"). These definitions of the values which $b(t)$ may take hint at the restrictions on the state transitions allowed; the single target is "born" only when it is first detected and cannot be detected again once it dies.

Because it now involves more than just detection, we rename $d(t)$ the event state of the 1 target; it includes all of the discrete components of the complete state of the 1 target. The event state is Markovian because we assume

$$\text{Prob}[d(t)|d(\tau) \text{ for } \tau \leq t-1] = \text{Prob}[i(t)|b(t)]\text{Prob}[b(t)|b(t-1)] \text{ for all } t > 0 \quad (2-19)$$

$$\begin{aligned} \text{Prob}[i(t)|b(t)] &= 1/L(t) \text{ for } b(t)=D \text{ and } 1 \leq i(t) \leq L(t) \\ &0 \text{ otherwise ,} \end{aligned} \quad (2-20)$$

$$\begin{aligned} \text{Prob}[b(t)|b(t-1)] &= 1-P_B \quad \text{for } b(t)=\bar{B} \text{ and } b(t-1)=\bar{B} \\ &P_B \quad \text{for } b(t)=D \text{ and } b(t-1)=\bar{B} \\ &P_D \quad \text{for } b(t)=D \text{ and } b(t-1)=D \\ &1-P_D-P_X \quad \text{for } b(t)=\bar{D} \text{ and } b(t-1)=D \\ &P_X \quad \text{for } b(t)=X \text{ and } b(t-1)=D \\ &P_D \quad \text{for } b(t)=D \text{ and } b(t-1)=\bar{D} \\ &1-P_D \quad \text{for } b(t)=\bar{D} \text{ and } b(t-1)=\bar{D} \\ &1 \quad \text{for } b(t)=X \text{ and } b(t-1)=X \\ &0 \quad \text{otherwise ,} \end{aligned} \quad (2-21a)$$

and

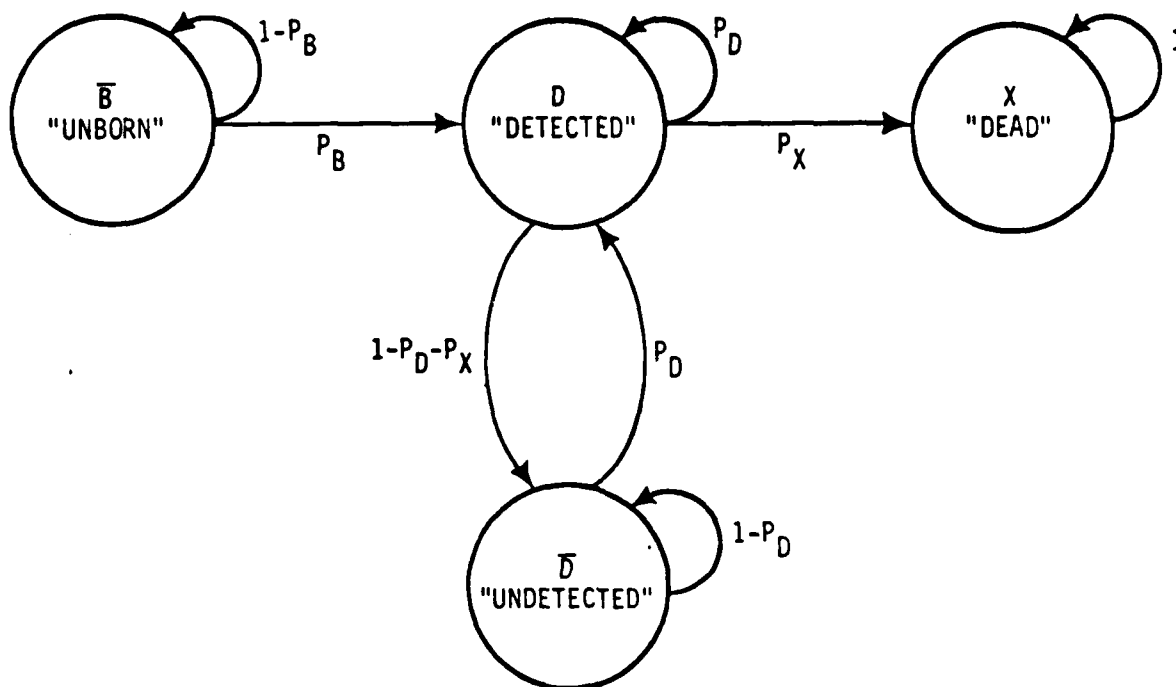
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$$\text{Prob}[b(0)] = 1 \text{ for } b(0)=\bar{B}$$

(2-21b)

0 otherwise

The state transitions of $b(t)$ are diagrammed in Fig. 2-1.



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Figure 2-1. State Transition Diagram for $b(t)$ with Associated Transition Probabilities.

The figure clearly illustrates that we have intimately coupled "mortality," a target-related phenomenon, and detection, a radar-related phenomenon. On the surface, it would seem preferable to have less coupling; to associate a target's "birth" not with its first detection but rather with its entry into the radar's coverage (or some other such event external to the radar). To do so would cause additional complexity in the resulting tracking algorithm.

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Detection is an observable event to the radar tracking algorithm, but target entry into the radar's coverage is not observable in the absence of target detection; the radar receives no information about target positions if the target is not detected. If one were to model without the coupling introduced here, the resulting algorithm would take into account the possibility of existing targets which have not yet been detected. Clearly such hypotheses are indistinguishable from ones which avoid hypothesizing undetected targets. This point illustrates the care which must be taken in modeling the radar environment; models which seem natural or intuitively pleasing on the surface may introduce subtle but substantial complexities in the tracking algorithm.

The model of the single target's dynamic state must also be modified for this case. It becomes the following:

$$x(t) = \begin{array}{ll} Ax(t-1)+w(t-1) & \text{if } b(t)=D \text{ or } \bar{D} \text{ and } b(t-1)=D \text{ or } \bar{D} \\ x_0 & \text{if } b(t)=D \text{ and } b(t-1)=\bar{D} \end{array} \quad (2-22)$$

where x_0 is Gaussian distributed with mean 0 and covariance Σ_0 . Effectively, x_0 is the dynamic state with which the target is "born." Once "born," the single targets dynamic state evolves in the same manner as Case 1 until the target "dies." The dynamic state of the target before its "birth" or after its "death" is undefined.

2.1.3 Case 3

In this case, the number of targets is greater than one. We model the total number of targets as indefinitely large, but assume that a finite number are "born" on any given scan. Thus, the number "born" at or before t , denoted

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by $N(t)$, is always finite; it also is monotonically increasing with time. As with the previous case, it is necessary to extend the definition of $d(t)$. In this case, we let

$$d(t) = [N(t), d'(1,t)^T, d'(2,t)^T, \dots, d'(N(t),t)^T]^T \quad (2-23)$$

where

$$d'(\ell, t) = [b(\ell, t), i(\ell, t)]^T, \quad (2-24)$$

$$b(\ell, t) \in \{\bar{B}, \bar{D}, \bar{D}, X\}, \quad (2-25)$$

and

$$i(\ell, t) \in \{1, \dots, L(t)\}. \quad (2-26)$$

Effectively, $d'(\ell, t)$ is the event state of the ℓ -th target where that state is as defined for the 1 target in Case 2. The total discrete valued state of the system of targets $d(t)$, is finite dimensional because it only includes the individual event states $d'(\ell, t)$ of the $N(t)$ targets "born" on or before scan t , but the dimension grows with time.

This event state is Markovian. In particular, we assume

$$\begin{aligned} \text{Prob}(d(t)|d(t-1)) &= \text{Prob}(N(t)|N(t-1)) \prod_{\ell=1}^{N(t)} \text{Prob}[b(\ell, t)|b(\ell, t-1), N(t), N(t-1)] \\ &\times p(i(1, t), \dots, i(N(t), t) | b(1, t), \dots, b(N(t), t)) \end{aligned} \quad (2-27)$$

where

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$$\begin{aligned}
 \text{Prob}[b(l,t)|b(l,t-1),N(t),N(t-1)] &= 1 && \text{for } b(l,t)=B \text{ and } N(t)<l \\
 &1 && \text{for } b(l,t)=D \text{ and } N(t-1)<l\leq N(t) \\
 &P_D && \text{for } b(l,t)=D \text{ and } b(l,t-1)=D \\
 &1-P_D-P_X && \text{for } b(l,t)=\bar{D} \text{ and } b(l,t-1)=D \\
 &P_X && \text{for } b(l,t)=X \text{ and } b(l,t-1)=D \\
 &P_D && \text{for } b(l,t)=D \text{ and } b(l,t-1)=\bar{D} \\
 &1-P_D && \text{for } b(l,t)=\bar{D} \text{ and } b(l,t-1)=\bar{D} \\
 &1 && \text{for } b(l,t)=X \text{ and } b(l,t-1)=X \\
 &0 && \text{otherwise} \qquad (2-28)
 \end{aligned}$$

$$\begin{aligned}
 \text{Prob}[N(t)|N(t-1)] &= e^{\frac{-\lambda_B [N(t)-N(t-1)]}{\lambda_B}} / [N(t)-N(t-1)]! \text{ for } N(t) \geq N(t-1) \\
 &\text{and } t > 0, \qquad (2-29a)
 \end{aligned}$$

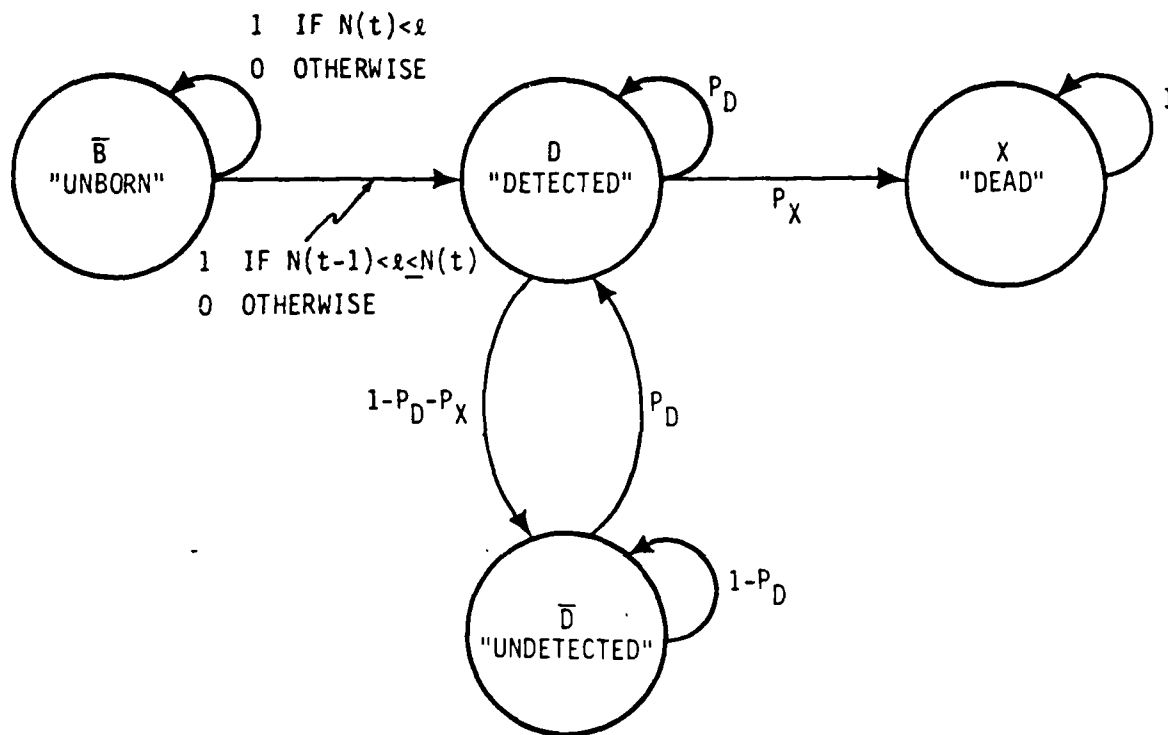
and

$$\begin{aligned}
 \text{Prob}[N(0)] &= 1 \text{ for } N(0)=0 \\
 &0 \text{ otherwise} \qquad (2-29b)
 \end{aligned}$$

We will define the last term in Eq. 2-27 in a moment, but it is useful to pause at this point to provide an interpretation of the above expressions which actually are simpler than they may appear. The state transitions of $b(k,t)$ are diagrammed in Fig. 2-2. This diagram is virtually identical to Fig. 2-1; the difference is that the transition from $\bar{B}$ to D, i.e., the "birth"

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of the target is governed by the $N(t)$ process. When a target's number comes up, it is "born." The number of targets "born" on a given scan is Poisson distributed with mean λ_b and is independent from scan to scan.



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Figure 2-2. State Transition Diagram for $b(\ell, t)$ with Associated Transition Probabilities.

We now define the probabilistic description of the data association variables $i(\ell, t)$. The key here is to note that specifying the $b(\ell, t)$, $\ell=1, \dots$, $N(t)$ determines which $i(\ell, t)$ must be defined (i.e., which targets are to have measurements associated with them at time t). It is useful to divide this set of targets into three groups:

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$$\Psi_{DB}^-(t) = \{\ell | b(\ell, t) = D \& b(\ell, t-1) = \bar{B}\} \quad (2-30a)$$

$$\Psi_{DD}(t) = \{\ell | b(\ell, t) = D \& b(\ell, t-1) = D\} \quad (2-30b)$$

$$\Psi_{DD}^- = \{\ell | b(\ell, t) = D \& b(\ell, t-1) = \bar{D}\} \quad (2-30c)$$

We use the lower-case letter $\psi_{DB}^-(t)$, $\psi_{DD}^-(t)$, and $\psi_{DD}(t)$ to denote the cardinalities of these sets. The probability distribution for the $i(\ell, t)$ for ℓ in the union of these three sets can be described as follows: of the total set of $L(t)$ returns at time t , it is equally likely that any subset of cardinality

$$\psi_{DB}^-(t) + \psi_{DD}(t) + \psi_{DD}^-(t) \quad (2-31)$$

corresponds to the set of returns from targets; out of this subset, it is equally likely that any subset of cardinality

$$\psi_{DD}(t) + \psi_{DD}^-(t) \quad (2-32)$$

corresponds to the set of returns from targets which have been detected at previous times, and any permutation of the elements of this subset corresponds to an equally likely association of measurements in this subset with the set of previously existing targets which are detected at time t . The remaining $\psi_{DB}^-(t)$ returns to be associated correspond to returns from new targets. Note that here there are a number of absolutely indistinguishable possibilities, corresponding to the ordering of the new targets in our list. We remove this ambiguity, as we describe in more detail later, by ordering these targets in a unique manner, corresponding to the magnitude of the range measurement

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associated with each. Given the above discussion, one can compute the probability for any allowable set of values of

$$i(l,t), l \in \Psi_{DB}(t) \cup \Psi_{DD}(t) \cup \Psi_{DD}(t) \quad . \quad (2-33)$$

Here "allowable" means, for example that no two of the $i(l,t)$'s can take on the same value, as individual returns correspond to individual targets. The resulting probability is:

$$\begin{aligned} p(i(1,t), \dots, i(N(t),t) | b(1,t), \dots, b(N(t),t)) \\ = p(i(l,t), l \in \Psi_{DB}(t) \cup \Psi_{DD}(t) \cup \Psi_{DD}(t)) \\ = \frac{[L(t) - \Psi_{DD}(t) - \Psi_{DD}(t) - \Psi_{DB}(t)]! \Psi_{DB}!}{L(t)!} \quad . \quad (2-34) \end{aligned}$$

This probability is, as expected, uniform over the set of allowable values.

Just as it was necessary to define a total discrete valued state for the system of targets, made up of individual event states, it is necessary to define a total continuous valued state, made up of the individual target's dynamic states. Thus we let

$$x(t) = [N(t), x'(1,t)^T, x'(2,t)^T, \dots, x'(N(t),t)^T]^T \quad \text{for } t \geq 0 \quad (2-35)$$

where

$$\begin{aligned} x'(l,t) &= Ax'(l,t-1) + w(l,t-1) \quad \text{if } b(l,t)=D \text{ or } \bar{D} \text{ and } b(l,t-1)=D \text{ or } \bar{D} \quad , \\ x'_0(l) & \quad \quad \quad \text{if } b(l,t)=D \quad \quad \quad \text{and } b(l,t-1)=\bar{B} \quad (2-36) \end{aligned}$$

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and where $x'_o(l)$ is independently Gaussian distributed for all l with mean 0 and covariance Σ'_o . Each target's dynamic state is modeled in this case as the single target's dynamic state was modeled in Case 2.

The measurement model must also be modified to account for multiple targets and to be consistent with the data associations specified by the $i(l,t)$ and $b(l,t)$. Specifically,

$$z(i(l,t),t) = Cx'(l,t) + v(k,t) \quad \text{for } l \in \Psi_{DB}(t) \cup \Psi_{DD}(t) \quad (2-37a)$$

$$z(j,t) = v'(j,t) \quad \text{for } j \in \Phi(t) \quad (2-37b)$$

where $v(k,t)$ is independently Gaussian distributed with mean 0 and covariance V , where $v'(j,t)$ is uniformly distributed over the surveillance set Ξ , as in Case 1, and where

$$\Phi(t) = \{1, \dots, L(t)\} - \{i(l,t) | l \in \Psi_{DB}(t) \cup \Psi_{DD}(t)\} \quad (2-38)$$

As discussed earlier, in order to remove ambiguity in ordering new targets we place the following constraint on the $i(l,t)$: should $\Psi_{DB}(t)$ contain more than one element, we restrict the indices it contains, $N(t-1)$ through $N(t)$, to be ordered such that

$$\|z(i(l,t),t)\| < \|z(i(l',t),t)\| \quad (2-39)$$

for all l and l' in $\Psi_{DB}(t)$ such that $l < l'$. That is to say, if more than one target is "born" at t , we assume they are indexed in magnitude order of the measurements they produce. Because each measurement is a random value, this ordering is unique.

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2.1.4 Environment Model Accuracy

Certain aspects of these models are somewhat unrealistic. For example, it is assumed that the airborne surveillance radar provides the tracker with a 360° "snapshot" of detected target positions once per scan. In typical airborne surveillance radars, each azimuth is revisited once per scan, but in a rotating search pattern. More significantly, position measurement accuracy, detection probability, and the distribution of false detections are all assumed to be independent of range and azimuth. In typical airborne surveillance radars, measurement accuracy degrades with range, because of the signal-to-thermal noise power ratio decreases with range and the width of the radar beam (in meters, not radians) increases with range. Also, clutter, and the signal processing techniques used to suppress its impact, can have a very non-uniform effect, blocking target detection or producing dense clusters of false detections in local regions of the surveillance volume.

The obvious question is whether a tracking algorithm based on a somewhat unrealistic model can perform well. There is reason to believe that an unrealistic model need not produce poor tracking performance. In simpler, single target tracking problems, Kalman filters are often applied even when the uncertainties in target motion or measurement are known to be non-Gaussian in distribution and of variance different from that assumed. Yet these Kalman filters produce position and velocity estimates and predictions which are quite satisfactory; they perform quite robustly. There may even be an advantage to basing a tracking algorithm on a somewhat unrealistic model if it reduces the sensitivity of model performance to mismatches between the actual and modeled environments. Consider a tracking algorithm based on an

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exceedingly accurate model of sea clutter returns over water; its performance may be better, but how will its performance be degraded by ground clutter when used over land, or over an archipelago?

The question of whether satisfactory performance can be achieved by a tracking algorithm based on a somewhat unrealistic model of the radar environment cannot be definitively answered using analytic techniques. The use of analytic techniques requires the assumption of an environment model (possibly different from that upon which the tracking algorithm is based), leading to the question of how accurate this model must be. A definitive answer requires the use of actual radar data to drive the algorithm and "truth" data which reliably reports the actual positions and velocities of the tracked aircraft. Of course, such data is expensive to obtain. Simulated data can be clearly as valuable. Simulation also requires use of an environment model, but allows a very complex model. By using a significantly more complex model to produce simulated radar data than the model upon which the tracking algorithm is based, the robustness of the tracking algorithm in the face of environment modeling inaccuracies can be tested.

2.2 SIMULATION MODEL

As noted immediately above, an environment model is needed in any radar simulation producing data to drive a tracking algorithm and that model should be more complex than (or at least different from) the model upon which the algorithm is based in order to test the algorithm's robustness. Early in this project we produced a high-level design for an ideal airborne surveillance radar simulation for testing tracking algorithms. In concert with our tracking algorithm software development, we began developing software for a

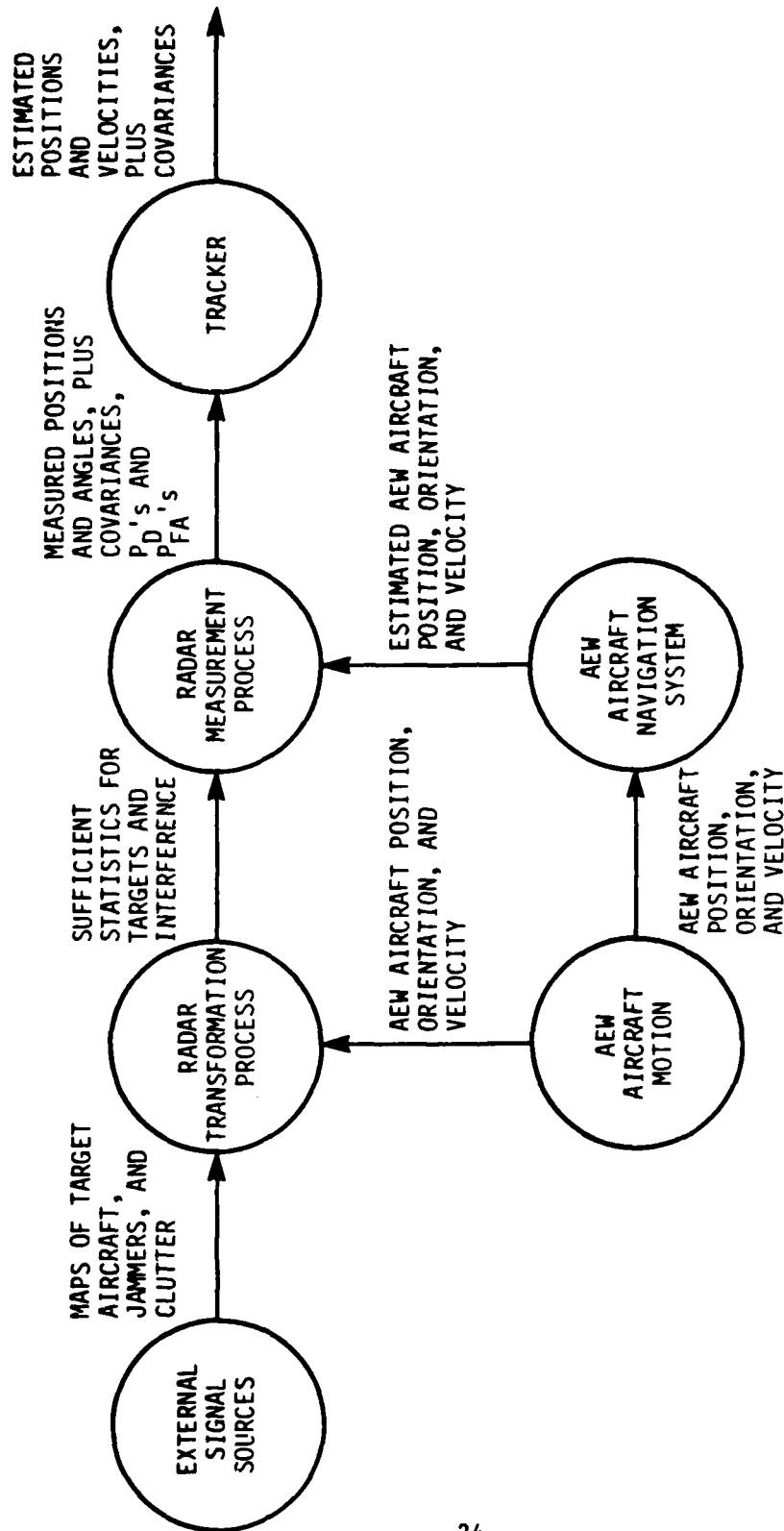
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simplified simulation with a goal of building toward the ideal simulation. The high-level design of the ideal simulation is described in this subsection.

Figure 2-3 illustrates our conceptual model of the context in which the tracking algorithm operates. We have decomposed the conceptual model into several linked submodels which can be usefully isolated intellectually. The "external signal sources" are target aircraft, jammers, and ground clutter; the "external signal sources" submodel describes these sources, including target aircraft motion. Motion of the airborne early warning (AEW) aircraft is described in another submodel. All pretracking functions and phenomena of the AEW radar system are described in the "radar transformation process" and the "radar measurement process" submodels. The division of the radar system into two submodels is somewhat arbitrary, but convenient. Functionally, the division is between the output of the Doppler filters and the input to the detection processor. In order to suppress ground clutter returns in the antenna's main lobe, the "radar measurement process" must have available an estimate of the AEW aircraft ground speed and heading. We assume that estimate is provided by the "AEW aircraft navigation system" which we describe rather simply. The figure names the information provided by each submodel to the others; this information, and the submodels, are briefly described in the next few paragraphs. Time is treated as discrete, not continuous, in all of the submodels.

2.2.1 "External Signal Sources" Submodel

We model individual target aircraft motion as arbitrary within realistic constraints on accelerations and velocities. This approach proved successful in recent ALPHATECH research for MICON on aircraft maneuver detection. The



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Figure 2-3. Conceptual Simulation Model.

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number of target aircraft is also considered arbitrary but constrained to be reasonable. Targets flying in formation can be modeled; since they would typically be unresolvable, they are considered collocated. Jammers may also be collocated with aircraft or they may be stationary. Ground clutter is modeled as both diffuse (producing noise-like returns) and discrete (producing target-like returns). At each discrete time step, the "external signal sources" submodel supplies maps of the signal sources describing:

1. current target aircraft positions,
2. current jammer positions and effective radiated power,
3. diffuse clutter densities, and
4. positions of discrete clutter sources.

The map coordinates are "absolute" in that they are rectangular and are referenced to a fixed location, not to the current position of the AEW aircraft.

We initially are making several simplifying assumptions about jamming and clutter. Jammers are assumed to be stationary, all of equal power, and uniformly distributed. We similarly assume that discrete clutter sources are all of equal size and uniformly distributed. Diffuse clutter is assumed to be of uniform density everywhere.

2.2.2 "AEW Aircraft" Submodels

Motion of the AEW aircraft is assumed to be periodic, along a racetrack course. The "AEW aircraft motion" submodel also outputs a map in "absolute" coordinates at each discrete time step, giving the current AEW aircraft position, orientation, and velocity. The "AEW aircraft navigation system" submodel presently is assumed to pass these values through without alteration at each time step. In reality, there are errors introduced into the tracking

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process by use of estimates of AEW aircraft position, orientation, and velocity. But we believe that such errors are small compared to others and so have chosen not to model this source at this time.

2.2.3 "Radar Transformation Process" Submodel

The AEW aircraft's radar is modeled as doubly transforming the maps of the external signal sources in the course of producing the Doppler filter outputs. The first transformation is a geometric one: using the current AEW aircraft position, the maps are translated into radar-centered polar coordinates. The second transformation is into sufficient statistics at the output of the Doppler filters. Actually, the outputs of the Doppler filters are random voltages. But we are not interested in modeling these voltages themselves; we are interested in modeling the detection and location of target aircraft using these voltages. Thus, it is efficient to compute only statistics sufficient to describe the random voltages from the viewpoint of the detection and location processes. Both the overall model and the simulation based upon it are simplified by using sufficient statistics at this stage. In the "radar transformation process" submodel we are also making some simplifying assumptions initially. For example, all antenna and Doppler filter side-lobes assume constant magnitude while the main lobes are "squared off."

The sufficient statistics are described by two range/azimuth/Doppler frequency maps. One is for target returns (including multipath returns) and discrete clutter returns. It gives the expected range, azimuth, and Doppler of the peak return as well as the expected magnitude of the peak. The second map is for noise-like interference (jamming, diffuse clutter returns, and receiver noise combined). It gives the expected interference power as a function of

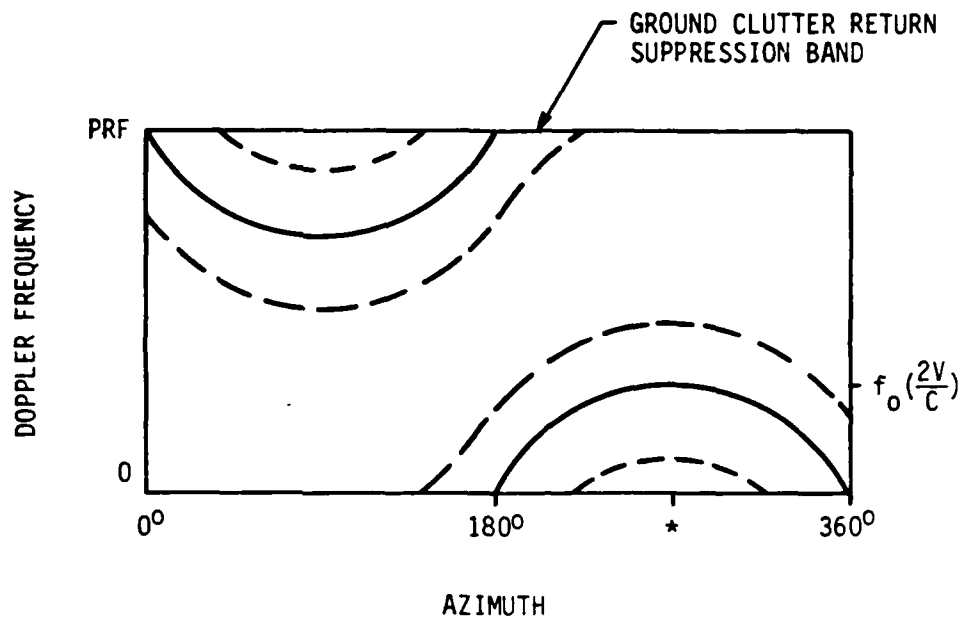
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range, azimuth, and Doppler. The sufficient statistics are calculated for each azimuth as if that azimuth were at the center of the beam and the beam were stationary. Thus, the rotation of the radar antenna and all its effects are not modeled. This omission should have little impact on tracking algorithm performance and greatly simplifies the model (and the simulation).

2.2.4 "Radar Measurement Process" Submodel

The "radar measurement process" models all detection and post-detection radar system features short of the tracker. The detection algorithm is quite simple: response peaks in range, azimuth, and Doppler above a fixed threshold are declared detections except those occurring in the azimuth/Doppler band predicted for main lobe ground clutter returns or those occurring along azimuths where excessive jamming creates a very high interference level. Figure 2-4 illustrates the azimuth/Doppler band. For each azimuth value, that band is constant width in Doppler and is centered on the currently estimated AEW aircraft ground speed along that azimuth. Detection statistics can be calculated from the two maps of sufficient statistics using standard formulae for the detection of signals in noise or noise-like interference. False alarm statistics can be similarly calculated from the map of sufficient statistics for noise-like interference.

Interpolation of detection range and azimuth is modeled by assuming independent Gaussian measurement errors with variances inversely proportional to mean target response-to-mean interference ratio. The resultant polar, AEW-relative measurements are translated into "absolute" coordinates for input to the tracker using the current estimate of the AEW aircraft position.



* = HEADING OF AIRCRAFT
 V = AEW AIRCRAFT VELOCITY

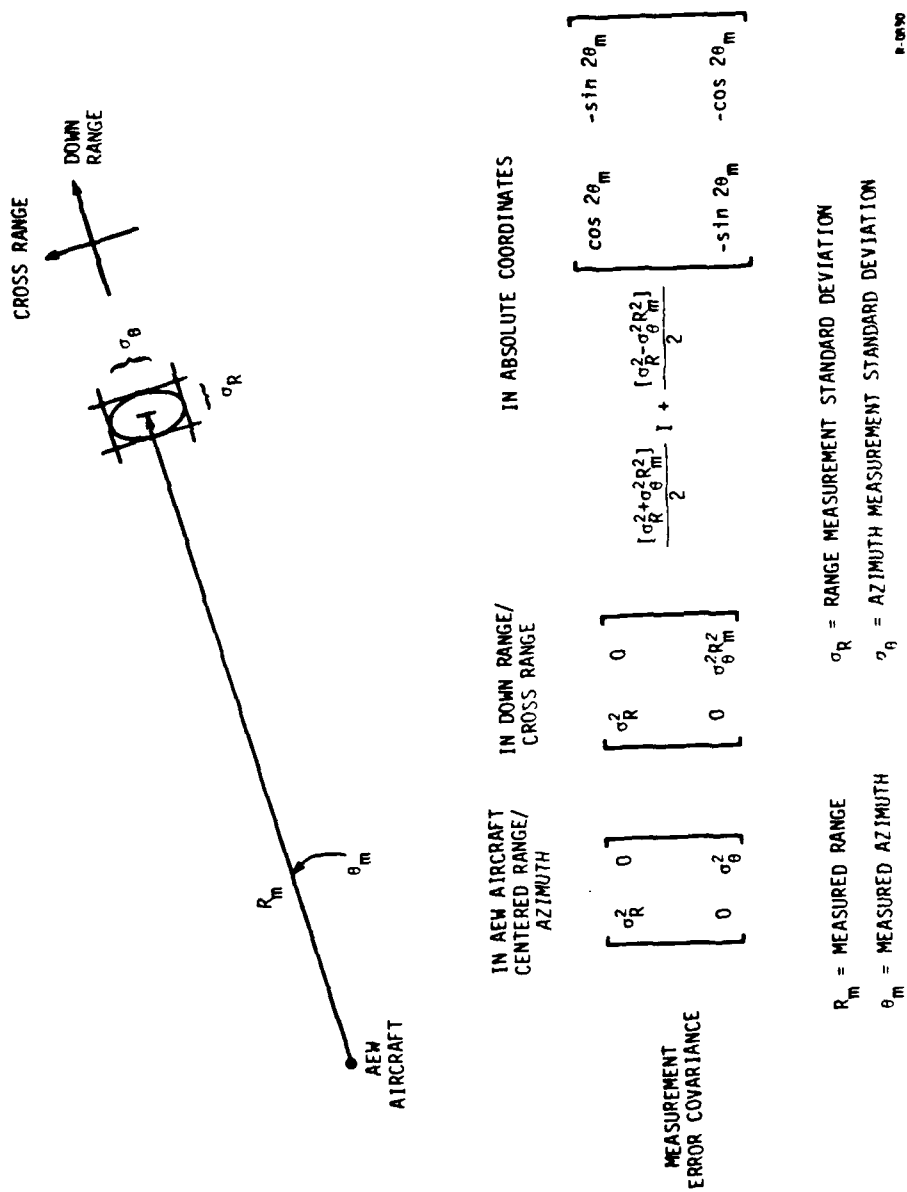
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Figure 2-4. Azimuth/Doppler Band.

It is necessary also to translate the measurement covariance into absolute coordinates. Figure 2-5 illustrates the translation. Azimuthal uncertainty must be translated into cross range uncertainty and then the down range and cross range uncertainties must be translated into absolute coordinate uncertainties.

2.2.5 "Tracker" Submodel

The tracking algorithm requires estimates of target aircraft detection probabilities and of false alarm rates in order to correctly account for missed and false detections. In some AEW radar systems, these quantities may



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Figure 2-5. Measurement Covariance Transformation.

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be estimated from signal processor outputs by sophisticated means while in other systems nominal values are assumed. For simplicity, we have chosen to assume nominal values. The values are modeled as provided by the "radar measurement process" as they would be in more sophisticated cases.

SECTION 3

ALGORITHM DEVELOPMENT: OPTIMAL ALGORITHM

Optimal linear estimation algorithms are by now well understood from both a theoretical and applied point of view. In contrast, aside from the adhoc extended Kalman filter, no general nonlinear estimation algorithms are available. But for a specific class of problems, specifically, problems that would be linear except for the presence of certain unknown discrete or continuous parameters, the family of so-called adaptive estimation algorithms are available. The problems of target tracking in the environment described in the previous section fall into this class. Such algorithms are designed to be optimal by some probabilistic criterion, e.g., Bayesian, maximum likelihood, or maximum a posteriori probability.

This section begins with a description of the most basic technique for adaptive estimation, the multiple model estimation algorithm. This basic technique assumes a finite number of unknown discrete parameters; its generalization to a number of discrete parameters which grow without bound is then described. The optimal algorithms are next presented for the three cases of environment phenomena in the previous section (see pp. 5 and 6). Each algorithm is more complex than the preceding, but the progression through the cases aids understanding of the algorithms. The section finishes with a useful reformulation of the algorithm for the most complex case; it is the formulation which was used in implementing the algorithm.

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3.1 MULTIPLE MODEL ADAPTIVE ESTIMATION (MMAE) ALGORITHM

3.1.1 Basic Algorithm

The basic MMAE algorithm is defined for a linear system of the form

State Dynamics

$$\underline{x}(t+1) = \underline{A}(t)\underline{x}(t) + \underline{w}(t) \quad (3-1)$$

Measurement Equation

$$\underline{z}(t+1) = \underline{C}(t+1)\underline{x}(t+1) + \underline{v}(t+1) \quad (3-2)$$

where $t=0,1,2,\dots$ is the time index,

$\underline{x}(t) \in \mathbb{R}^J$ is the state vector (nonwhite stochastic sequence),

$\underline{w}(t) \in \mathbb{R}^J$ is the white plant noise,

$\underline{v}(t) \in \mathbb{R}^K$ is the white measurement noise, and

$\underline{z}(t) \in \mathbb{R}^K$ is the measurement vector.

Probabilistic Information

The initial state $\underline{x}(0)$ is Gaussian with

$$E\{\underline{x}(0)\} = \bar{\underline{x}}(0) \quad (3-3)$$

$$\text{cov}[\underline{x}(0); \underline{x}(0)] = \underline{\Sigma}_0 = \underline{\Sigma}_0' > \underline{0} \quad (3-4)$$

The plant noise $\underline{w}(t)$ is Gaussian discrete white-noise with

$$E\{\underline{w}(t)\} = \underline{0} \quad (3-5)$$

$$\text{cov}[\underline{w}(t), \underline{w}(\tau)] = \underline{W}(t) \delta_{t\tau} \quad (3-6)$$

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$$\underline{w}(t) = \underline{w}^T(t) > \underline{0} \quad . \quad (3-7)$$

The measurement noise $\underline{v}(t)$ is Gaussian discrete white-noise with

$$E\{\underline{v}(t)\} = \underline{0} \quad (3-8)$$

$$\text{cov}[\underline{v}(t); \underline{v}(\tau)] = \underline{V}(t) \delta_{t\tau} \quad (3-9)$$

$$\underline{V}(t) = \underline{V}^T(t) > \underline{0} \quad (3-10)$$

(i.e., every measurement is corrupted by white noise)

$$\underline{x}(0) \quad , \quad \underline{w}(t) \quad , \quad \underline{v}(\tau) \quad (3-11)$$

are independent for all t, τ .

It is assumed that the system of concern has been modeled in the above form, but that some parameters of the model are undetermined. If we denote the unknown parameters by a vector $\underline{d}$, the dependence of the model matrices can be made explicit by the notation $\underline{A}(t; \underline{d})$, $\underline{W}(t; \underline{d})$, etc. it is assumed that the parameter or model set is finite and discrete, $\underline{d} \in \{\underline{D}_1, \underline{D}_2, \dots, \underline{D}_N\}$. This means, in essence, that N hypotheses are possible concerning the system and that the goal is to identify which is correct as well as to estimate the system state.

The solution the MMAE estimation algorithm provides is a means to find the optimal (conditional expectation) estimate $\hat{\underline{x}}(t|t)$ of the state $\underline{x}(t)$ and a means to compute the probability $p_i(t)$ that the i -th parameter is the correct parameter (alternatively, that the i -th hypothesis is correct), given the observations $\underline{z}(0), \dots, \underline{z}(t)$. Several authors have considered this problem; the

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original derivation is apparently due to Magill [1].* At any rate, straightforward Bayesian manipulations show that the solution is given by the relations

$$p_i(t) = \frac{\beta_i(t) \exp \left[-\frac{1}{2} \underline{r}_i^T(t) \underline{S}_i^{-1}(t) \underline{r}_i(t) \right]}{\sum_{j=1}^N \beta_j(t) \exp \left[-\frac{1}{2} \underline{r}_j^T(t) \underline{S}_j^{-1}(t) \underline{r}_j(t) \right]} p_i(t-1) \quad (3-12)$$

$$\hat{\underline{x}}(t|t) = \sum_{i=1}^N \hat{\underline{x}}_i(t|t) p_i(t) \quad (3-13)$$

In Eqs. 3-12 and 3-13, the subscript i denotes a quantity computed assuming that model i is the correct model, i.e., that $\underline{d} = \underline{D}_i$. Thus $\hat{\underline{x}}_i(t|t)$ is the standard Kalman filter estimate for the model of Eqs. 3-1 through 3-11 with $\underline{d} = \underline{D}_i$, $\underline{r}_i(t)$ is the corresponding filter residual

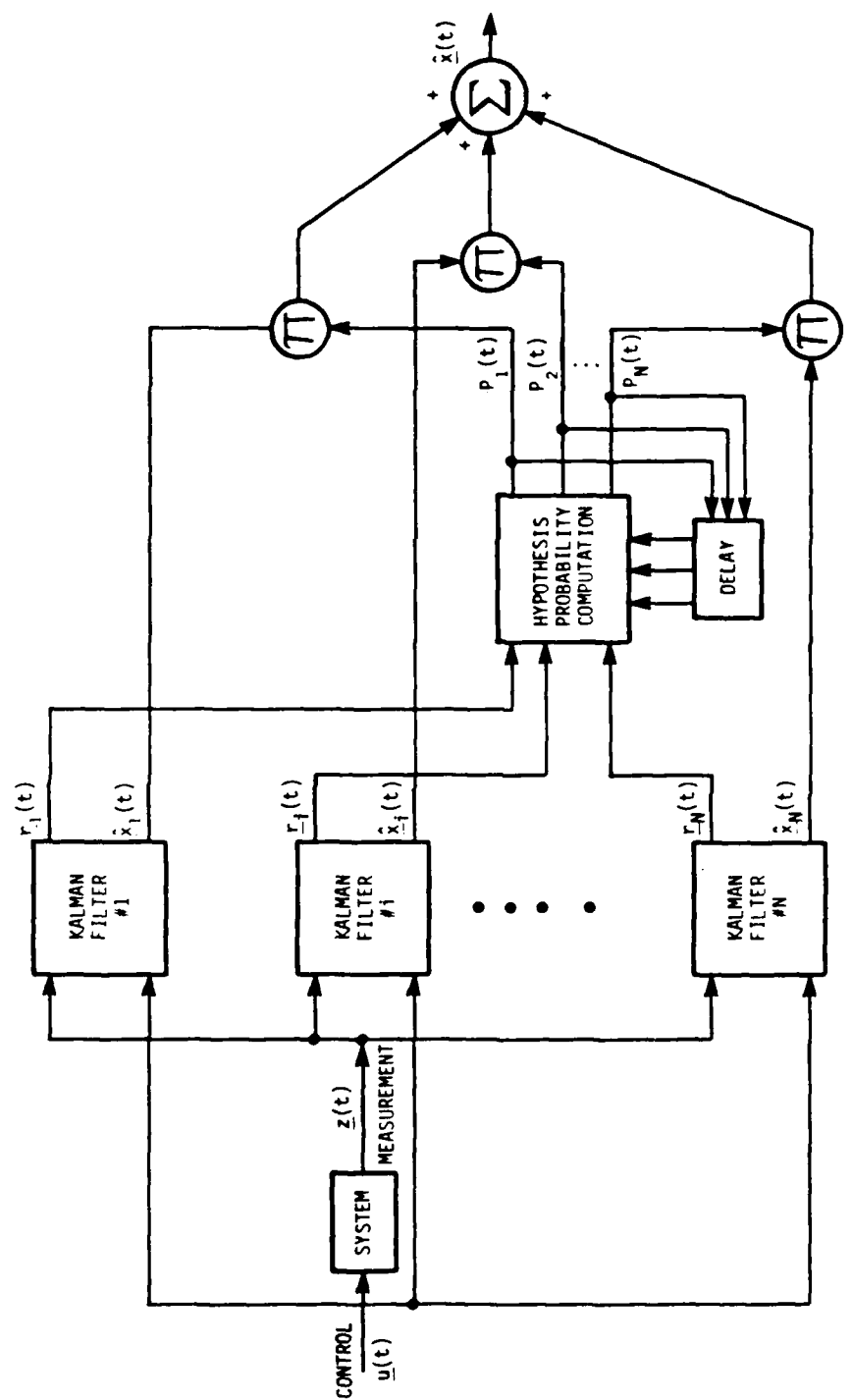
$$\underline{r}_i(t) = \underline{z}(t) - \underline{C}(t; \underline{D}_i) \hat{\underline{x}}_i(t|t-1) \quad (3-14)$$

$\underline{S}_i(t)$ is the residual covariance matrix, and

$$\beta_i(t) = |\underline{S}_i(t)|^{1/2} \quad (3-15)$$

The solution is illustrated in Fig. 3-1.

*References are indicated by numbers in square brackets and appear at the end of this report.



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Figure 3-1. Multiple Model Adaptive Estimation Algorithm.

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The MMAE algorithm has been the object of considerable study, both analytic and by simulation, e.g., [2]-[7]. It has been known for some time that if the true system is in the model set and is, say, model k , then under reasonable assumptions

$$p_k(t) \rightarrow 1 \quad (3-16)$$

$$p_i(t) \rightarrow 0, \quad i \neq k \quad (3-17)$$

as $t \rightarrow \infty$. More interesting is the realistic situation in which the true model is not in the model set, but may be some high order, even nonlinear system. In this case, it has been shown that

$$p_k(t) \rightarrow 1 \quad (3-18)$$

$$p_i(t) \rightarrow 0, \quad i \neq k \quad (3-19)$$

where k minimizes a certain information distance between the set of admissible models and the true system, [8]-[10]. This information distance is readily computed (in the case in which the true system is linear) by standard covariance calculations associated with mismatched Kalman filter performance evaluation. Moreover, it can be shown that the convergence in Eqs. 3-18 and 3-19 (in an appropriate probabilistic sense made precise in [8]) is exponential with coefficient equal to the information distance.

3.1.2 Generalizations of MMAE Algorithm

Two generalizations of the above described MMAE algorithm are necessary before it can be applied to multitarget tracking. The first of these restrictions is that the dimension J of the state vector is assumed not dependent on

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d in the preceding subsection. But there are many situations in which the dimension of the state vector, i.e., the order of the system, is one of the unknown parameters; it will be demonstrated below that tracking multiple targets is one such situation. It is then impossible to combine the conditional state estimates into an unconditional estimate as per Eq. 3-13. Under such circumstances, a maximum a posterior probability criterion is adopted, i.e., for each t

$$\hat{x}(t|t) = \hat{x}_i(t|t) \quad (3-20)$$

where i is such that

$$p_i(t) > p_j(t) \quad (3-21)$$

for all j . As above, if the true system is in the model set and is, say, model k , then under similar reasonable assumptions,

$$p_k(t) \rightarrow 1 \quad (3-22a)$$

and

$$p_j(t) \rightarrow 0 \quad \text{for } i \neq k \quad (3-22b)$$

as $t \rightarrow \infty$. Thus,

$$\hat{x}(t|t) \rightarrow \hat{x}_k(t|t) \quad (3-23)$$

in probability as $t \rightarrow \infty$.

The other assumption which must be relaxed is that the parameter set is fixed. There are many situations in which the size of the parameter set is

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always finite but increases with time, i.e., the number of plausible hypotheses can grow steadily with time. The simplest such situation is when $d=d(t)$ and $d(t)$ takes on values from the usual finite, discrete set, $\{\underline{D}_1, \dots, \underline{D}_N\}$; the situation is similar, if more complex, when tracking multiple targets. In this simplest situation, there are N hypotheses at time $t=1$, each corresponding to one possible value for $d(1)$. At $t=2$, there are N^2 hypotheses, each corresponding to a plausible pair of values for $d(1)$ and $d(2)$, and so forth as indicated in Fig. 3-2. Each node in that figure represents a hypothesis and associated with each hypothesis is a state estimate $\hat{x}_i(t|t)$ which is conditioned on the hypothesis being correct and the posterior probability of the hypothesis' correctness, $p_i(t)$.

The conditional estimate $\hat{x}_i(t|t)$ is the standard Kalman filter estimate for the model of Eqs. 3-1 through 3-11 with $d(t)=d_{i-[1/N]N}$, $\underline{r}_i(t)$ is the corresponding filter residual

$$\underline{r}_i(t) = \underline{z}(t) - \underline{C}(t; d(t)) \hat{x}_{[1/N]}(t|t-1) \quad , \quad (3-24)$$

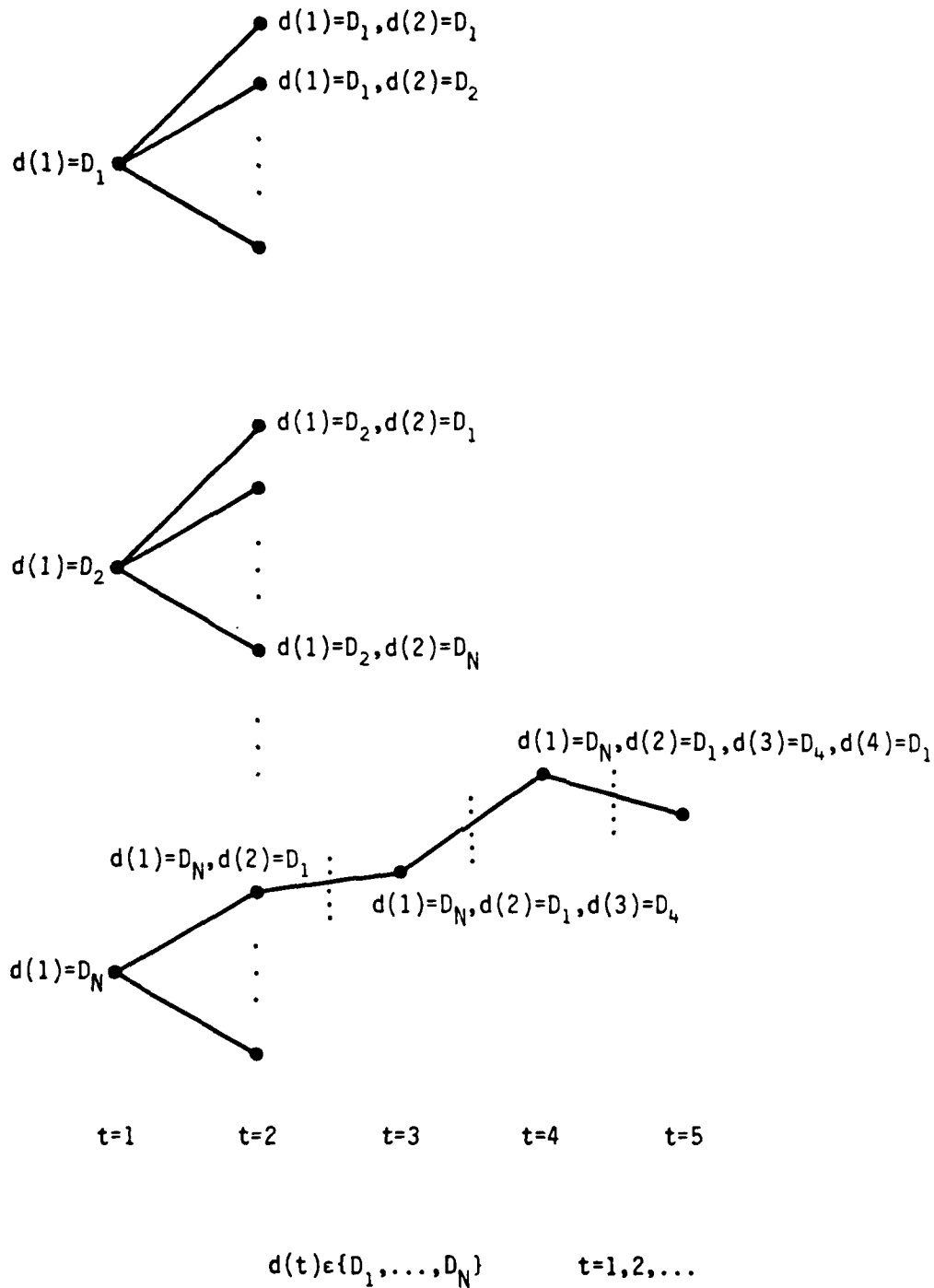
$\underline{S}_i(t)$ is the residual covariance matrix,

$$\beta_i(t) = |\underline{S}_i(t)|^{1/2} \quad , \quad (3-25)$$

and

$$p_i(t) = \frac{\beta_j \exp \left[-\frac{1}{2} \underline{r}_j(t)^T \underline{S}_j(t)^{-1} \underline{r}_j(t) \right]}{\sum_{j=1}^{N^t} \beta_j(t) \exp \left[-\frac{1}{2} \underline{r}_j(t)^T \underline{S}_j(t)^{-1} \underline{r}_j(t) \right]} p_{[1/N]}(t-1) \quad . \quad (3-26)$$

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Figure 3-2. Illustrating Growing Trees of Hypotheses.

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The indices are "coded" so that the first ($i=1$) hypothesis is that $\underline{d}(\tau)=\underline{D}_1$ for $\tau \leq t$, the second ($i=2$) is that $\underline{d}(\tau)=\underline{D}_1$ for $\tau \leq t-1$ and $\underline{d}(t)=\underline{D}_2$, and the last ($i=N^t$) is that $\underline{d}(\tau)=\underline{D}_N$ for $\tau \leq t$. The notation $[i/N]$ denotes the largest integer n strictly less than i/N . For example, $[1/2]=[1]=0$, $[4/3]=[2]=1$, etc. If the dimension of the state vector is not a function of $\underline{d}$, then it is possible to form an unconditional state estimate as in Eq. 3-13. Otherwise, a maximum a posteriori criterion must be used to select one of the conditional state estimates as the state estimate.

3.2 OPTIMAL TRACKING ALGORITHMS

As with our model development effort, our algorithm development effort has proceeded by considering three cases of increasing complexity. The cases we have considered include:

1. one target (known) with measurement errors, missed detections, and false detections, but no maneuvers, etc.;
2. one target (known) with measurement errors, missed detections, false detections, "mortality," (appearance and disappearance) but no maneuvers, etc.; and
3. an unknown number of targets with measurement errors, missed detections, false detections, "mortality," but no maneuvers, etc.

Case 1 is the simplest combination of phenomena which requires an MMAE algorithm. The only hypotheses concern which detection on a given scan is caused by one target, if any. This is the simplest sort of data association hypothesis. In Case 2 it is necessary to hypothesize whether the target has been "born" and if so, whether it has also "died." These hypotheses are, of course, in addition to the simple hypotheses about which detection, if any, is caused by the target. Case 3 provides far more complexity in the data association hypotheses, as there are many possible pairings of targets and

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detections. Hypotheses concerning the number of targets born by a given time (as well as which, if any, have died) are also essential. Each case will be discussed in varying detail in the succeeding subsections.

3.2.1 Case 1

In this case there is a single target (and it is known there is just one) which is "immortal" in the sense that its "birth" and "death" are not modeled. The unknown parameters are the single target's detection state, which varies with time and which takes on one of $L(t)+1$ values at time t . For this reason, a generalized MMAE algorithm of the form described above is needed. The algorithm creates an ever increasing number of hypotheses, one corresponding to each possible sequence of values that can be taken on by the sequence of detection states, i.e., at time t there is one for each possible sequence $\{d(\tau)\}_{\tau=-\infty}^t$.

All of the information associated with the i -th hypothesis at t can be gathered into a global hypothesis structure, denoted by $H_G(i,t)$. It has four components:

$$H_G(i,t) = (\hat{D}_G(i,t), \hat{x}(t|i,t), \hat{z}(t|i,t), P_G(i,t)) \quad (3-27)$$

The first component represents the hypothesized detection state sequence. As follows:

$$\hat{D}_G(i,t) = \{\hat{d}_G(\tau|i,t)\}_{\tau=-\infty}^t \quad (3-28)$$

and

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$$\hat{d}_G(\tau|i,t) = [\hat{b}_G(\tau|i,t), \hat{i}_G(\tau|i,t)]^T \text{ for } \tau \leq t. \quad (3-29)$$

Effectively, $\hat{d}_G(\tau|i,t)$ is the value of $d(\tau)$ assumed by the i -th hypothesis existing at t ; $\hat{b}_G(\tau|i,t)$ and $\hat{i}_G(\tau|i,t)$ are similarly related to $b(\tau)$ and $i(\tau)$. The i -th hypothesis at t is correct if and only if

$$\hat{d}_G(\tau|i,t) = d(\tau) \text{ for all } \tau \leq t. \quad (3-30)$$

For convenience, we denote this event by $\Theta_G(i,t)$.

The second and third components of $H_G(i,t)$ represent the optimal estimate of the single target's dynamic state $x(t)$, as follows:

$$\hat{x}(t|i,t) = E[x(t)|\Theta_G(i,t) \& Z_G(t)] \quad (3-31)$$

and

$$\Sigma(t|i,t) = \text{Cov}[x(t)|\Theta_G(i,t) \& Z_G(t)] \quad (3-32)$$

where $E[\cdot|\cdot]$ and $\text{Cov}[\cdot|\cdot]$ are respectively the conditional mean and conditional covariance operators, and where

$$Z_G(t) = \{Z_S(\tau)\}_{\tau=-\infty}^t \text{ for all } t \quad (3-33)$$

and

$$Z_S(\tau) = \{z(j,\tau)\}_{j=1}^{L(\tau)} \text{ for all } \tau \leq t. \quad (3-34)$$

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The $Z_s(\tau)$ sequences include all of the detections for each scan τ while the $Z_G(t)$ sequences include all of the detections in all of the scans up through t . Since $x(t)$ is Gaussian distributed for all t (see Eq. 2-1), $\hat{x}(t|i,t)$ and $\Sigma(t|i,t)$ together give the conditional distribution of $x(t)$. Note that the definitions of $\hat{x}(t|i,t)$ and $\Sigma(t|i,t)$ can be extended to making $\hat{x}(\tau|i,t)$ and $\Sigma(\tau|i,t)$ the equivalent conditional mean and covariance of $x(\tau)$ for $\tau \neq t$.

The fourth component of $H_G(i,t)$ represents the probability that the hypothesis is supported by the measurement data as follows:

$$P_G(i,t) = \text{Prob}[\theta_G(i,t)|Z_G(t)] \quad . \quad (3-35)$$

We denote the number of hypotheses at t by $M_G(t)$.

The hypothesis structures are the data structures manipulated by the optimal algorithm. It is necessary to define how the components are calculated. Before doing so, it is convenient to define one more data structure, the scan hypothesis structure, denoted by $H_S(j,t)$. It has one component:

$$H_S(j,t) = (\hat{d}_S(t|j,t)) \quad \text{for all } t \quad (3-36)$$

where

$$\hat{d}_S(t|j,t) = [\hat{b}_S(t|j,t), \hat{i}_S(t|j,t)]^T \quad \text{for all } t \quad . \quad (3-37)$$

Effectively, $\hat{d}_S(t|j,t)$ is the value of $d(t)$ assumed by the j -th scan hypothesis at t ; $\hat{b}_S(t|j,t)$ and $\hat{i}_S(t|j,t)$ are similarly related to $b(t)$ and $i(t)$.

The j -th scan hypothesis is correct if and only if

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$$\hat{d}_s(t|j,t) = d(t) \quad . \quad (3-38)$$

For convenience, we denote this event by $\Theta_s(j,t)$. We denote the number of scan hypotheses at t by $M_s(t)$. In this case, the only plausible scan hypotheses are that the single target caused one of the $L(t)$ detections or that it was not detected, so

$$M_s(t) = L(t) + 1 \quad \text{for all } t \quad . \quad (3-39)$$

Each global hypothesis structure is constructed from a sequence of consecutive scan hypothesis structures. Thus, for each global hypothesis structure at $t-1$ and scan hypothesis structure at t , one can construct a new global hypothesis structure for t . Symbollically,

$$H_G(i,t-1) * H_s(j,t) \Rightarrow H_G(k,t) \quad (3-40)$$

for every i and j pair. It is appropriate to note at this point that the indices of global and scan hypothesis structures are arbitrary. One could cleverly encode the value of $\hat{D}_G(i,t)$ in the index i and of $\hat{d}_s(j,t)$ in the index j , making the hypothesis structures "content addressable." But the choice of whether to do so or not is basically an implementation issue which we wish to avoid. In defining the optimal tracking algorithm, we will simply state it generally in terms of arbitrary indices i , j , and k as in Eq. 3-40 without stating how k should be chosen for a particular i and j pair.

The new hypothesized detection state sequence $\hat{D}_G(k,t)$ is generated from $\hat{D}_G(i,t-1)$ and $\hat{d}_s(j,t)$ by letting

$$\hat{d}_G(\tau|k,t) = \hat{d}_G(\tau|i,t-1) \quad \text{for } \tau \leq t-1 \quad (3-41a)$$

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and

$$\hat{d}_G(t|k,t) = \hat{d}_S(t|j,t) \quad (3-41b)$$

Assuming that $\hat{b}_S(t|j,t)=D$, the dynamic state estimate is updated by letting

$$\hat{x}(t|k,t) = \hat{x}(t|i,t-1) + K(t|i,t-1)[z(\hat{b}_S(t|j,t),t) - C\hat{x}(t|i,t-1)] \quad (3-41c)$$

and

$$\Sigma(t|k,t) = [I - K(t|i,t-1)C^T]\Sigma(t|i,t-1) \quad (3-41d)$$

If $\hat{b}_S(t|j,t)=\bar{D}$, there is no measurement to incorporate, and

$$\hat{x}(t|k,t) = \hat{x}(t|i,t-1) \quad (3-41e)$$

Here

$$\hat{x}(t|i,t-1) = A\hat{x}(t-1|i,t-1) \quad (3-42a)$$

$$\Sigma(t|i,t-1) = A\Sigma(t-1|i,t-1)A^T + W \quad (3-42b)$$

$$K(t|i,t-1) = \Sigma(t|i,t-1)C^T[V + C\Sigma(t|i,t-1)C^T]^{-1} \quad (3-42c)$$

The probability is updated by letting

$$P_G(k,t) = P_G(i,t-1)(1-P_D)Q(t) \quad \text{if } \hat{b}_S(t|j,t) = \bar{D} \quad (3-43a)$$

$$P_G(i,t-1)P_D[G(z(\hat{b}_S(t|j,t),t) - \hat{x}(t|i,t-1), V + C\Sigma(t|i,t-1)C^T) / \rho_{FA}]Q(t) \quad (3-43b)$$

if $\hat{b}_S(t|j,t) = D$

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where $G(\cdot, \cdot)$ is the Gaussian probability density function, i.e.,

$$G(y, Y) = (2\pi)^{-K/2} |Y|^{-1/2} e^{-y^T Y^{-1} y / 2}, \quad (3-44)$$

and

$$Q(t) = [e^{-\lambda_{FA} L(t)} / \rho_{FA} L(t)!] / \text{Prob}[Z_S(t) | Z_G(t-1)] \quad (3-45)$$

This algorithm is carried out for every pair of i and j such that $1 \leq i \leq M_G(t-1)$ and $1 \leq j \leq M_S(t)$. It follows that

$$M_G(t) = M_G(t-1) M_S(t) = M_G(t-1) [L(t) + 1] \quad \text{for all } t, \quad (3-46)$$

The practical infeasibility of the algorithm is here made clear; the number of global hypotheses grows geometrically with t .

Note that it would be possible to form an unconditional state estimate

$$\hat{x}(t|t) = \sum_{k=1}^{M_G(t)} \hat{x}(t|k, t) P_G(k, t) \quad (3-47)$$

in this case because the dimension of x is always 4. But we assume for consistency with more complex cases that a maximum a posteriori criterion is used. That is, for each t

$$\hat{x}(t|t) = \hat{x}(t|k^*, t) \quad (3-48)$$

where k^* is such that

$$P_G(k^*, t) > P_G(k, t) \quad \text{for all } k. \quad (3-49)$$

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The equations generating the new hypothetical detection state sequence are obviously appropriate. The equations generating the new dynamic state estimate are nearly as obvious; they are the Kalman filter equations specialized to the particular pairing of hypotheses. This is the optimum way to update a dynamic state estimate for a Gaussian distributed dynamic state, given a measurement based on that dynamic state. The equations generating the probability of the new global hypothesis are less obvious. Their derivation is sketched in the next few paragraphs.

By definition,

$$P_G(k,t) = \text{Prob}[\theta_G(k,t) | Z_G(t)] \quad . \quad (3-50)$$

Observing that the event $\theta_G(k,t)$ occurs if and only if the events $\theta_G(i,t-1)$ and $\theta_S(j,t)$ occur and that

$$Z_G(t) = Z_G(t-1) \cup \{Z_S(t)\} \quad , \quad (3-51)$$

one can demonstrate that

$$\begin{aligned} P_G(k,t) &= \text{Prob}[Z_S(t) | \theta_S(j,t) \& \theta_G(i,t-1) \& Z_G(t-1)] \\ &\times \text{Prob}[\theta_S(j,t) | \theta_G(i,t-1) \& Z_G(t-1)] \\ &\times P_G(i,t-1) / \text{Prob}[Z_S(t) | Z_G(t-1)] \quad . \end{aligned} \quad (3-52)$$

The first factor on the right-hand side of the above equation can be further expanded as follows

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$$\text{Prob}[Z_S(t) | \Theta_S(j, t) \& \Theta_G(i, t-1) \& Z_G(t-1)]$$

$$= \prod_{\ell=1}^{L(t)} \text{Prob}[z(\ell, t) | L(t) \& \Theta_S(j, t) \& \Theta_G(k, t-1) \& Z_G(t-1)]$$

$$\times \text{Prob}[L(t) | \Theta_S(j, t) \& \Theta_G(i, t-1) \& Z_G(t-1)] \quad (3-53)$$

because the measured locations of all detections are statistically independent. Further simplification of Eqs. 3-52 and 3-53 can be accomplished by noting similar independence, leading to the observation that

$$P_G(k, t) = \prod_{\ell=1}^{L(t)} \text{Prob}[z(\ell, t) | \Theta_S(j, t) \& \Theta_G(i, t-1) \& Z_G(t-1)]$$

$$\times \text{Prob}[L(t) | \Theta_S(j, t)] \text{Prob}[\Theta_S(j, t)] P_G(i, t-1) / \text{Prob}[Z_S(t) | Z_G(t-1)] \quad (3-54)$$

Further simplification requires assumptions about $H_S(j, t)$.

Assume that j is such that $\hat{d}_S(j, t) = \bar{D}$. This implies all detections are false alarms. The measurements of all of the detections are uniformly distributed and $L_{FA}(t)$ equals $L(t)$. Thus

$$P_G(k, t) = \left[\prod_{\ell=1}^{L(t)} |\Xi|^{-1} \right] [e^{-\lambda_{FA} L(t)} \lambda_{FA}^{L(t)} / L(t)!] [1 - P_D] P_G(i, t-1) / \text{Prob}[Z_S(t) | Z_G(t-1)] \quad (3-55)$$

A little manipulation yields Eq. 3-43a.

Now instead assume that j is such that $\hat{d}_S(t | j, t) = D$. This implies that all detections but the $\hat{d}_S(t | j, t)$ -th are false alarms. The measurements of all the false detections are uniformly distributed and $L_{FA}(t)$ is one less than

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$L(t)$. The measurement $z(\hat{i}(t|j,t),t)$ is Gaussian distributed if $\theta_S(j,t)$. From Eq. 2-12a it is clear that the mean and covariance of the measurement, conditioned as above are

$$\hat{C}x(t|i,t-1) \quad (3-56a)$$

and

$$V + C\Sigma(t|i,t-1)C^T \quad (3-56b)$$

respectively. It follows that

$$\begin{aligned} & \text{Prob}[z(\hat{i}_S(t|j,t),t) | \theta_S(j,t) \& \theta_G(i,t-1) \& Z_G(t-1)] \\ & = G(z(\hat{i}_S(t|j,t),t) - \hat{C}x(t|i,t-1), V + C\Sigma(t|i,t-1)C^T) \end{aligned} \quad (3-57)$$

and so

$$\begin{aligned} P_G(k,t) &= \left[\prod_{\substack{l=1 \\ l \neq i_S(t|j,t)}}^{L(t)} |\Xi|^{-1} \right] G(z(\hat{i}_S(t|j,t),t) - \hat{C}x(t|i,t-1), V + C\Sigma(t|i,t-1)C^T) \\ & \times [e^{-\lambda_{FA} L(t)-1} / \{\lambda_{FA}^{L(t)-1} L(t)!\}] [P_D/L(t)] P_G(i,t-1) / \text{Prob}[Z_S(t) | Z_G(t-1)] \end{aligned} \quad (3-58)$$

A little manipulation yields Eq. 3-43b.

3.2.2 Case 2

In this case, there is again a simple target (and it is again known there is just one), but it is "mortal" in that its "birth" and "death" are modeled.

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The unknown parameters are again the target's detection state, which varies with time and which takes on one of $L(t)+3$ values at time t . Moreover, the dynamic state of the target is effectively of dimension 0 (i.e., it is undefined) if $d(t)=\bar{B}$ or X . For both of these reasons, a generalized MMAE algorithm of the form described in subsection 3.1.2 is needed. Again, the algorithm creates an ever increasing number of hypotheses, one corresponding to each possible sequence of values that can be taken on by the sequence of detection states, i.e., at time t , there is one for each possible sequence $\{d(\tau)\}_{\tau=0}^t$.

The modifications to the model going from Case 1 to Case 2 are not extensive; the modifications of the optimal tracking algorithm are also not extensive. The global and scan hypothesis structures are defined exactly as in Case 1. Only the range of values of $b_G(i,t)$ and $b_S(i,t)$ differ. We can again symbolize the generation of new global hypothesis structures for old global hypothesis structures and current scan hypotheses by

$$H_G(i,t-1)*H_S(j,t) \Rightarrow H_G(k,t) \quad (3-59)$$

but with two restrictions. The first restriction is that this generative procedure applies only if $t>0$. For $t=0$, we have but one global hypothesis structure, $H_G(1,0)$, such that

$$\hat{b}_G(1,0) = \bar{B} \quad (3-60)$$

and

$$P_G(1,0) = 1 \quad (3-61)$$

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All of the other components of this global hypothesis structure are undefined. The second restriction is that Eq. 3-59 does not apply for every i and j pair. It applies only if the event state $\hat{d}_s(j,t)$ is reachable from $\hat{d}_G(i,t-1)$ in one step, i.e., if either

$$\hat{b}_s(t|j,t) = \bar{B} \text{ and } \hat{b}_G(t-1|i,t-1) = \bar{B} ,$$

$$\hat{b}_s(t|j,t) = D \text{ and } \hat{b}_G(t-1|i,t-1) \neq X ,$$

$$\hat{b}_s(t|j,t) = \bar{D} \text{ and } \hat{b}_G(t-1|i,t-1) = D \text{ or } \bar{D} , \text{ or}$$

$$\hat{b}_s(t|j,t) = X \text{ and } \hat{b}_G(t-1|i,t-1) = D \text{ or } X . \quad (3-62)$$

Given the aforementioned restrictions, we can describe the generative procedure. The new hypothetical event state sequence $\hat{D}_G(k,t)$ is generated from $\hat{D}_G(i,t-1)$, and $\hat{d}_s(j,t)$ by letting

$$\hat{d}_G(\tau|k,t) = \hat{d}_G(\tau|i,t-1) \text{ for } 0 \leq \tau \leq t-1 \quad (3-63a)$$

and

$$\hat{d}_G(t|k,t) = \hat{d}_s(t|j,t) , \quad (3-63b)$$

exactly as in Case 1.

Updating the dynamic state is a bit more complex in this case, the formulae depending on the hypothesized event state in a manner paralleling Eq. 2-21. If $\hat{b}_s(t|j,t)=D$ and $\hat{b}_G(t-1|i,t-1)=D$ or $\bar{D}$,

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$$\hat{x}(t|k,t) = \hat{x}(t|i,t-1) + K(t|i,t-1)[z(\hat{i}_s(t|j,t),t) - \hat{x}(t|i,t-1)] \quad (3-64a)$$

and

$$\Sigma(t|k,t) = [I - K(t|i,t-1)C^T]\Sigma(t|i,t-1) \quad (3-64b)$$

while if $\hat{b}_s(t|j,t) = \bar{D}$, then

$$\hat{x}(t|k,t) = \hat{x}(t|i,t-1) \quad (3-65a)$$

and

$$\Sigma(t|k,t) = \Sigma(t|i,t-1) \quad (3-65b)$$

where

$$\hat{x}(t|i,t-1) = A\hat{x}(t-1|i,t-1) \quad , \quad (3-66a)$$

$$\Sigma(t|i,t-1) = A\Sigma(t-1|i,t-1)A^T + W \quad , \quad (3-66b)$$

and

$$K(t|i,t-1) = \Sigma(t|i,t-1)C^T[V + C\Sigma(t|i,t-1)C^T]^{-1} \quad . \quad (3-66c)$$

But if $\hat{b}_s(t|j,t) = D$ and $\hat{b}_G(t-1|i,t-1) = \bar{B}$, then

$$\hat{x}(t|k,t) = K_0 z(\hat{i}_s(t|j,t),t) \quad (3-67a)$$

and

$$\Sigma(t|k,t) = [I - K_0 C^T]\Sigma_0 \quad (3-67b)$$

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where

$$K_0 = \Sigma_0 C^T [V + C \Sigma_0 C^T]^{-1} \quad (3-68)$$

For all other circumstances, $\hat{x}(t|k, t)$ and $\Sigma(t|k, t)$ are undefined.

The updating of the probability is similarly dependent on the values of $\hat{b}_s(t|j, t)$ and $\hat{b}_G(t-1|i, t-1)$.

$$\begin{aligned} P_G(k, t) &= P_G(i, t-1) [1 - P_B] Q(t) && \text{if } \hat{b}_s(t|j, t) = \bar{B} \text{ and } \hat{b}_G(t-1|i, t-1) = \bar{B} \\ &P_G(i, t-1) P_B [G(z(\hat{i}_s(t|j, t), t), V + C \Sigma_0 C^T) / \rho_{FA}) Q(t) && \\ &&& \text{if } \hat{b}_s(t|j, t) = D \text{ and } \hat{b}_G(t-1|i, t-1) = \bar{B} \\ &P_G(i, t-1) P_D [G(z(\hat{i}_s(t|j, t), t) - Cx(t|i, t-1), V + C \Sigma(t|i, t-1) C^T) / \rho_{FA}) Q(t) && \\ &&& \text{if } \hat{b}_s(t|j, t) = D \text{ and } \hat{b}_G(t-1|i, t-1) = d \text{ or } \bar{D} \\ &P_G(i, t-1) [1 - P_D - P_X] Q(t) && \text{if } \hat{b}_s(t|j, t) = \bar{D} \text{ and } \hat{b}_G(t-1|i, t-1) = D \\ &P_G(i, t-1) P_X Q(t) && \text{if } \hat{b}_s(t|j, t) = X \text{ and } \hat{b}_G(t-1|i, t-1) = D \\ &P_G(i, t-1) [1 - P_D] Q(t) && \text{if } \hat{b}_s(t|j, t) = \bar{D} \text{ and } \hat{b}_G(t-1|i, t-1) = \bar{D} \text{ ,} \\ &P_G(i, t-1) Q(t) && \text{if } \hat{b}_s(t|j, t) = X \text{ and } \hat{b}_G(t-1|i, t-1) = X \text{ .} \end{aligned} \quad (3-69)$$

where

$$G(y, Y) = (2\pi)^{-K/2} |Y|^{-1/2} e^{-y^T Y^{-1} y / 2} \quad (3-70)$$

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and

$$Q(t) = [e^{-\lambda_{FA}} \lambda_{FA}^{L(t)} / L(t)!] / \text{Prob}[Z_S(t) | Z_G(t-1)] \quad (3-71)$$

as before.

In this case, the plausible scan hypotheses at t are that the single target caused one of the $L(t)$ detections, that it has not been "born" yet, that it is already "dead" or that it simply is undetected but not yet "dead." So,

$$M_S(t) = L(t) + 3 \quad \text{for } t > 0 \quad (3-72)$$

Given the observation that not every combination of an old global hypothesis and a current scan hypothesis generates a new global hypothesis, the most that can be said is that

$$M_G(t) \leq M_G(t-1)[L(t)+3] \quad \text{for } t > 0 \quad (3-73)$$

meaning that the growth of the number of global hypotheses can be geometric.

The derivation of the probability update formulae is quite similar to that in Case 1. One difference appears in the equivalent of Eq. 3-54. In this case,

$$P_G(k, t) = \prod_{l=1}^{L(t)} \text{Prob}[z(l, t) | \theta_S(j, t) \& \theta_G(i, t-1) \& Z_G(t-1)] \\ \times \text{Prob}[L(t) | \theta_S(j, t)] \text{Prob}[\theta_S(j, t) | \theta_G(i, t-1)] P_G(i, t-1) / \text{Prob}[Z_S(t) | Z_G(t-1)] \quad (3-74)$$

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The third factor differs from Eq. 3-54; the probability of a hypothesized event state at t depends on the hypothesized event state at $t-1$. Another difference appears in the equivalent of Eq. 3-57 when $\hat{b}_s(t|j,t)=D$ and $\hat{b}_G(t-1|i,t)=\bar{B}$. The measurement $z(\hat{i}_s(t|j,t),t)$ is Gaussian distributed if $H_s(j,t)$ is true, but its mean and covariance are, respectively

$$CE[x_0] = 0 \quad (3-75a)$$

and

$$V + C \text{Cov}[x_0]C^T = V + C\Sigma_0C^T \quad (3-75b)$$

respectively. It follows that

$$\text{Prob}[z(\hat{i}_s(t|j,t),t) | \theta_s(j,t) \& \theta_G(i,t-1) \& Z_G(t-1)] = G(z(\hat{i}_s(t|j,t),t), V+C\Sigma_0C^T) \quad (3-76)$$

3.2.3 Case 3

In this case, there are an unknown number of targets, each of which can be "born" or "die" at any time. The unknown parameters include the number of targets having been born and their detection states, each of which can take on $L(t)+2$ values. The overall dynamic state vector is composed of the four dimensional dynamic state vectors of the targets which are currently "alive," making the dimension of the overall dynamic state vector a function of the unknown parameters. For both of these reasons, a generalized MMAE algorithm of the form described in subsection 3.1.2 is needed. Again, the algorithm creates an ever increasing number of hypotheses, one corresponding to each

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possible sequence of values which can be taken on by the sequence of composite discrete states, i.e., at time t , there is one for each possible sequence $\{d(\tau)\}_{\tau=0}^t$ where

$$d(\tau) = [N(\tau), d'(1, \tau)^T, d'(2, \tau)^T, \dots, d'(N(\tau), \tau)^T]^T \quad (3-77)$$

as in subsection 2.1.3.

The global and scan hypotheses are defined exactly as in Case 1, but the variables $\hat{d}(t)$ and $\hat{x}(t)$ now have new components. Hypotheses about and estimates of these new components are denoted as usual. Again we can symbolize the generation of new global hypothesis structures from old global hypothesis structures and current scan hypotheses by

$$H_G(i, t-1) * H_S(j, t) \Rightarrow H_G(k, t) \quad (3-78)$$

but with restriction, as we did in Case 2. The restrictions are fewer, but slightly more complex. For $t=0$, we again have but one global hypothesis structure, $H_G(1, 0)$. Its components are

$$\hat{N}_G(1, 0) = 0 \quad (3-79)$$

and

$$P_G(1, 0) = 1 \quad (3-80)$$

The second restriction is that Eq. 3-77 applies only if the total event state $\hat{d}_S(j, t)$ is reachable from $\hat{d}_G(i, t-1)$ in one step, i.e., only if

$$\hat{N}_S(j, t) > \hat{N}_G(i, t-1) \quad (3-81)$$

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and if for every ℓ either

$$\hat{b}_S(\ell, t | j, t) = \bar{B} \text{ and } \hat{b}_G(\ell, t-1 | i, t-1) = \bar{B} , \quad (3-82a)$$

$$\hat{b}_S(\ell, t | j, t) = D \text{ and } \hat{b}_G(\ell, t-1 | i, t-1) \neq X , \quad (3-82b)$$

$$\hat{b}_S(\ell, t | j, t) = \bar{D} \text{ and } \hat{b}_G(\ell, t-1 | i, t-1) = D \text{ or } \bar{D} , \quad (3-82c)$$

or

$$\hat{b}_S(\ell, t | j, t) = X \text{ and } \hat{b}_G(\ell, t-1 | i, t-1) = D \text{ or } X . \quad (3-82d)$$

Some additional notation is needed before the generation procedure can be derived. We partition the set of target indices as follows:

$$\hat{\Psi}_{DB}(k, t) = \{\ell | \hat{b}_S(\ell, t | j, t) = D \& \hat{b}_G(\ell, t-1 | j, t-1) = \bar{B}\} \quad (3-83a)$$

$$\hat{\Psi}_{DD}(k, t) = \{\ell | \hat{b}_S(\ell, t | j, t) = D \& \hat{b}_G(\ell, t-1 | j, t-1) = D\} \quad (3-83b)$$

$$\hat{\Psi}_{\bar{D}\bar{D}}(k, t) = \{\ell | \hat{b}_S(\ell, t | j, t) = \bar{D} \& \hat{b}_G(\ell, t-1 | j, t-1) = D\} \quad (3-83c)$$

$$\hat{\Psi}_{XD}(k, t) = \{\ell | \hat{b}_S(\ell, t | j, t) = X \& \hat{b}_G(\ell, t-1 | i, t-1) = D\} \quad (3-83d)$$

$$\hat{\Psi}_{D\bar{D}}(k, t) = \{\ell | \hat{b}_S(\ell, t | j, t) = D \& \hat{b}_G(\ell, t-1 | j, t-1) = \bar{D}\} \quad (3-83e)$$

$$\hat{\Psi}_{\bar{D}D}(k, t) = \{\ell | \hat{b}_S(\ell, t | j, t) = \bar{D} \& \hat{b}_G(\ell, t-1 | j, t-1) = \bar{D}\} \quad (3-83f)$$

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$$\hat{\Psi}_{XX}(k,t) = \{\ell | b_s(\ell,t|j,t)=X \& b_G(\ell,t-1|j,t-1)=X\} \quad (3-83g)$$

The cardinality of each of these sets is denoted by using the corresponding lower case symbol, e.g.,

$$\hat{\Psi}_{DB}(k,t) = \text{Card}[\hat{\Psi}_{DB}(k,t)] \quad (3-84)$$

The new hypothesized total event state sequence $\hat{D}_G(k,t)$ is generated from $\hat{D}_G(i,t-1)$ and $\hat{d}_s(j,t)$ by letting

$$\hat{d}_G(\tau|k,t) = \hat{d}_G(\tau|i,t-1) \quad \text{for } 0 \leq \tau \leq t-1 \quad (3-85a)$$

and

$$\hat{d}_G(t|k,t) = \hat{d}_s(t|j,t) \quad , \quad (3-85b)$$

exactly as in Case 1 but for the restrictions on i and j .

Updating the dynamic state in this case resembles the process in Case 2:

$$\hat{x}'(\ell,t|k,t) = \hat{x}'(\ell,t|t-1) + K(\ell,t|i,t-1)[z(\hat{i}_s(\ell,t|j,t),t) - C\hat{x}'(\ell,t|i,t-1)] \quad (3-86a)$$

and

$$\Sigma'(\ell,t|k,t) = [I - K(\ell,t|i,t-1)C^T]\Sigma'(\ell,t|i,t-1) \quad (3-86b)$$

for $\ell \in \hat{\Psi}_{DD}(k,t) \cup \hat{\Psi}_{DB}(k,t)$ and

$$\hat{x}'(\ell,t|k,t) = \hat{x}'(\ell,t|i,t-1) \quad (3-87a)$$

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and

$$\Sigma(\ell, t | k, t) = \Sigma(\ell, t | i, t-1) \quad (3-87b)$$

for $\ell \in \Psi_{DD}(k, t) \cup \Psi_{DD}(k, t)$ where

$$\hat{x}'(\ell, t | i, t-1) = A x'(\ell, t-1 | i, t-1) \quad (3-88a)$$

$$\Sigma'(\ell, t | i, t-1) = A \Sigma'(\ell, t-1 | i, t-1) A^T + W \quad (3-88b)$$

and

$$K(\ell, t | i, t-1) = \Sigma'(\ell, t | i, t-1) C^T [V + C \Sigma'(\ell, t-1 | i, t-1) C^T]^{-1} \quad , \quad (3-88c)$$

plus

$$\hat{x}'(\ell, t | k, t) = K_0 z(\hat{i}_s(\ell, t | j, t), t) \quad (3-89a)$$

$$\Sigma'(\ell, t | k, t) = [I - K_0 C^T] \Sigma'_o \quad (3-89b)$$

for $\ell \in \Psi_{DB}(k, t)$ where

$$K_0 = \Sigma'_o C^T [V + C \Sigma'_o C^T]^{-1} \quad . \quad (3-90)$$

Under all other circumstances, $\hat{x}'(\ell, t | k, t)$ and $\Sigma'(\ell, t | k, t)$ are undefined.

Updating the probability more extensively involves the partitions of the target indices:

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$$\begin{aligned}
 P_G(k, t) = & P_G(i, t-1) \prod_{\ell \in \hat{\Psi}_{DB}^-(k, t)} \lambda_B [G(z(\hat{i}_S(\ell, t|j, t), V + C\Sigma'_0 C^T)/\rho_{FA}) \times \\
 & \prod_{\ell \in \hat{\Psi}_{DD}^-(k, t) \cup \hat{\Psi}_{DD}^-(k, t)} P_D [G(z(\hat{i}_S(\ell, t|j, t), t) - Cx(\ell), t|i, t-1) \\
 & V + C\Sigma'(\ell, t|i, t-1)C^T)/\rho_{FA}] \times \\
 & (1-P_D-P_X) \hat{\Psi}_{DD}^-(k, t) P_X \hat{\Psi}_{XD}^-(k, t) (1-P_D) \hat{\Psi}_{DD}^-(k, t) Q(t) \quad (3-91)
 \end{aligned}$$

where

$$G(y, Y) = (2\pi)^{-K/2} |Y|^{-1/2} e^{-y^T Y^{-1} y/2} \quad (3-92)$$

and

$$Q(t) = e^{-\lambda_B} [e^{-\lambda_{FA}} L(t) / \rho_{FA} L(t)!] / \text{Prob}[Z_S(t)/Z_G(t-1)] \quad (3-93)$$

Note that $Q(t)$ does differ from the previous case, but still is independent of the hypothesis indices.

In this case, the plausible scan hypotheses at t are quite large. As many as $L(\tau)$ new targets or as few as 0 could have been born on each scan $\tau \leq t$, so one knows only that

$$0 \leq N(t) \leq \sum_{\tau=1}^t L(\tau) \quad (3-94)$$

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In terms of the $\hat{N}_S(t)$ components of the scan hypothesis structure alone, there can be

$$\left[\begin{array}{c} t \\ \sum_{\tau=1} L(t) \end{array} \right] + 1 \quad (3-95)$$

distinct scan hypotheses. The various possible values of $\hat{d}_S(t|j,t)$ are naturally larger but can be bounded loosely as follows:

$$M_S(t) < [L(t)+2] \left[\begin{array}{c} t \\ \sum_{\tau=1} L(t) \end{array} \right] + 1 \quad \text{for } t > 0 \quad (3-96)$$

Because the observation that not every combination of an old global hypothesis and a current scan hypothesis generates a new global hypothesis is especially true in this case, it can be fairly said that

$$M_G(t) < M_G(t-1)[L(t)+2] \left[\begin{array}{c} t \\ \sum_{\tau=1} L(t) \end{array} \right] + 1 \quad \text{for } t > 0 \quad (3-97)$$

is a very weak bound. This bound does reflect a potentially faster than geometric growth of the number of hypotheses in this case.

The derivation of the probability update formulae is naturally more complex in this case, but does parallel that of Cases 1 and 2. Equations 3-52 and 3-53 are still valid, for example. The latter equation's terms can be further expanded as follows:

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$$\prod_{\ell=1}^{L(t)} \text{Prob}[z(\ell, t) | L(t) \& \theta_S(j, t) \& \theta_G(i, t-1) \& Z_G(t-1)]$$

$$= \prod_{\ell \in \Psi_{DB}^-(k, t) \cup \Psi_{DD}^-(k, t)} \text{Prob}[z(\ell, t | j, t), t) | \theta_S(j, t) \& \theta_G(i, t-1) \& Z_G(t-1)] \times$$

$$\prod_{\ell \in \Phi(k, t)} \text{Prob}[z(\ell, t)] \quad (3-98)$$

and

$$\text{Prob}[L(t) | \theta_S(j, t) \& \theta_G(i, t-1) \& Z_G(t-1)] = \text{Prob}[\hat{\phi}(k, t)] \quad (3-99)$$

where

$$\hat{\phi}(k, t) = \{1, \dots, L(t)\} - \{\ell_S(\ell, t | j, t) | \ell \in \Psi_{DB}^-(k, t) \cup \Psi_{DD}^-(k, t) \cup \Psi_{DD}^-(k, t)\} \quad (3-100)$$

is the set of indices of the detections implicitly hypothesized to be false,

and

$$\hat{\phi}(k, t) = \text{Card}[\hat{\phi}(k, t)] \quad (3-101)$$

Reasoning about the conditional means and variances of the measurements resulting in target detections as in Cases 1 and 2 leads to the conclusion that

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$$\text{Prob}[Z_S(t) | \theta_S(j, t) \& \theta_G(1, t-1) \& Z_G(t-1)] =$$

$$\prod_{l \in \Psi_{DB}(k, t)} G(z(l_S(l, t | j, t), t), V + C \Sigma_o' C^T) \times$$

$$\prod_{l \in \Psi_{DD}(k, t)} G(z(l_S(l, t | j, t), t) - C x'(l, t | i, t-1), U \Psi_{DD}(k, t)) \times$$

$$V + C \Sigma^T(l, t | i, t-1) C^T) \times$$

$$| \Xi | = \frac{e^{-\hat{\phi}(t)} \lambda_{FA}^{\hat{\phi}(t)}}{\lambda_{FA}^{\hat{\phi}(t)} / \hat{\phi}(t)!} \quad (3-102)$$

The observation that

$$\hat{\phi}(t) = L(t) - \hat{\psi}_{DB}(t) - \hat{\psi}_{DD}(t) - \hat{\psi}_{DD}(t) \quad (3-103)$$

is used later to eliminate $\hat{\phi}(t)$ from the above equation.

Equation 3-102 gives a detailed expansion of the first term of Eq. 3-52 for this case. The expansion of the second term is sketched next. First, we note that

$$\text{Prob}[\theta_S(j, t) | \theta_G(t, t-1) \& Z_G(t-1)] =$$

$$\text{Prob}[d(l, t) = d(l, t | j, t) \text{ for } l \in N(t) | N(t) = \hat{N}_S(j, t) \& \theta_G(1, t-1) \& Z_G(t-1)] \times$$

$$\text{Prob}[N(t) = \hat{N}_S(j, t) | \theta_G(1, t-1) \& Z_G(t-1)] \quad (3-104)$$

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The second factor can be manipulated to show that

$$\text{Prob}[N(t)=\hat{N}_S(j,t) | \Theta_G(i,t-1) \& Z_G(t-1)] = e^{-\lambda_B} \frac{\psi_{DB}^-(\ell,t)}{\lambda_B} / \psi_{DB}^-(\ell,t)! \quad (3-105)$$

by observing that the number of targets "born" in the scan hypothesis structure simply equals the number already "born" in the old global hypothesis structure plus those just born.

The first factor on the right-hand side of Eq. 3-104 can be further expanded and simplified to yield

$$\text{Prob}[d(\ell,t)=\hat{d}(\ell,t) | j,t) \text{ for } \ell \leq N(t) | N(t)=\hat{N}_S(j,t) \& \Theta_G(i,t-1) \& Z_G(t-1)]$$

$$= \text{Prob}[i(\ell,t)=\hat{i}_S(\ell,t) | j,t) \text{ for } \ell \in \psi_{DB}^-(k,t) \cup \psi_{DD}^-(k,t) \cup \psi_{DD}^-(k,t) |$$

$$\psi_{DB}^-(t) = \psi_{DB}^-(k,t) \& \psi_{DD}^-(t) = \psi_{DD}^-(t) \& \psi_{DD}^-(t) = \psi_{DD}^-(k,t) \} \times$$

$$\prod_{\ell=1}^{\hat{N}_S(\ell,t)} \text{Prob}[b(\ell,t)=\hat{b}_S(\ell,t) | j,t) | N(t)=\hat{N}_S(j,t) \&$$

$$N(t-1) = \hat{N}_G(i,t-1) \& b(\ell,t-1)=\hat{b}_G(\ell,t-1) | i,t-1] \quad (3-106)$$

The number of different ways $\psi_{DB}^-(k,t) + \psi_{DD}^-(k,t) + \psi_{DD}^-(k,t)$ indices can be "drawn" from the $L(t)$ measurement indices is

$$L(t)! / [L(t) - \psi_{DB}^-(t) - \psi_{DD}^-(t) - \psi_{DD}^-(t)]! \quad (3-107)$$

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But the requirement that the indices in $\hat{\Psi}_{DB}^-(k,t)$ be ordered by the magnitudes of the corresponding measurements reduces that quantity by $\hat{\Psi}_{DB}^-(t)!$, so the first factor of Eq. 3-106 can be simplified as follows:

$$\text{Prob}[i(\ell,t)=i_s(\ell,t)|j,t] \text{ for } \ell \in \hat{\Psi}_{DB}^-(k,t) \cup \hat{\Psi}_{DD}^-(k,t) \cup \hat{\Psi}_{DD}^-(k,t) \}$$

$$\hat{\Psi}_{DB}^-(t) = \hat{\Psi}_{DB}^-(k,t) \& \hat{\Psi}_{DD}^-(t) = \hat{\Psi}_{DD}^-(k,t) \& \hat{\Psi}_{DD}^-(t) = \hat{\Psi}_{DD}^-(k,t) \}$$

$$= [L(t) - \hat{\Psi}_{DB}^-(t) - \hat{\Psi}_{DD}^-(t) - \hat{\Psi}_{DD}^-(t)]! \hat{\Psi}_{DB}^-(t)! / L(t)! \quad (3-108)$$

The remaining factors of Eq. 3-106 are simply state transition probabilities, each repeated as many times as a particular transition is hypothesized to occur. Thus,

$$\text{Prob}[\theta_s(j,t) | \theta_G(i,t-1) \& Z_G(t-1)] = ([L(t) - \hat{\Psi}_{DB}^-(t) - \hat{\Psi}_{DD}^-(t) - \hat{\Psi}_{DD}^-(t)]! \hat{\Psi}_{DB}^-(t)! / L(t)!) \times$$

$$\begin{matrix} \hat{\Psi}_{DD}^-(k,t) & \hat{\Psi}_{DD}^-(k,t) & \hat{\Psi}_{XD}^-(k,t) & \hat{\Psi}_{DD}^-(k,t) & \hat{\Psi}_{DD}^-(k,t) & \hat{\Psi}_{XX}^-(k,t) \\ P_B & [1-P_D-P_X] & P_X & P_D & [1-P_D] & 1 \end{matrix} \times$$

$$e^{-\lambda_B} \frac{\hat{\Psi}_{DB}^-(k,t)}{\lambda_B} / \hat{\Psi}_{DB}^-(t)! \quad (3-109)$$

When this equation and Eq. 3-102 are substituted in Eq. 3-52, the formula for $P_G(k,t)$ can be obtained by a little rearrangement of terms.

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3.2.4 Case 3 Revisited

A remarkable feature of the formula in Eq. 3-91 for computing the probability of the k-th hypothesis at t is that the actual number of detections appears only in the term $Q(t)$, common to all of the hypotheses at that time. While different hypotheses may implicitly involve hypothesizing different numbers of false detections, the differing numbers do not appear explicitly; the weighting of each Gaussian density function by the inverse of p_{FA} effectively accounts for the false detections. Another remarkable feature is the presence of a term corresponding to each target hypothesized to have been born at that time. This suggests a different organization of hypothesis structures and of the optimal algorithm which may be more readily implemented in a practical manner.

The first step in defining this alternative approach is to define the target hypothesis structure, $H_T(i,t)$. It has four components:

$$H_T(i,t) = (\hat{D}_T'(i,t), \hat{x}(t|i,t), \Sigma(t|i,t), P_T(i,t)) \quad (3-110)$$

The first component represents a hypothesized event state sequence for some target, index unspecified, as follows:

$$\hat{D}_T(i,t) = \{\hat{d}_T(\tau|i,t)\}_{\tau=0}^t \text{ for } t \geq 0 \quad (3-111)$$

and

$$\hat{d}_T'(\tau|i,t) = [\hat{b}_T(\tau|i,t), \hat{i}_T(\tau|i,t)]^T \text{ for } \tau \leq t \quad (3-112)$$

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and where $\hat{d}_T(\tau|i,t)$ is the value of $d'(\ell,\tau)$ assumed by the i -th target hypothesis for some unspecified ℓ ; $b_T(\tau|i,t)$ and $\hat{v}_T(\tau|i,t)$ are similarly related to $b(\ell,\tau)$ and $v(\ell,\tau)$. The i -th target hypothesis at t is correct if and only if

$$\hat{d}_T(\tau|i,t) = d'(\ell,\tau) \text{ for } 0 \leq \tau \leq t \text{ and some } \ell. \quad (3-113)$$

For convenience, we denote this event by $\Theta_T(i,t|\ell)$.

The second and third components of $H_T(i,t)$ represent the optimal estimate of the target's dynamic state $x(\ell,t)$, as follows:

$$\hat{x}_T(t|i,t) = E[x(\ell,t) | \Theta_T(i,t|\ell) \& Z_G(t)] \quad (3-114)$$

and

$$\Sigma_T(t|i,t) = \text{Cov}[x(\ell,t) | \Theta_T(i,t|\ell) \& Z_G(t)] \quad (3-115)$$

for some ℓ . Thus far, there are strong parallels to the definition of the global hypothesis structure in Case 2. However,

$$P_T(i,t) \neq \text{Prob}[\Theta_T(i,t|\ell) | Z_G(t)] \quad (3-116)$$

The definition of $P_T(i,t)$ is ad hoc, but carefully chosen, as will be seen.

The number of track hypothesis structures at t is denoted by $M_T(t)$.

To define how the components of track hypothesis structures are calculated, it is convenient to define the look hypothesis structure, denoted by $H_L(j,t)$. It has one component:

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$$H_L(j,t) = (\hat{d}_L(t|j,t)) \text{ for } t > 0 \quad (3-117)$$

where

$$\hat{d}_L(t|j,t) = [\hat{b}_L(t|j,t), \hat{i}_L(t|j,t)]^T \text{ for } t > 0 \quad (3-118)$$

and where $\hat{d}_L(t|j,t)$ is the value of $d'(\ell,t)$ assumed by the j -th look hypothesis at t for some unspecified ℓ ; $\hat{b}_L(t|j,t)$ and $\hat{i}_L(t|j,t)$ are similarly related to $b(\ell,t)$ and $i(\ell,t)$ for the same value of ℓ . The j -th look hypothesis at t is correct if and only if

$$\hat{d}_L(t|i,t) = d'(\ell,t) \text{ for } t > 0 \text{ and some } \ell. \quad (3-119)$$

For convenience, we denote this event by $\Theta_L(j,t|\ell)$. We denote the number of look hypotheses at t by $M_L(t)$. On any scan t , any one target can be "unborn," can be "undetected," can be "dead," or can cause any one of the $L(t)$ detections on that scan. Thus,

$$M_L(t) = L(t) + 3 \text{ for } t > 0. \quad (3-120)$$

Each target hypothesis structure is constructed from a sequence of consecutive look hypothesis structures. Thus each target hypothesis structure at t can be formed from a target hypothesis structure at $t-1$ and a look hypothesis structure at t . We symbolize this relationship in the usual manner:

$$H_T(i,t-1) * H_L(j,t) \Rightarrow H_T(k,t). \quad (3-121)$$

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As in Case 2, this generative formula applies only for $t > 0$ and for certain i and j pairs. For $t=0$, we have but one track hypothesis structure $H_T(1,0)$, such that

$$\hat{b}_T(1,0) = \bar{B} \quad (3-122)$$

and

$$P_T(1,0) = 1 \quad (3-123)$$

All of the other components of this hypothesis structure are undefined. The indices i and j are restricted to be such that $\hat{d}_L(j,t)$ is reachable from $\hat{d}_T(i,t-1)$ in one step. These restrictions exactly parallel those in Case 2:

$$\hat{b}_L(t|j,t) = \bar{B} \quad \text{and} \quad \hat{b}_T(t-1|i,t-1) = \bar{B}$$

$$\hat{b}_L(t|j,t) = D \quad \text{and} \quad \hat{b}_T(t-1|i,t-1) \neq X$$

$$\hat{b}_L(t|j,t) = \bar{D} \quad \text{and} \quad \hat{b}_T(t-1|i,t-1) = D \text{ or } \bar{D} \quad ,$$

or

$$\hat{b}_L(t|j,t) = X \quad \text{and} \quad \hat{b}_T(t-1|i,t-1) = D \text{ or } X \quad (3-124)$$

The generative procedure also closely parallels that in Case 2. The new hypothesized event state sequence $\hat{D}_T(k,t)$ is generated from $\hat{D}_T(i,t-1)$ and $\hat{d}_L(j,t)$ by letting

$$\hat{d}_T(\tau|k,t) = \hat{d}_T(\tau|i,t-1) \quad \text{for} \quad 0 \leq \tau \leq t-1 \quad (3-125a)$$

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and

$$\hat{d}_T(t|k,t) = \hat{d}_L(t|j,t) \quad (3-125b)$$

This definition gives rise to the observation that

$$\Theta_T(i,t-1|\ell)\Theta_L(j,t|\ell) = \Theta_T(k,t|\ell) \quad (3-126)$$

for $t > 0$ and $\ell > 0$. This observation can be used to justify the following procedures for updating the second and third components of the track hypothesis structures:

$$\hat{x}_T(t|k,t) = \hat{x}_T(t|i,t-1) + K(t|i,t-1)[z(\hat{i}_L(t|j,t),t) - C\hat{x}_T(t|i,t-1)] \quad (3-127a)$$

and

$$\Sigma_T(t|k,t) = [I - K(t|i,t-1)C^T]\Sigma_T(t|i,t-1) \quad (3-127b)$$

if $\hat{b}_L(t|j,t) = D$ and $\hat{b}_T(t-1|i,t-1) = D$ or $\bar{D}$,

$$\hat{x}_T(t|k,t) = \hat{x}_T(t|i,t-1) \quad (3-128a)$$

and

$$\Sigma_T(t|k,t) = \Sigma_T(t|i,t-1) \quad , \quad (3-128b)$$

if $\hat{b}_L(t|j,t) = \bar{D}$, and

$$\hat{x}_T(t|k,t) = K_0 z(\hat{i}_L(t|j,t),t) \quad (3-129a)$$

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and

$$\Sigma_T(t|k,t) = [I - K_O C^T] \Sigma_O \quad (3-129b)$$

if $\hat{b}_L(t|j,t)=D$ and $\hat{b}_T(t-1|i,t-1)=\bar{B}$ where

$$\hat{x}_T(t|i,t-1) = A\hat{x}_T(t-1|i,t-1) \quad , \quad (3-130a)$$

$$\Sigma_T(t|i,t-1) = A\Sigma_T(t-1|i,t-1)A^T + W \quad , \quad (3-130b)$$

$$K(t|i,t-1) = \Sigma_T(t|i,t-1)C[V+C\Sigma_T(t|i,t-1)C^T]^{-1} \quad , \quad (3-130c)$$

and

$$K_O = \Sigma C_O[V+C\Sigma_O C^T]^{-1} \quad . \quad (3-130d)$$

The update of $P_T(i,t)$ depends on $\hat{b}_L(t|j,t)$ and $\hat{b}_T(t-1|i,t-1)$ as follows:

$$P_T(k,t) = P_T(i,t-1) \quad \text{if} \quad \hat{b}_L(t|j,t)=\bar{B} \quad \text{and} \quad \hat{b}_T(t-1|i,t-1) = \bar{B}$$

$$P_T(i,t-1)\lambda_B[G(z(\hat{b}_L(t|j,t),t),V+C\Sigma_O C^T)/\rho_{FA}]$$

$$\text{if} \quad \hat{b}_L(t|j,t)=D \quad \text{and} \quad \hat{b}_T(t-1|i,t-1)=\bar{B}$$

$$P_T(i,t-1)P_D[G(z(\hat{b}_L(t|j,t),t)-C\hat{x}_T(t|i,t-1),V+C\Sigma_T(t|i,t-1)C^T)/\rho_{FA}]$$

$$\text{if} \quad \hat{b}_L(t|j,t)=D \quad \text{and} \quad \hat{b}_T(t-1|i,t-1)=D \text{ or } \bar{D}$$

$$P_T(i,t-1)[1-P_D-P_X] \quad \text{if} \quad \hat{b}_L(t|j,t)=\bar{D} \quad \text{and} \quad \hat{b}_T(t-1|i,t-1)=D$$

$$P_T(i,t-1)P_X \quad \text{if} \quad \hat{b}_L(t|j,t)=X \quad \text{and} \quad \hat{b}_T(t-1|i,t-1)=D$$

$$P_T(i,t-1)[1-P_D] \quad \text{if} \quad \hat{b}_L(t|j,t)=\bar{D} \quad \text{and} \quad \hat{b}_T(t-1|i,t-1)=\bar{D} \quad ,$$

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and

$$P_T(i, t-1) \quad \text{if} \quad \hat{b}_L(t|j, t)=X \quad \text{and} \quad \hat{b}_T(t-1|i, t-1)=X \quad (3-131)$$

where

$$G(y, Y) = (2\pi)^{-K/2} |Y|^{-1/2} e^{-y^T Y^{-1} y/2} \quad (3-132)$$

The expression $Q(t)$ does not appear in this update unlike previous cases.

Growth in the number of target hypothesis structures can be bounded as follows:

$$M_T(t) \leq M_T(t-1)[L(t)+3] \quad \text{for} \quad t > 0 \quad (3-133)$$

As with the global hypothesis structures in Case 2, the rate of growth can be geometric.

The second step in this alternative formulation of the optimal tracking algorithm requires an alternative definition of the global hypothesis structure. The i -th alternative global hypothesis structure has three components:

$$H'_G(i, t) = (\hat{N}_G(i, t), \hat{K}_G(i, t), P_G(i, t)) \quad (3-134)$$

where $\hat{N}_G(i, t)$ and $P_G(i, t)$ have their usual meanings, where

$$\hat{K}_G(i, t) = \{\hat{\kappa}_G(\ell|i, t)\}_{\ell=1}^{\hat{N}_G(i, t)} \quad (3-135)$$

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and where each $\hat{\kappa}(\ell|i,t)$ designates a target hypothesis structure. In effect, each alternative global hypothesis assumes a number of targets and associates a track hypothesis with each one.

There are two restrictions on the target hypothesis structure index set $\hat{K}_G(i,t)$. One restriction is that

$$\hat{1}_T(\tau|\hat{\kappa}_G(\ell|i,t),t) \neq \hat{1}_T(\tau|\hat{\kappa}_G(\ell'|i,t),t) \quad (3-136)$$

for all $\ell \neq \ell'$ and $0 < \tau \leq t$. This restriction simply means that an alternative global hypothesis cannot include two target hypotheses based on a common detection. The second restriction is that for ℓ and ℓ' such that $0 < \ell < \ell' \leq \hat{N}_G(i,t)$ then either

$$\hat{b}_T(\tau|\hat{\kappa}_G(\ell'|i,t),t) = \bar{B} \quad \text{and} \quad \hat{b}_T(\tau|\hat{\kappa}_G(\ell|i,t),t) = D \quad (3-137a)$$

i.e., one target is born before the other; or, if both targets are born at the same time t

$$\|z(\hat{1}_T(\tau|\hat{\kappa}_G(\ell'|i,t),t))\| > \|z(\hat{1}_T(\tau|\hat{\kappa}_G(\ell|i,t),t))\| \quad (3-137b)$$

This restriction simply means that targets are indexed first in the order of the "birth" and second by the order of their "birth" measurement's magnitude.

The method of calculating $P_T(i,t)$ was chosen so that

$$P_G(i,t) = \prod_{\ell=1}^{\hat{N}_G(i,t)} \hat{P}_T(\hat{\kappa}_G(\ell|i,t),t) \prod_{\tau=1}^t Q(t) \quad (3-138)$$

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where

$$Q(\tau) = e^{-\lambda_B} [e^{-\lambda_{FA}} \rho_{FA}^{L(\tau)} / L(\tau)!] / \text{Prob}[Z_S(\tau) | Z_G(\tau-1)]$$

(3-139)

It remains to demonstrate the correctness of this formula. The first step is to note that the number of alternative global hypotheses at t equals the number of global hypotheses, since both sets of hypotheses must include all possible hypothetical associations of detections with targets. For convenience, we assume that the indices of the original and alternative hypothesis structures are equivalent. That is, we assume

$$\hat{d}'_G(\ell, \tau | i, t) = \hat{d}_T(\tau | \kappa_G(\ell | i, t), t) \quad \text{for } \tau \leq t \quad (3-140a)$$

and

$$\hat{x}'(\ell, t | i, t) = \hat{x}'_T(t | \kappa_G(\ell | i, t), t) \quad , \quad (3-140b)$$

both for $t > 0$.

The second step is to observe that Eq. 3-85b implies

$$\hat{d}'_G(\ell, t | k, t) = \hat{d}'_S(\ell, t | j, t) \quad (3-141)$$

for $1 \leq \ell \leq N_G(k, t)$ and for some j corresponding to every k . Thus,

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$$\hat{d}'_s(\ell, t | j, t) = \hat{d}_T(t | \kappa_G(\ell | k, t), t) \quad (3-142)$$

for $1 \leq \ell \leq \hat{N}_G(k, t)$ and for some j corresponding to every k . Using the relation between j and k implied in this last equation, one can define the target index sets $\hat{\Psi}_{DB}(k, t)$, etc. as in the last subsection with a slightly different interpretation, e.g.,

$$\hat{b}_T(t | \kappa_G(\ell | k, t), t) = D \quad \text{and} \quad \hat{b}_T(t-1 | \kappa_G(\ell | k, t), t) = \bar{B} \quad (3-143)$$

if and only if $\ell \in \hat{\Psi}_{DB}(k, t)$.

The third step is then to rewrite Eq. 3-138 as follows:

$$\begin{aligned} P_G(k, t) = & \hat{\prod}_{\ell \in \hat{\Psi}_{DB}(k, t)} P_T(\hat{\kappa}_G(\ell | k, t), t) \hat{\prod}_{\ell \in \hat{\Psi}_{DD}(k, t)} P_T(\hat{\kappa}_G(\ell | k, t), t) \times \\ & \hat{\prod}_{\ell \in \hat{\Psi}_{DD}(k, t)} P_T(\hat{\kappa}_G(\ell | k, t), t) \hat{\prod}_{\ell \in \hat{\Psi}_{DD}(k, t)} P_T(\hat{\kappa}_G(\ell | k, t), t) \times \\ & \hat{\prod}_{\ell \in \hat{\Psi}_{DD}(k, t)} P_T(\hat{\kappa}_G(\ell | k, t), t) \hat{\prod}_{\ell \in \hat{\Psi}_{DD}(k, t)} P_T(\hat{\kappa}_G(\ell | k, t), t) \times \\ & \hat{\prod}_{\ell \in \hat{\Psi}_{XX}(k, t)} P_T(\hat{\kappa}_G(\ell | k, t), t) \prod_{\tau=1}^t Q(\tau) \end{aligned} \quad (3-144)$$

Using Eqs. 3-125 and 3-131, it is possible to further the rewriting process:

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$$\begin{aligned}
 P_G(k, t) = & \prod_{m=1}^{\hat{N}_G(i, t-1)} P_T(\kappa_G(m|i, t-1), t-1) \prod_{\tau=1}^{t-1} Q(\tau) \times \\
 & \prod_{\ell \in \Psi_{DB}(k, t)} \lambda_B[G(z(\iota_T(t|\hat{\kappa}_G(\ell|k, t), t), V + C\Sigma_0 C^T)/\rho_{FA})] \times \\
 & \prod_{\ell \in \Psi_{DD}(k, t) \cup \Psi_{DD}(k, t)} P_D[G(z(\iota_T(t|\hat{\kappa}_G(\ell|k, t), t) - Cx_T(t|\hat{\kappa}_G(\ell|i, t-1)t-1), \\
 & \quad V + C\Sigma_T(t|\hat{\kappa}_G(\ell|i, t-1), t-1)C^T)] \times \\
 & [1 - P_D - P_X] \frac{\bar{\Psi}_{DD}(k, t)}{P_X} \frac{\Psi_{XD}(k, t)}{[1 - P_D]} \frac{\bar{\Psi}_{DD}(k, t)}{Q(t)} \quad (3-145)
 \end{aligned}$$

for some i corresponding to each k . Because the first two factors of this last equation simply equal $P_G(i, t-1)$, the correctness of Eq. 3-138 is demonstrated intuitively.

The motivation for this alternative form for the hypothesis structures and for the optimal algorithm is not obvious at this point. It is in simplifying and then implementing the algorithm that the advantages reveal themselves. The advantages are partially illuminated in the next section which sketches an implementation of the optimal algorithm.

SECTION 4

ALGORITHM DEVELOPMENT: PRACTICAL ALGORITHMS

Defining an algorithm which is optimal given all of the phenomena which must be captured (false and missing detections, target maneuvers, data association, etc.) is difficult even in the absence of computational constraints. To take such an algorithm and make it computationally practical without sacrificing much performance is also difficult. Practicality requires that the number of hypotheses actually generated and tested by a tracking algorithm be bounded by some value dependent on the host computer. Thus some hypotheses must be ignored. This fact leads to the necessity of defining rules for the pruning, combining, and ignoring hypotheses in an efficient fashion while maintaining a high level of performance. Here we must be careful in defining, even informally, what we mean by a "high level of performance." One obvious measure of performance is the probability that the correct hypothesis is not ignored or discarded. However, if one ignores or discards even a single hypothesis there is a nonzero probability that it will be the true hypothesis that is ignored or discarded. Furthermore, if all but a bounded number of hypotheses are ignored, then the probability that the true hypothesis is ignored or discarded grows as $t \rightarrow \infty$, and, although we have not yet attempted to prove it, we conjecture that in many cases this probability approaches unity as $t \rightarrow \infty$.

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It is very important that the last sentence be understood thoroughly, as it clearly points out the inadequacy of using the probability of keeping the true hypothesis as the critical measure of performance and in fact suggests both alternative measures of performance and potential pruning strategies. Specifically, in our Case 3, the true hypothesis includes the precise specification of exactly when each target is born and dies, the complete list of scans on which each target is detected, and the data associations for detected targets. If one were to include maneuvers and formations, the true hypothesis would include the precise times and descriptions of every maneuver of every target and the precise times of the splitting of targets from formation or the merging of targets into formation. With this definition, an hypothesis corresponding to absolute truth, except for a single misclassification of one return as a false alarm rather than a detected target, is a false hypothesis, even if this one error corresponds to an event several hundred scans in the past! From this example it is clear that there are many hypotheses that are close to the truth and consequently will produce estimates virtually indistinguishable from that of the true hypothesis, except, perhaps, for small intervals of time corresponding to points at which the "nearby" hypothesis is in error. Thus, one is led to the notion of the resilience of a suboptimal MMAE algorithm. There are a variety of ways in which one can quantify this intuitive idea. For example, one might take as a measure of resilience the probability that at least one hypothesis "sufficiently close" to the true hypothesis is retained or the expected percentage of time that such an hypothesis is retained.

While we have not pursued the detailed calculation of such measures or the optimal choice of pruning rules (which is a very difficult problem),

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having specified the optimal algorithm provides us with an excellent foundation both for devising promising rules and for evaluating their performance, both through simulations and eventually via analysis. To date our work has followed the forms of these methods of evaluation, but before we turn to describing several rules and subsequently the evaluation of their performance, let us make several comments about analytical methods. Specifically, to develop such methods, what is needed are two types of tools:

1. methods for measuring the distance between hypotheses and for determining the set of hypotheses that are "sufficiently close to the truth;" and
2. methods for evaluating the probability that all hypotheses that are "sufficiently close" are discarded when particular pruning rules are used.

While neither of these tasks is an easy one, there are existing tools that should prove of value for each. Specifically, as we have indicated, "sufficiently close" can be defined in terms of estimation accuracy. Thus, standard results on suboptimal linear filtering can be used. Alternatively, one might consider using the recent results of Baram [8],[9],[18] and others on distance measures between different models (i.e., hypotheses) and on the selection of suboptimal modes for filter design. The problem of evaluating probabilities for specific pruning rules is essentially a complex level crossing problem, as all such rules can be viewed as consisting of a set of threshold or comparison tests. There exists a large literature on this topic, and in particular the recent computationally efficient approximate methods of Gallager and Helstrom [19], and researchers at ALPHATECH [20] working on a different project should be of value. In the remainder of this section we focus our attention on several specific pruning rules which have clear and obvious advantages and interpretations.

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One type of rule that might be used is to explicitly discard track hypotheses using much the same criteria as are used implicitly in currently fielded airborne surveillance radar systems. Those systems often employ tracking "correlation gates" to decide which detection should be used to update which tracks. In terms of the algorithm described in subsection 3.2.4, such gating would discard the k -th track hypothesis if, in the course of generating $P_T(k, t)$ from $P_T(i, t-1)$ as per Eqs. 3-131 and 3-132

$$G(\hat{z}(i_L(t|j, t), t) - \hat{C}x_T(t|i, t-1), V + \hat{C}\Sigma_T(t|i, t-1)\hat{C}^T) > T_G \quad (4-1)$$

In essence, this equation establishes an elliptical track correlation gate about the predicted measurement coordinates $\hat{C}x_T(t|i, t-1)$, with orientation and axes determined by the covariance of that prediction and of the measurements. For this correlation gating scheme, one can explicitly determine the probability of discarding the correct hypothesis on any particular scan with this test; it is

$$e^{-T_G/2} \quad (4-2)$$

This result illustrates the advantage of using the optimal algorithm as a starting point for defining a tracking algorithm even if familiar ad hoc approaches are used to reduce storage and computational requirements. Specifically, having the optimal algorithm available allows one to ascertain precisely the nature of the suboptimality introduced by any particular decision rule and to quantify the extent of suboptimality.

The approach in the preceding paragraph discards track hypotheses. We presume every global hypothesis which involves a discarded track hypothesis is also discarded. Another technique can be adopted which begins by discarding

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global hypotheses and then goes on to discard track hypotheses which are not a component of some surviving global hypothesis. In this case one retains the T_M most probable global hypotheses and discards all the rest.

While both of these approaches should reduce to a trivial level the probability of discarding the correct global hypothesis if T_G and T_M are sufficiently large, they still allow the possibility that the correct global hypothesis will be discarded. However, as indicated previously, discarding the correct global hypothesis need not be a catastrophe or even a serious problem. For simplicity, consider two track hypotheses, $H_T(1,t)$ and $H_T(2,t)$. Both are based on detections of the same target, with one exception. Suppose that

$$\hat{d}_T(\tau|1,t) = d_T(\tau|2,t) = d'(\ell,\tau) \quad (4-3)$$

for some ℓ and for all $\tau < t$ except τ_0 . For τ_0 , let

$$\hat{b}_T(\tau_0|1,t) = b(\ell,\tau_0) = D, \quad (4-4)$$

$$\hat{i}_T(\tau_0|1,t) = i(\ell,\tau_0), \quad (4-5)$$

and

$$\hat{b}_T(\tau_0|2,t) = \bar{D}. \quad (4-6)$$

That is, $H_T(1,t)$ is the correct hypothesis while $H_T(2,t)$ differs in assuming that the target was not detected at τ_0 although it actually was.

If $\tau_0 = t$, then the state estimates and associated covariance will show a difference, although not necessarily a large one unless the target was very

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recently born. As $t - \tau_0$ becomes larger and the difference in the hypotheses recedes into the past, the state estimates and associated covariances become closer and closer in value. When $t - \tau_0$ is large, the estimates and covariances become indistinguishable. Thus, if $H_T(1,t)$ had been discarded for some reason, $H_T(2,t)$ would eventually become essentially equivalent. The point of this example is that our tracking algorithm is quite resilient; it can recover from the incorrect discarding of the correct hypothesis with a transient in the state estimates and associated covariances.

This observation suggests that storage and computational resources can be saved by combining hypotheses, either track hypotheses or global hypotheses, which are essentially equivalent. We term the process "hypothesis fusion." The most obvious criterion for deciding when to fuse track hypotheses is a simple threshold test, a weighted difference in state estimates. For $H_T(1,t)$ and $H_T(2,t)$, the hypotheses are fused if

$$\| \hat{x}_T(t|1,t) - \hat{x}_T(t|2,t) \|^2 [\Sigma_T(t|1,t)/2 + \Sigma_T(t|2,t)/2]^{-1} \leq T_F \quad (4-7)$$

Then, one hypothesis or the other is discarded and the other appropriately modified. Continuing with our example, a reasonable modification is to use as an estimate the weighted average of the estimates of the hypotheses being fused and to use the average of their covariances:

$$\begin{aligned} \hat{x}_T(t|1,t) \leq & [\Sigma_T(t|1,t)/2 + \Sigma_T(t|2,t)/2] \times \\ & [\Sigma_T(t|1,t)^{-1/2} \hat{x}_T(t|1,t) + \Sigma_T(t|2,t)^{-1/2} \hat{x}_T(t|2,t)] \end{aligned} \quad (4-8)$$

$$\Sigma_T(t|1,t) \leq \Sigma_T(t|1,t)/2 + \Sigma_T(t|2,t)/2 \quad (4-9)$$

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Also, the probability mass distributed between the hypotheses being fused is summed:

$$P_T(t|1,t) \leq P_T(t|1,t) + P_T(t|2,t) \quad , \quad (4-10)$$

creating a new $H_T(1,t)$; $H_T(2,t)$ would be discarded. We would then similarly merge any global hypotheses differing only by the two track hypotheses, $H_T(1,t)$ and $H_T(2,t)$.

An even simpler "hypothesis fusion" technique would be to combine $H_T(1,t)$ and $H_T(2,t)$ if

$$d_T(\tau|1,t) = d_T(\tau|2,t) \quad \text{for} \quad t - T_T < \tau < t \quad . \quad (4-11)$$

Then the two hypotheses would be merged as in Eqs. 4-8 through 4-10, again producing a new $H_T(1,t)$ and discarding the old $H_T(2,t)$. Some global hypotheses would then be merged as needed.

In judging the efficacy of any particular rule for reducing the number of hypotheses that are kept one must consider several issues. The first of these is, of course, the effectiveness of the rule in reducing the number of hypotheses in a resilient manner. As indicated earlier in this section we have not developed detailed analytical tools for evaluating resilience (although we have briefly outlined how this might be done). Rather, in Section 6 we will demonstrate the resilience and qualitative behavior of algorithms using some of these rules by describing a series of simulations that have been performed.

The second issue is the complexity of the additional calculations required for the implementation of the rule. While we have not examined this issue in great detail for any of the rules we have proposed, it is not difficult to see the key differences among these rules in terms of complexity.

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Gating rules as in Eq. 4-1 offer the greatest computational savings. This is not only because the calculations in Eq. 4-1 are simple. In fact the critical point is that this rule determines hypotheses which need not be generated at all. Such a rule is termed a "rule for ignoring," and additional rules of this type should be considered if for no other reason than the computational savings they may offer. As a second example, consider the rule which keeps all but a specified number of the most probable hypotheses. This is a "rule for pruning" which requires that hypotheses be generated before being discarded. Such rules are no doubt essential but intuitively should be used subsequent to using rules for ignoring to reduce the number of hypotheses that are generated. Finally, the rule described in Eqs. 4-3 through 4-10 is an example of a "rule for merging" which is the most complex type of rule, as not only does one generate hypotheses but one also must search for hypotheses to be merged and then perform operations to combine the hypotheses. Again such rules will certainly be necessary, and in fact, they are of critical importance in assuming that pruning rules work in a desirable fashion.

The third issue is a bit more subtle, as it involves the intuitive simplicity of the rule. Specifically, in a large-scale application in which numerous rules are used, a critical element in understanding an overall algorithm is a precise understanding of what each individual rule is meant to do. This is especially important in algorithm development, modification, and troubleshooting: there are too many existing decision tree algorithms in which the sheer complexity of the system precludes one being able to deduce how the algorithm will respond under any specified conditions; by starting from the complete, optimal algorithm and proceeding systematically we have

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begun to develop a set of rules that will allow us to avoid this difficulty and to determine a set of rules which together reduce overall complexity to a satisfactory level while maintaining a high level of performance.

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SECTION 5 IMPLEMENTATION

5.1 INTRODUCTION

The multitarget tracker has two major tasks: generation of data associations, and generation of consistent interpretations of data associations. To accomplish these tasks, the tracker maintains and processes corresponding data structures: the association list, and the global hypothesis list. The association list stores numerical data which describes postulated trajectories. The global hypothesis list stores combinations of trajectories each of which is given a numerical likelihood. At any time, the global hypothesis of highest likelihood summarizes the tracker's best estimate of the number of trajectories as well as the current location and velocity of the targets traversing these trajectories. The association list is updated once in each scan cycle. The global hypothesis list is generated anew in each cycle by expanding the list which was present at the end of the previous scan.

In a supporting role is the trajectory list which stores the coordinates of simulated returns and false detections. Based on parameters entered by the user, the trajectory generator produces lists of radar returns with Gaussian random noise added. The trajectory list is a dually-linked list. Individual trajectories are generated over a series of scans, a single return in each scan. The same data is presented to the tracker, however, as sets of returns, one set per scan. The parameters upon which trajectories are based are not

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available to the tracker itself. All elements of the description of trajectories, including the number of trajectories, must be deduced by the generation and ranking of global hypotheses.

The operation of the trajectory generator is straightforward, but the processing of the association list and the global hypothesis list is quite complex. The rest of Section 5 describes the building of hypotheses and the devices employed to limit their number.

5.2 THE ASSOCIATION LIST

The association list is constructed from the primitive elements referred to as track nodes or track hypotheses. A track node stores the information which uniquely describes one possible trajectory: the estimated position and velocity of the target, the estimated errors in these estimates, and the numerical likelihood of this target state. Procedure ASSOCIATE, which processes this list, calls most of the computational submodules of the tracker. These include the Kalman filter, the likelihood calculator, and lower-level matrix mathematics routines.

Each simulated return is represented in two ways in the association list, first of all as a new target, and secondly as a group of continuations of existing tracks. A track node which represents a new target becomes the root node of a potential tree of track nodes - a track tree. As track continuations, the return is multiply represented as track nodes which occupy new branches on preexisting track trees. Each terminal track node in each track tree receives one additional branch for each simulated return (an exception to

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this is noted below). The Kalman filter bases its state estimate for a new branch node on the updated state estimate associated with the parent node and the coordinates of the return.

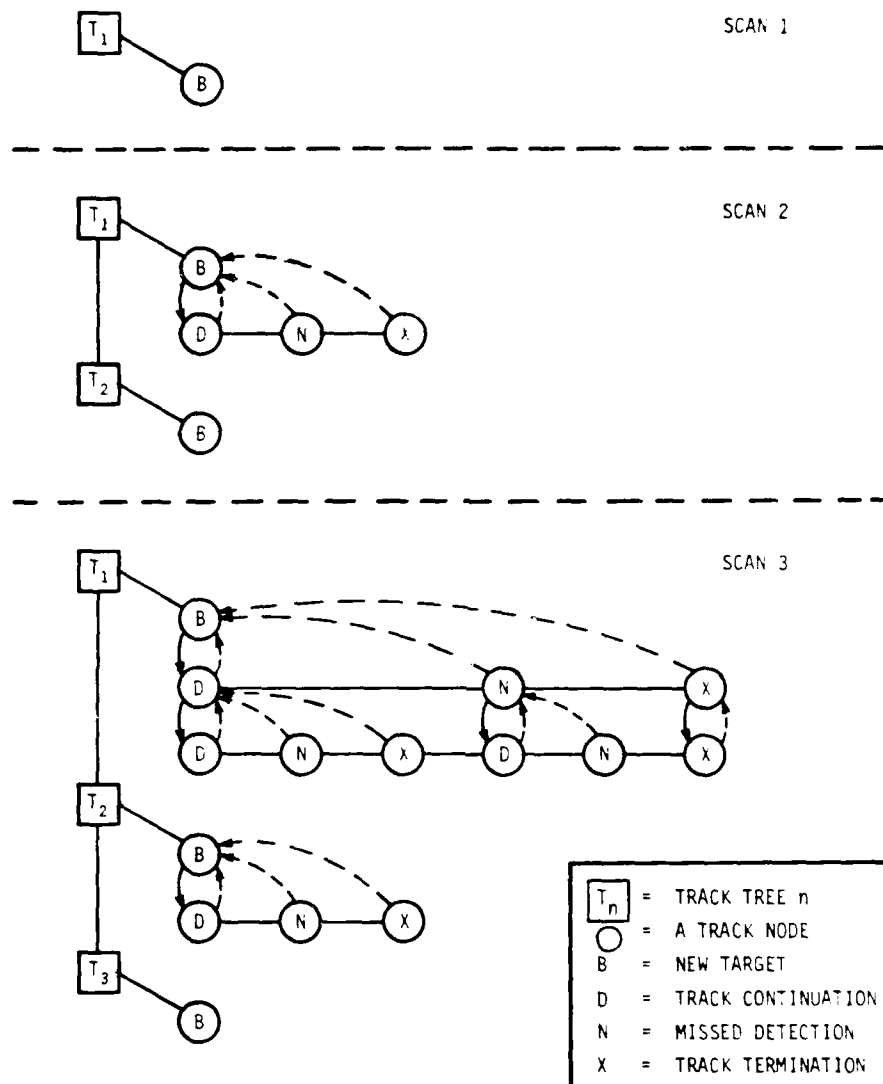
Besides the branch nodes associated with returns, two additional branch nodes are added to the descendants of some parent track nodes, one node which corresponds to a postulated missed detection, and a second which corresponds to a track termination. Parent nodes representing missed detections, and nodes corresponding to track terminations are given special handling. Missed detections are not given branches corresponding to terminations. Terminations are given only terminations; they never receive branches corresponding to returns or to missed detections.

The number of track trees at the end of any scan is equal to the total number of returns up to that time. The depth of a track tree equals the number of scans which have been processed beginning with the scan in which the root node entered the association list up until the present scan. The breadth of a track tree is a function of its depth, and the number of returns per scan. Figure 5-1 traces the evolution of the association list for a simple case.

5.3 THE GLOBAL HYPOTHESIS LIST

The global hypothesis list is a bilevel list. Each entry in the list, a global hypothesis, is itself a list of elements each of which stores the address of a track node. These elements are referred to here as hypothesis nodes. The entire global hypothesis list stores these lower-order lists in descending order of hypothesis likelihood.

ONE RETURN/SCAN



R-0243

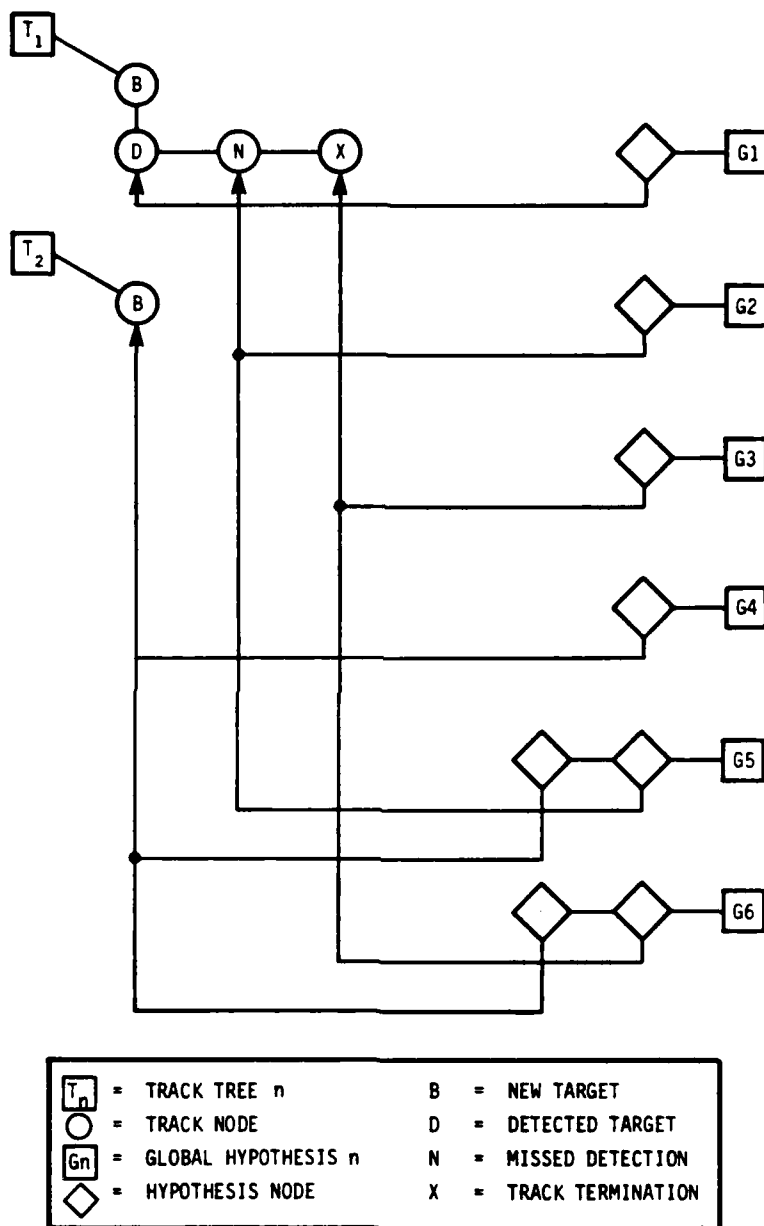
Figure 5-1. Evolution of the Association List.

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The track nodes to which hypothesis nodes refer are terminal track nodes on some branch of a track tree. In any global hypothesis, each hypothesis node selects a track node in a unique track tree. Since each track tree corresponds to a different postulated target, each hypothesis node refers to a different postulated trajectory. If a global hypothesis postulated N trajectories, it will contain N hypothesis nodes referring to track nodes in N different track trees. The likelihood of a track hypothesis equals the sum of the likelihoods assigned to each track node in the track. The likelihood of a global hypothesis equals the sum of the likelihoods of the track hypotheses to which it refers. (Throughout this discussion, the term "likelihood" should be interpreted as the natural logarithm of the likelihood value.)

Figure 5-2 illustrates the appearance of the global hypothesis list after two scans with a single return in each scan. No attempt is made to represent ranking by likelihood. Note that global hypotheses G2 and G3 in Fig. 5-2 are present in two versions, one which does not postulate the presence of a new target (G2,G3) and a second version which does (G5,G6). Each global hypothesis is produced as multiple version equal in number to the number of combinations of possible new targets, whenever these versions are not inconsistent with the total number of returns in the scan. Referring again to Fig. 5-2, you will note that there is no global hypothesis which include references to both the D node of track tree 1 and the B node of track tree 2. This hypothesis, which states that the return is both a continuation of a previous track and a new target, is logically inconsistent. Constraints built into the global hypothesis generator (logical constraints - discussed in subsection 5.4) screen out logically inconsistent hypotheses.

ONE RETURN/SCAN



R-0894

Figure 5-2. Global Hypothesis List After Two Scans.

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The trajectories postulated by the six global hypotheses in Fig. 5-2 and their interpretations are given as follows:

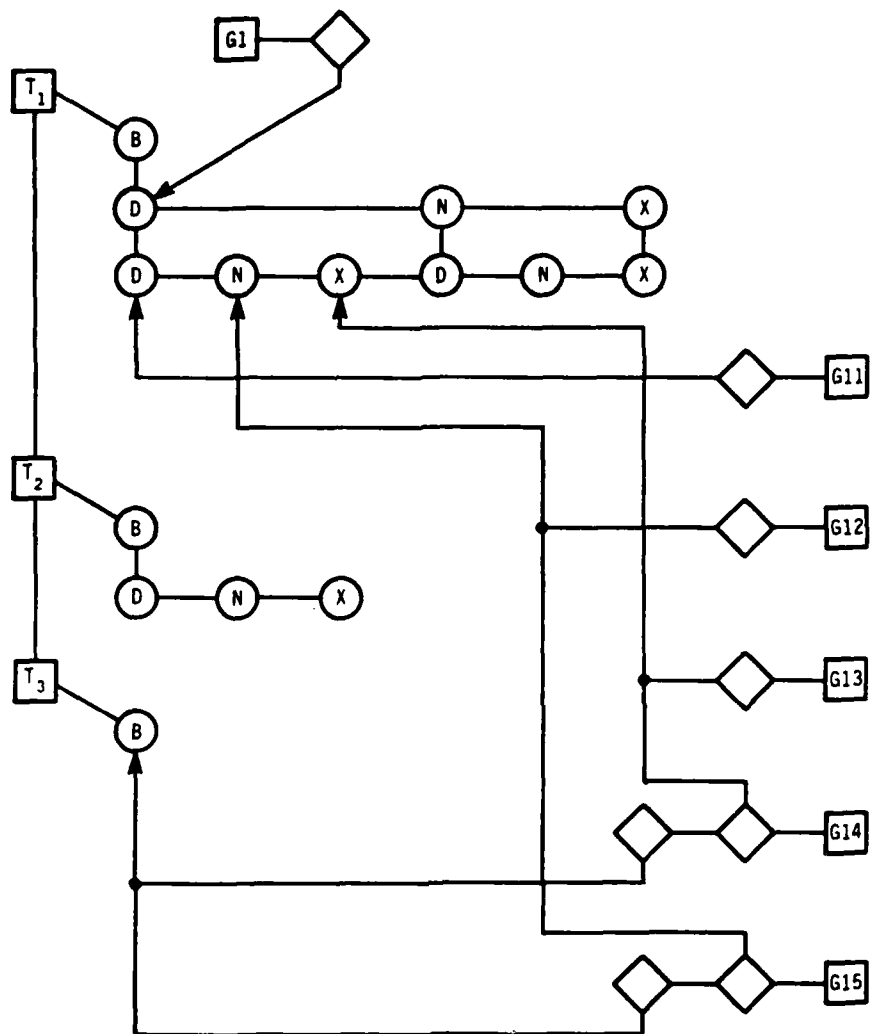
- G1.BD: one target, born in scan 1, observed in scan 2;
- G2.BN: one target, born in scan 1, not observed in scan 2;
- G3.BX: one target, born in scan 1, no longer existing at scan 2;
- G4.B: one target, seen first in scan 2;
- G5.BNB: two targets; one born in scan 1 and missed in scan 2; one born in scan 2; and
- G6.BXB: two targets; one born in scan 1, now dead; one born in scan 2.

These hypotheses implicitly postulate different numbers of false alarms:

- G1. 0 false alarms;
- G2. 1 false alarm, in scan 2;
- G3. 1 false alarm, in scan 2;
- G4. 1 false alarm, in scan 1;
- G5. 0 false alarms; and
- G6. 0 false alarms.

Figure 5-3 illustrates how one of these hypotheses, G1 in Fig. 5-2, is expanded into a family of global hypotheses in the next scan. Note that no descendant of G1 makes reference to track tree 2; none of its descendants postulates any trajectory which begins in scan 2. During expansion of G5 or G6, however, this would not be the case.

- G11.BDD: one target, observed in three scans;
- G12.BDN: one target, observed in scans 1 and 2;



NOTE: G1 IS THE PARENT GLOBAL HYPOTHESIS.
G11 THROUGH G15 ARE ITS DESCENDANTS IN THE NEXT SCAN.
THE SYMBOLS ARE DEFINED IN THE LEGEND OF FIG. 5-2.

R-0895

Figure 5-3. Expansion of a Global Hypothesis.

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G13.BDX: one target, observed for two scans, but now dead;

G14.BDXB: one target appearing anew in scan 3; a second target observed in scans 1 and 2, now dead; and

G15.BDNB: two targets, one observed in scans 1 and 2, a second appearing first in scan 3.

The generation of global hypotheses is the responsibility of procedure PARTITION which calls the recursive procedure SAMPLE. SAMPLE behaves as if it is constructed from nested loops, one loop for each track tree to which a parent hypothesis refers. The loops pass through all track nodes which are descendants of the track node in each tree, which belongs to the set of track nodes referenced by the parent hypothesis. The inner-most loop accesses the highest numbered track tree and varies most rapidly. In creating a descendant hypothesis, one track node is selected from each tree. The process is repeated until all relevant track nodes in all legal combinations are incorporated into descendant hypotheses. This technique constitutes a depth-first search of the association list.

5.4 IMPLEMENTATION OF CONSTRAINTS

The "optimal" tracker considers interpretations of radar returns exhaustively in the fashion outlined in subsections 5.2 and 5.3. Unless heuristic constraints are selected by the user, every internally consistent data interpretation is generated, and assigned a numerical likelihood value. For all but the most trivial cases, the operation of the tracker in optimal mode has proven to be a near impossibility owing to the demands on memory and CPU time. When heuristics are applied, the tracker runs in real time in many cases. Table 5-1 documents the rapid growth in the number of hypotheses with time,

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and the effectiveness of applying only a portion of the constraints available to the tracker, in limiting the growth of global hypotheses.

TABLE 5-1. GROWTH OF THE GLOBAL HYPOTHESIS LIST

CASE: ONE SIMULATED TRAJECTORY; ONE FALSE ALARM PER SCAN

Scan Number	Global Hypotheses	
	Without Constraints	With Constraints*
1	4 (2)	4 (2)
2	62 (10)	6 (3)
3	1,620 (34)	16 (6)
4	-	40 (12)
5	-	48 (22)

*The constraints include gating, elimination of track initializations not followed by a detection, and elimination of postulated trajectories which contain more than two successive missed detections. The number of track hypotheses is shown in parentheses.

Even the optimal tracker, which operates without heuristic constraints, must apply logical constraints on the hypotheses building in order to avoid logically inconsistent hypotheses. There are three logical constraints which are applied to hypotheses building, they are as follows.

1. No hypothesis may postulate a greater number of targets than the total number of returns in that scan. Returns are counted and a running total of the observed postulated by a global hypothesis under construction is compared against this count.
2. No hypothesis may postulate a greater number of trajectories than the total number of past and present returns. The fact that the number of track trees cannot exceed the total number of returns ensures that this constraint is obeyed.

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3. No returns may be assigned to more than one trajectory postulated by one global hypothesis. To prevent this type of inconsistency, the tracker assigns arbitrary indices to the returns in a scan. Once a return is assigned to a postulated trajectory, the index of the return is added to a set of disallowed indices. The set is examined each time a return is considered when building a global hypothesis.

Logical constraints are not sufficient to prevent the unmanageable growth in the number of hypotheses. Additional constraints - heuristic constraints - must be added to limit the size and complexity of the association list, and the number of global hypotheses. The choice of heuristic constraints is arbitrary, but the following seem reasonable and have proven effective.

1. Gating: Prior to adding to the association list a branch which represents a detected target, a numerical parameter is calculated which reflects the plausibility of the estimated target position relative to its estimated position in the previous scan. This gating parameter, which is a function of the filter innovation and estimated error in this innovation, is compared to a preselected constant. If the gating parameter exceeds the gating constant, the data association is rejected. The magnitude of the gating constant controls the rigor of the gating constraint.

Gating is an especially powerful constraint because it intervenes at a stage prior to global hypothesis building. Elimination of a single track node results in the elimination of numerous global hypotheses. For tracking multiple targets, gating is most effective with trajectories which are widely separated relative to the error in the measurements. In this case, only a minority of potential data associations pass the gate.

2. Born Screening: Recall that the tracker initiates a new track tree for each return in each scan. Under this constraint, the tracker will reject the root node of this track tree on the following scan unless there is a return which forms a gate-passing data association for the postulated target. The tracker requires confirmatory evidence in order to maintain a track initialization. This constraint has a strong effect on the complexity of the association list by eliminating tracks at an early stage in their existence.

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3. **Limitation on Missed Detections:** Under this constraint, any postulated trajectory can be given no more than a preselected number of missed detections as continuations. This constraint, which has the effect of removing spuriously postulated trajectories, is most effective when the false alarm rate is high. Under this condition there is an elevated likelihood that incorrect data associations will lead to faulty track initializations followed by gate-passing continuations which are also incorrect. Eventually these tracks will be eliminated when there are no data associations to support them.
4. **Pruning:** This constraint is a direct limitation on the number of global hypotheses. Only a preselected number of hypotheses are retained at the end of each scan: those hypotheses which are highest in likelihood. Pruning has a retroactive effect on the complexity of the association list; any terminal track node which is referred to by no surviving global hypothesis is ignored when the association list is expanded in the next scan. To implement retroactive pruning, the tracker keeps a count in each track node of the number of global hypotheses which reference it. When a global hypothesis is discarded during pruning, the count in each of its referenced track nodes is decremented by one. Only track nodes with counts exceeding zero are expanded further.

5.5 SUMMARY AND CONCLUSIONS

The multitarget tracker must form data associations and multiple interpretations of data associations, employing what might be termed a deep analysis. This means that the interpretation of events in a given scan is heavily determined by interpretations developed in previous scans. One of the principal tasks of the program, therefore, is to maintain a data structure which is capable of representing the relationships among observations which are distributed over scan time. The association list provides the necessary structuring of raw data and results of computations.

In developing interpretations of the information stored in the association list, that is to say, the building of global hypotheses, the program carries out what is essentially a depth-first search. The efficiency of this

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search is wholly determined by the depth and breadth of the association list. The complexity of this data structure is determined, in turn, by the effectiveness of heuristic and logical constraints in limiting its rate of growth. Whereas brute force pruning of the global hypothesis list would seem to be a most powerful constraint, in reality it is less effective than heuristics which focus on the association list itself. Pruning determines which global hypotheses are saved. Gating and associated constraints, which intervene before hypothesis building, determine which hypotheses will be formed.

The constraints available to the current version of the tracker are sufficiently powerful to allow real-time performance except in especially challenging cases: densely packed, crossing trajectories. For more complex models of the radar environment and target behavior, however, additional heuristic constraints will be necessary. These will most likely involve more aggressive restriction on the expansion of the association list, and additional postprocessing of the global hypothesis list. In addition to pruning, the merging of nearly identical global hypotheses should be valuable. In practice, the tracker has tended to produce and retain families of hypotheses which postulate nearly identical target coordinates. Reducing these families to single hypotheses should not impair performance and will lead to a greatly simplified association list.

SECTION 6

PERFORMANCE EVALUATION

In this section we examine the performance of the surveillance and tracking algorithm. In order to demonstrate the algorithm's major attributes, we select four representative scenarios, based on an ascending order of difficulty. Each of these scenarios is simulated, and in result, the surveillance and tracking performance of the algorithm is established. Common to all four scenarios is the surveillance volume Ξ , defined as a 20x20 kilometer plane at a distance of 200 kilometers away from the surveillance radar. For convenience we define the center of the surveillance range as the origin of a two-dimensional inertial coordinate system. Thus Ξ may be defined as

$$\Xi = \{x,y | -10,000 \leq x \leq 10,000, -10,000 \leq y \leq 10,000\} \quad , \quad (6-1)$$

where the positive y-axis direction points to the "north."

We further assume that the surveillance range is scanned every 10 seconds. For each scenario we simulate the total of nine scans. The simulation program generates at each scan

1. noisy position (x,y) returns originating from existing target(s);
2. false alarms; i.e., an arbitrary number of background noise returns, each of which is independent and uniformly distributed over the surveillance range; and
3. misses; i.e., the hypothesized target(s) does not produce a return. The accumulated number of misses for the entire trajectory of a particular target is arbitrary.

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6.1 SCENARIOS

In the following we list the details of the four scenarios examined. In all cases it is assumed that the target(s) velocity is 200 m/s.

1. Two crossing targets, no false alarms, no misses: the location of the targets at the first scan is $(-6500, 6500)$ and $(-6500, -6500)$ and their headings are 135° and 45° , respectively. The heading angle is measured from the "north" direction.
2. Two crossing targets, two false alarms/scan in first eight scans, no misses: the initial coordinates of the targets are the same as in Scenario 1.
3. Three targets, one false alarm/scan, some misses: two of the targets run in parallel, and are separated by 3000 meters. The third target crosses the two parallel trajectories. Target #1 (number assigned arbitrarily) is missed at the fifth scan, target #2 at the third, and target #3 at the seventh. The initial coordinates and headings (i.e., at the first scan) are:

target #1: $(-7900, 3500)$, 105° ;

target #2: $(-7900, 500)$, 105° ; and

target #3: $(-7900, -3500)$, 60° .

4. Three targets, no false alarms, no misses: Similar to Case 3, this scenario is characterized by two targets moving in parallel and a third one crossing. The difficulty in the present scenario is the proximity of the two parallel-moving targets: we assume a separation of 1000 meters. The initial coordinates and headings of the targets (numbered arbitrarily) are:

target #1: $(-7900, 500)$, 105° ;

target #2: $(-7900, -500)$, 105° ; and

target #3: $(-7900, -3500)$, 60° .

Finally, we assume that the target-originating returns are normally distributed, i.e., the (x,y) target position is actually measured (simulated) as $(x+v_x, y+v_y)$, where

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$$v_x \sim N(0, \sigma_x^2) \quad ; \quad v_y \sim N(0, \sigma_y^2) \quad , \quad (6-2)$$

and we further assume

$$\sigma_x = 5 \text{ m} \quad , \quad \sigma_y = 500 \text{ m} \quad . \quad (6-3)$$

This disparity in the measurement accuracy between the two axes emulates a realistic situation in which the accurate measurement is the range and the inaccurate is the line-of-sight angle.

6.2 ALGORITHM PARAMETERS

Next we list the algorithm/Kalman filter parameters that were used in the simulation. These were kept unchanged in all four scenarios, and are as follows:

ρ_{FA} = false alarm density = $10^{-10}/\text{meter}^2$;

λ_B = expected number of born targets per scan = 10^{-3} ;

P_D = probability of detection = 0.998; and

P_X = probability of target mortality = 10^{-4} .

The Kalman filter parameters are chosen as follows:

Process noise
covariance $= W = \text{diag}[0, 0, (10 \text{ m/sec})^2, (10 \text{ m/sec})^2]$;

Measurement noise
covariance $= V = \text{diag}[(5 \text{ m})^2, (500 \text{ m})^2]$; and

Initial state
estimate covariance $= \Sigma_0 = \text{diag}[(5 \text{ m})^2, (500 \text{ m})^2, (200 \text{ m/s})^2, (200 \text{ m/s})^2]$.

The initial state estimate position variables are taken as the (x,y) returns from scan #1; the initial velocity estimates are assumed to equal zero.

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As indicated in Section 5 only a suboptimal implementation of the surveillance/tracking algorithm is feasible. We therefore employ four heuristic modifications to the full-blown optimal case.

1. Gating: The gating parameter used is 10, implying that no more than approximately three standard deviations of the innovation process are allowed when associating new measurements with existing track hypotheses.
2. Track Initialization: The algorithm will not associate a miss or a track termination following a target-birth hypothesis.
3. Misses: If, on a scan following two successive misses pertaining to a particular track hypothesis, no return passes the associated "gate," that track is discounted.
4. Pruning: No more than 10 top ranking (i.e., with highest likelihood) global hypotheses are retained after the processing of each scan.

6.3 PERFORMANCE EVALUATION

In the performance analysis we present figures which illustrate the algorithm's surveillance and tracking for each scenario. In these figures, the following symbology is used.

Returns:	□; in the cases which involve false alarms, the returns are numbered by the order of appearance (scan number); the only exception is Fig. 6-18 in which all returns are enumerated, as explained in the sequel;
Hypothesized Trajectory Position Estimates:	▲, ◄, or ◆ (each symbol pertains to a particular track hypothesis);
Estimated Trajectories:	, -----, or ----.; and
Target Trajectories:	Solid Lines. Targets are ordered by encircled numbers (assigned arbitrarily) next to their trajectories.

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6.3.1 Scenario 1

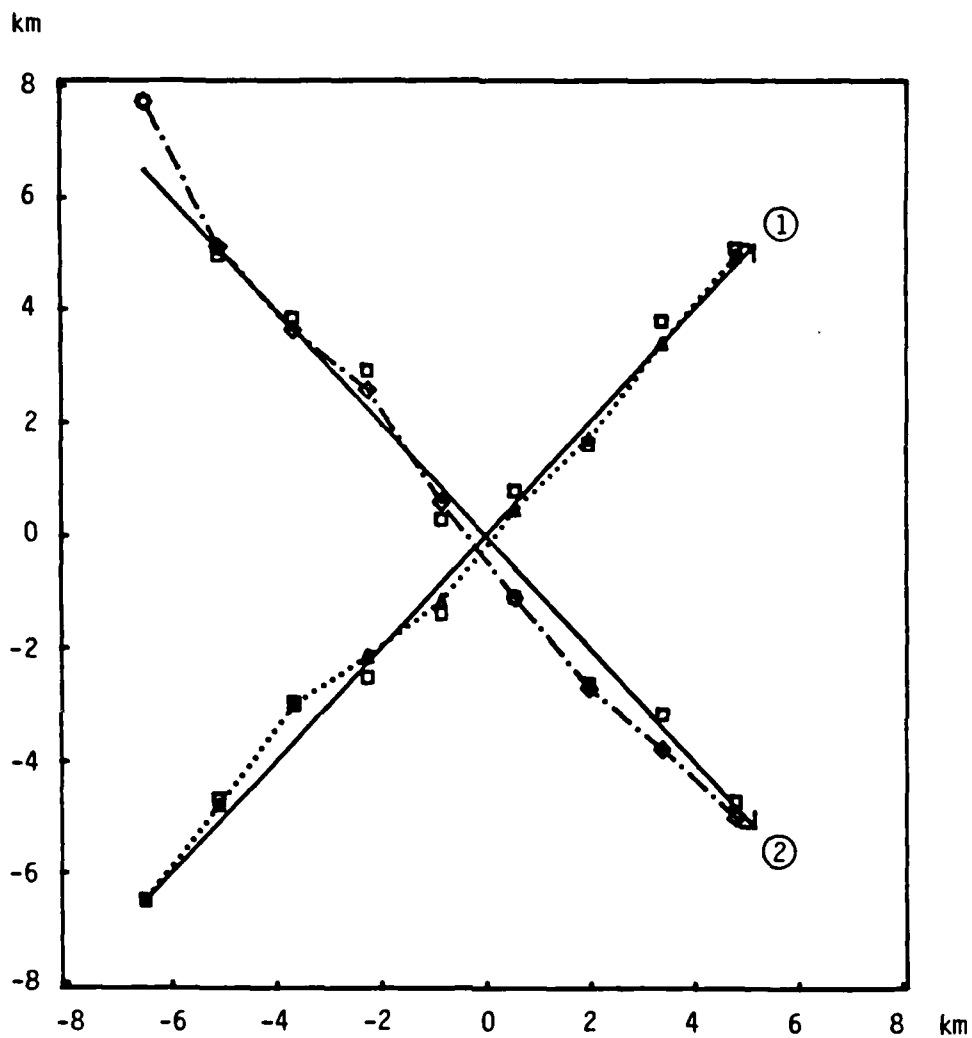
Figures 6-1 through 6-5 illustrate the surveillance/tracking performance for the simplest case considered. Shown are the five top-ranking hypotheses, i.e., those with the highest likelihoods of being correct, after the ninth scan. Figure 6-1 illustrates the Rank 1 hypothesis, Fig. 6-2 illustrates Rank 2, etc. In the case at hand, the correct hypothesis is ranked number 1 which is the desired result; i.e., all returns are associated by the algorithm, with the correct target positions as shown in Fig. 6-1.

Figure 6-2 illustrates the Rank 2 hypothesis, and it is evident that at the vicinity of the targets' crossing (sixth scan) an erroneous return/target association is hypothesized. In other words, after the ninth scan the Rank 2 hypothesis associates the sixth scan return from target #1 with target #2, and vice versa.

Figure 6-3 (hypothesis Rank 3) illustrates a different type of error: the Scan 1 return which originates from target #2 is interpreted as a false alarm; consequently, this target is assumed to be born only on the second scan. Naturally, this misinterpretation results in a different track estimate (compare with Fig. 6-1).

Figure 6-4 illustrates the Rank 4 hypothesis. This hypothesis is similar to the Rank 2 hypothesis but the erroneous target/return association occurs at the fifth rather than at the sixth scan.

Finally, the hypothesis ranked as fifth (Fig. 6-5), assumes that the ninth scan return from target #2 is a false alarm. Therefore, the hypothesis is that, on the ninth scan, target #2 is not detected.



R-0896

Figure 6-1. Scenario 1, Scan 9, Rank 1 Hypothesis (Truth Hypothesis).

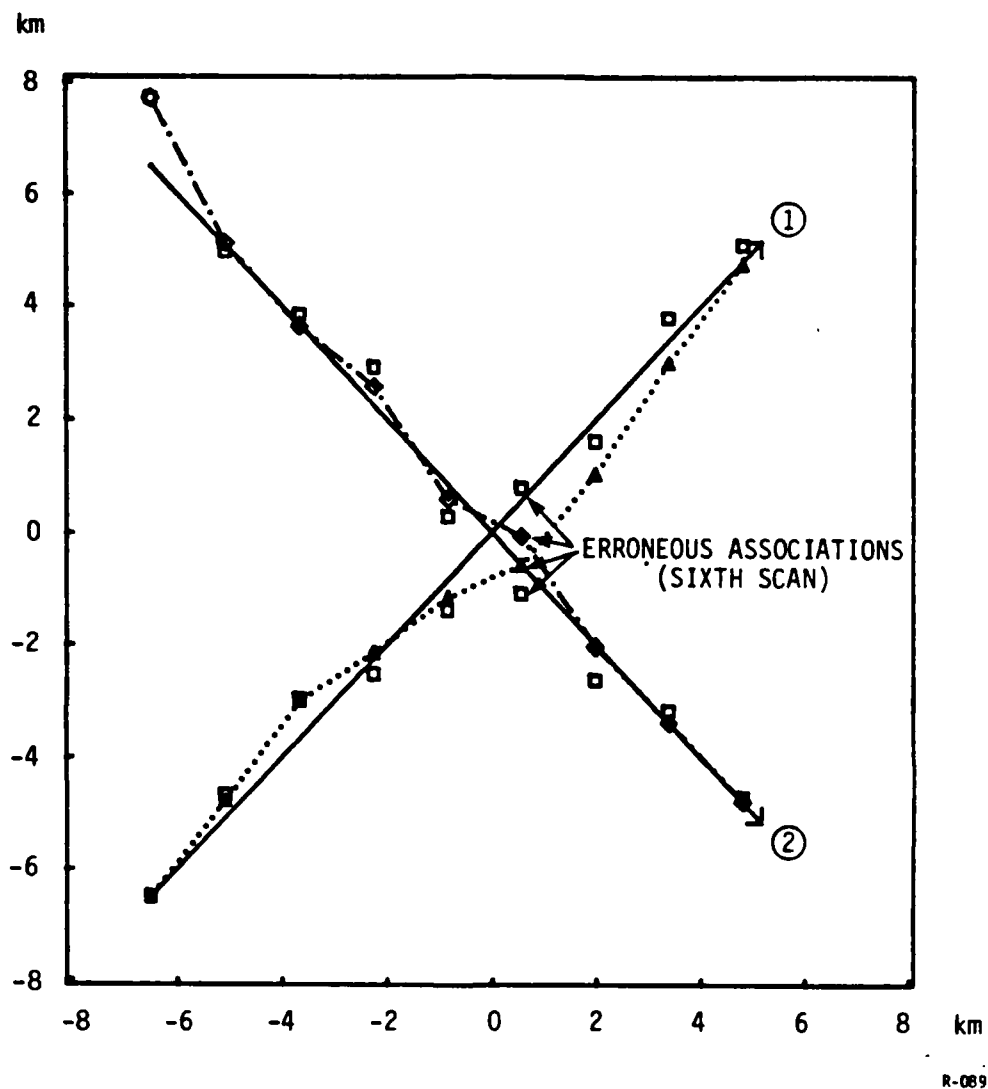


Figure 6-2. Scenario 1, Scan 9, Rank 2 Hypothesis.

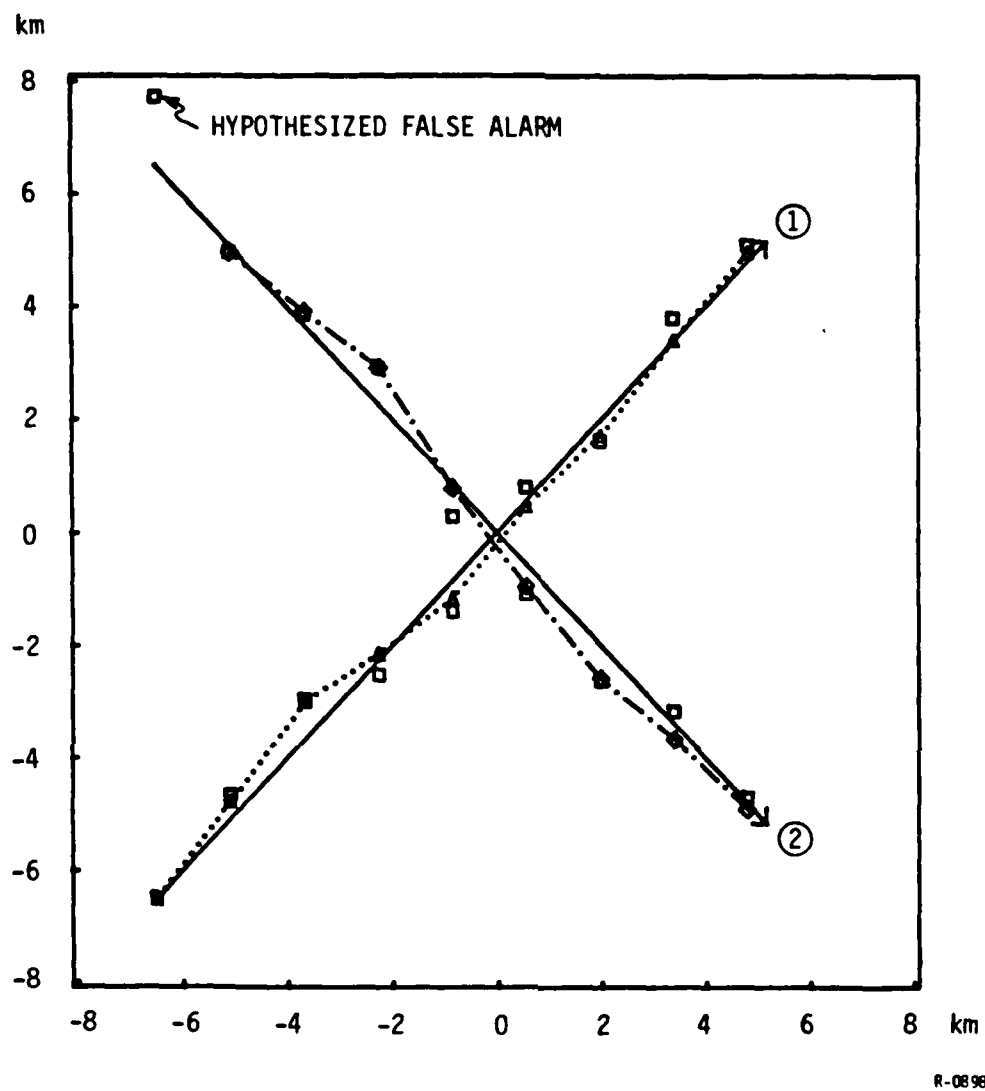
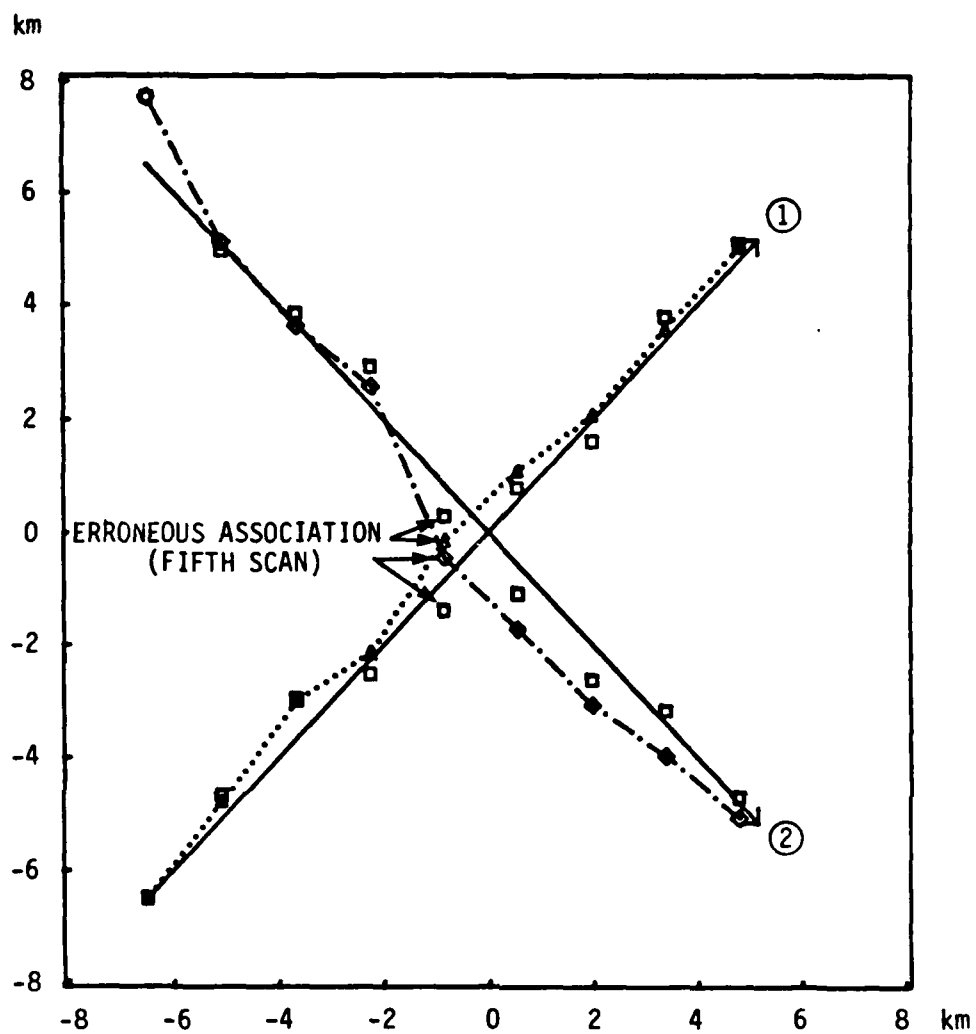


Figure 6-3. Scenario 1, Scan 9, Rank 3 Hypothesis.



R-0899

Figure 6-4. Scenario 1, Scan 9, Rank 4 Hypothesis.

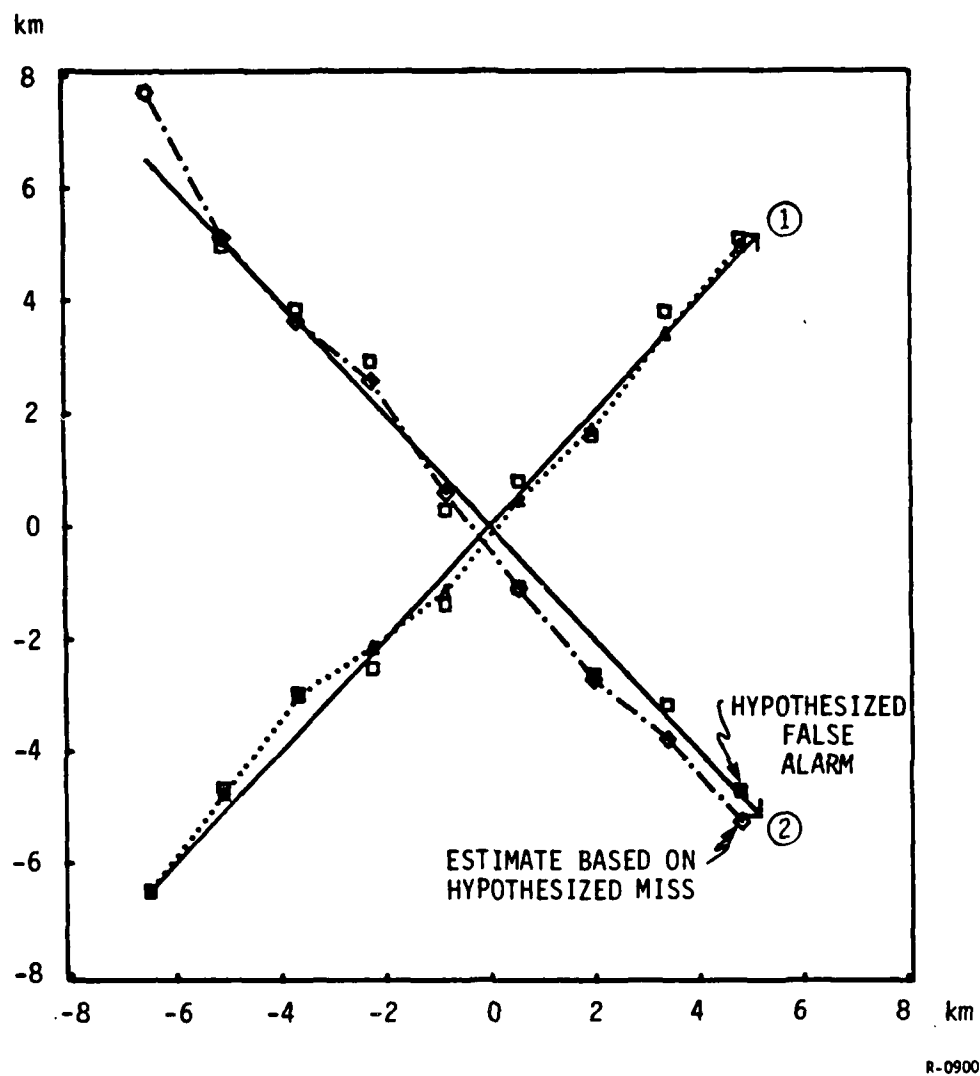


Figure 6-5. Scenario 1, Scan 9, Rank 5 Hypothesis.

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In summary, we have examined a simple but an interesting scenario. The truth hypothesis was correctly ranked first, and the subsequent rank/hypotheses illustrate a variety of plausible track estimates, which, strictly speaking, are erroneous. However, note that the erroneous hypothesized tracks are relatively similar to the correct ones.

6.3.2 Scenario 2

Scenario 2 is similar to Scenario 1 in the sense that the simulated targets and their associated returns are identical. Presently, however, we complicate the hypotheses tree by augmenting the correct returns with simulated false alarms - two per scan, in the first eight scans. We will see that adding these false alarms does not degrade the algorithm's performance, but it produces a different type of erroneous hypotheses: it generates hypothetical new tracks, which, obviously, are false.

Figure 6-6 illustrates the Rank 1 hypothesis which is similar to the Rank 1 hypothesis of Scenario 1 (the truth hypothesis). The false alarms in the first eight scans (indicated by the scan number) have no effect in this case. Similarly, the second ranking hypotheses of the two scenarios are exactly the same. (Rank 2 hypothesis of the present scenario is not shown.) More interesting cases/hypotheses, however, are shown in Figs. 6-7 and 6-8.

Figure 6-7 illustrates the Rank 3 hypothesis. It is shown that targets #1 and #2 are tracked correctly, similar to the Rank 1 hypothesis. However, a false alarm at the sixth scan is taken by the algorithm as a birth of a new target. Subsequently, this "target" is "detected" at the seventh scan by hypothesizing an association with another false return. Note that these two subsequent false returns are sufficiently close so that an hypothesis

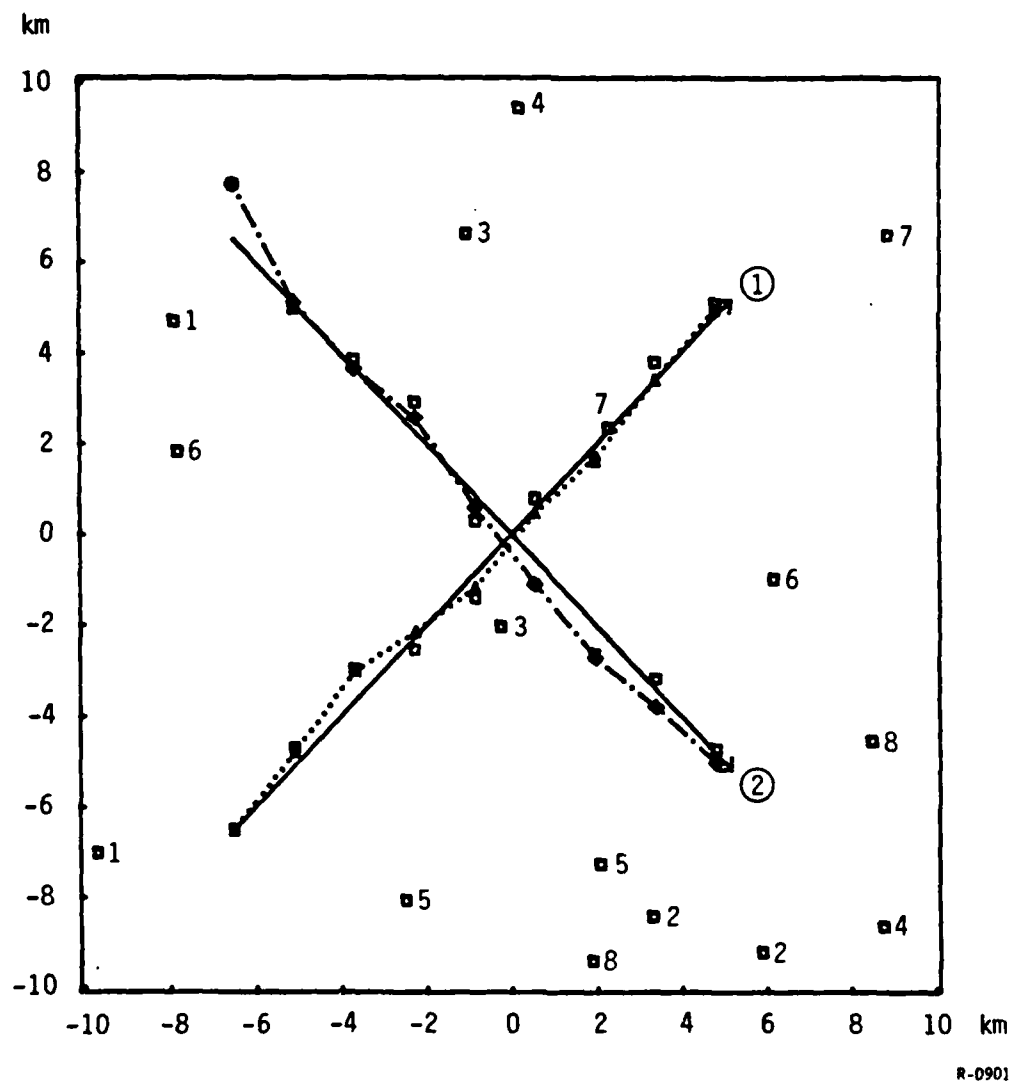
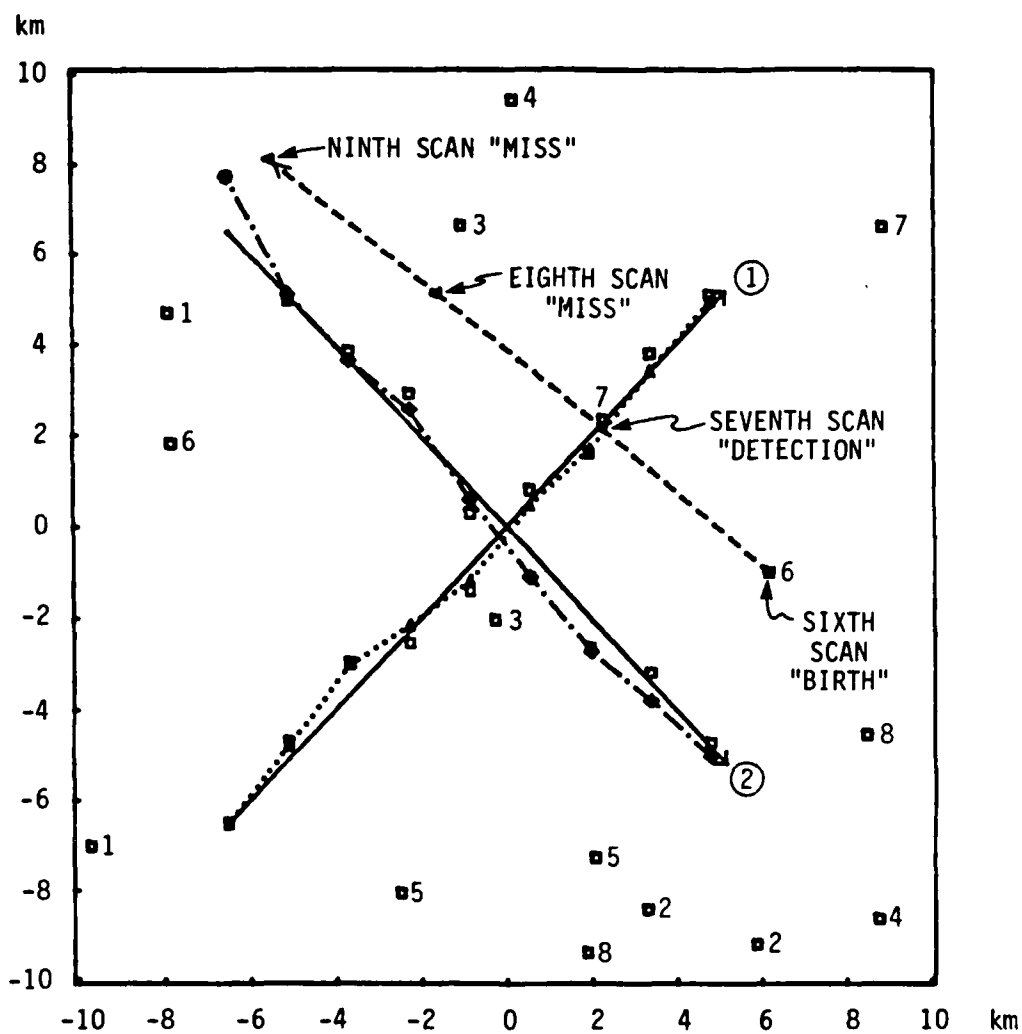


Figure 6-6. Scenario 2, Scan 9, Rank 1 Hypothesis (Truth Hypothesis).



R-0902

Figure 6-7. Scenario 2, Scan 9, Rank 3 Hypothesis.

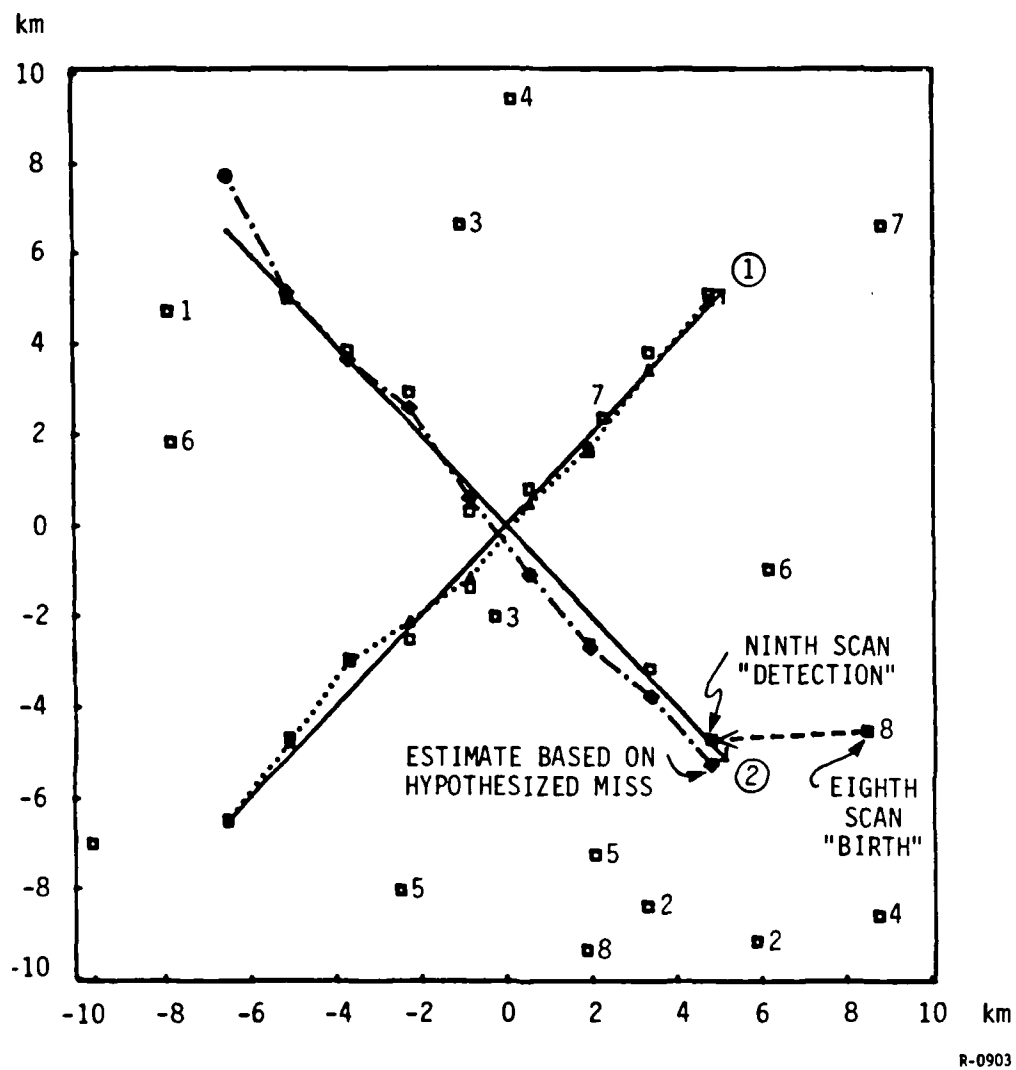


Figure 6-8. Scenario 2, Scan 9, Rank 4 Hypothesis.

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associating the two cannot be "gated-out." On the eight and ninth scans, however, this track makes no association which would pass the gate with any return. It is, therefore, postulated that the "target" was missed on these scans. Note that unless a new false return occurs on the path of this hypothetical track in the tenth scan, that track - on the basis of our suboptimality assumption - will be dropped entirely.

Figure 6-8 illustrates a similar situation in the Rank 4 hypothesis. A fictitious target is hypothesized to have been born by a false return on the eighth scan. This "target" is then "detected" in the ninth scan by associating with a return which actually originates from target #2. Therefore, the track associated with target #2 must assume that, in the ninth scan, a missed detection has taken place (see Fig. 6-5). Note that all of the falsely hypothesized trajectories are "young" and relatively short in duration.

6.3.3 Scenario 3

In this scenario we assume an engagement of three targets, two of which move in parallel and one of which is crossing. We also inject one false return per scan for the first eight scans, and simulate misses on the fifth, third, and seventh scans for the first, second, and third target, respectively. The scenario is not particularly difficult as the target returns are relatively sparse. We use it, however, to illustrate several interesting points:

1. we illustrate the difficulty in attempting to perform the surveillance and tracking task manually;
2. we show that if a finite number of scans is considered, the truth hypothesis does not necessarily rank first;

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3. the Rank 1 hypothesis, albeit erroneous, is not far from the truth: after a "reasonable" number of scans (greater than four), the tracking performance is adequate; and
4. we illustrate the mechanics of propagating the track-hypotheses throughout several scans.

We start by inspecting Fig. 6-9 which illustrates all the returns from the initial eight scans. Clearly, given this scenario, manual tracking would be very difficult, if not outright impossible. Indeed, certain patterns can be identified, but a mental hypothesis ranking seems to be unattainable.

Next, we examine Fig. 6-10 which is the Rank 1 hypothesis in the present scenario. Although it ranks first, this hypothesis is not the truth hypothesis, as it fails to interpret the absence of a return from target #2 on the third scan as a miss. As a result, it postulates a birth of target #2 only on the fourth scan. However, the tracking performance from the fifth scan on is correct. In particular, the two latter misses occurring in the two other trajectories are identified correctly.

Finally, we illustrate the propagation of the Rank 1 hypothesis through scan numbers 2, 3, 4, and 5 (Figs. 6-11, 6-12, 6-13, and 6-14, respectively). Only target #3 is tracked correctly throughout all four scans. Target #1 is detected only on the third scan, and target #2 only on the fifth (it is assumed to have been born on the fourth). It is also evident that on the second and the fourth scans, hypothetical tracks, effected by false returns, are postulated. These, however, disappear from the Rank 1 hypothesis thereafter.

6.3.4 Scenario 4

The final example illustrates perhaps the most interesting case, in which two very close targets move in parallel, and their trajectories are

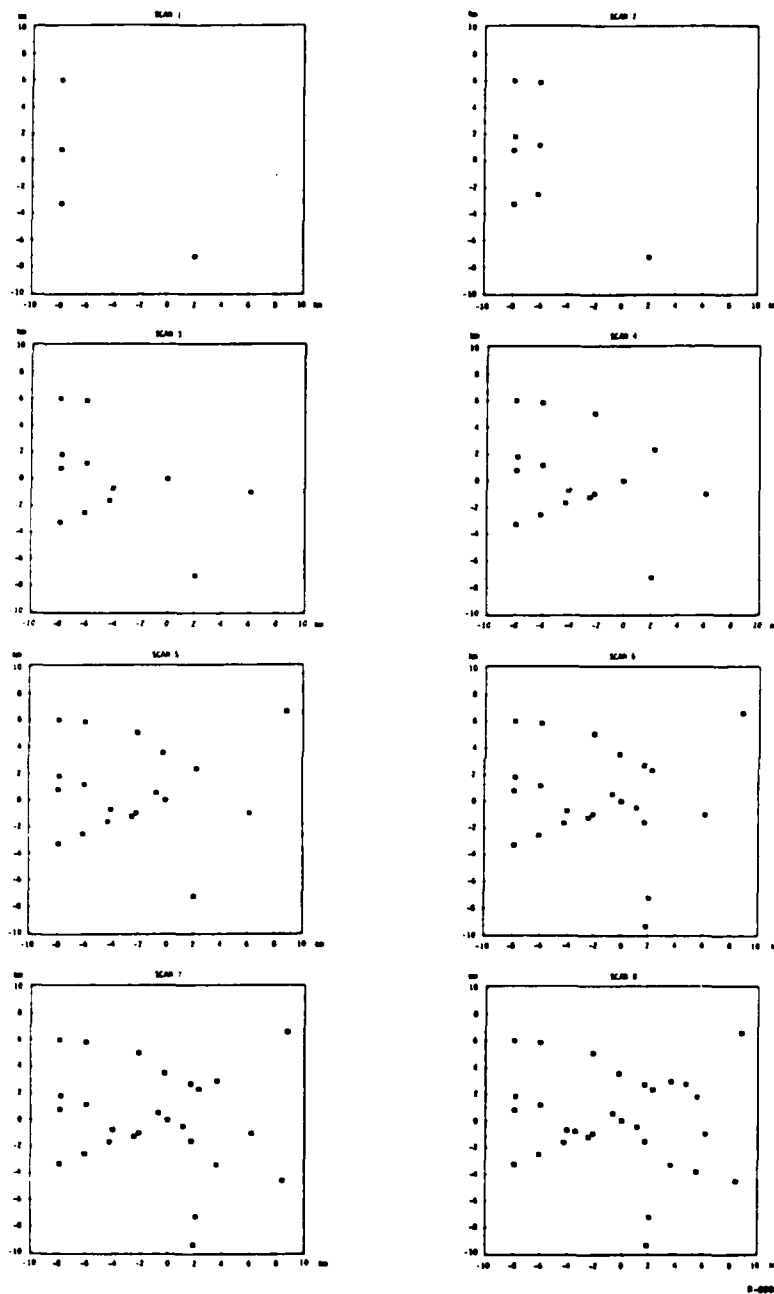


Figure 6-9. Eight Scan Returns of Scenario 3.

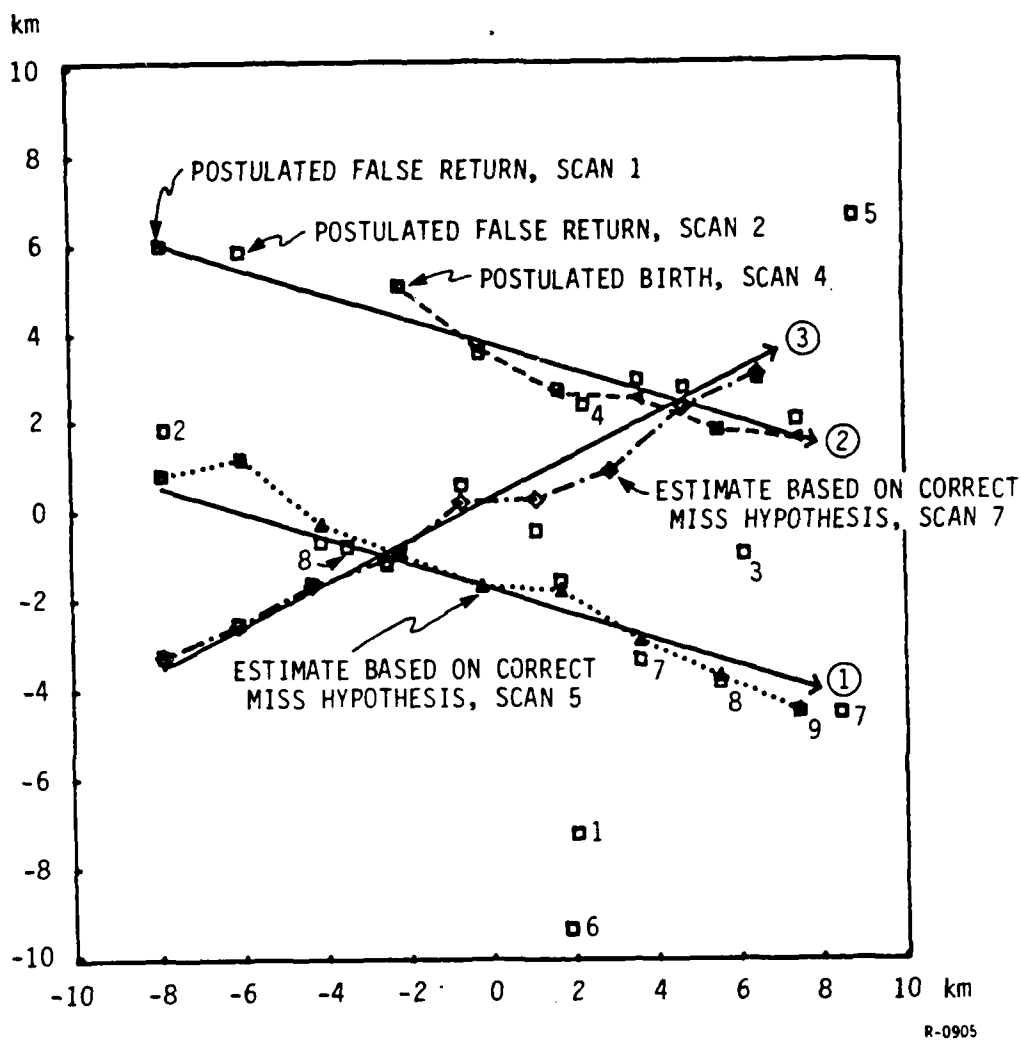


Figure 6-10. Scenario 3, Scan 9, Rank 1 Hypothesis.

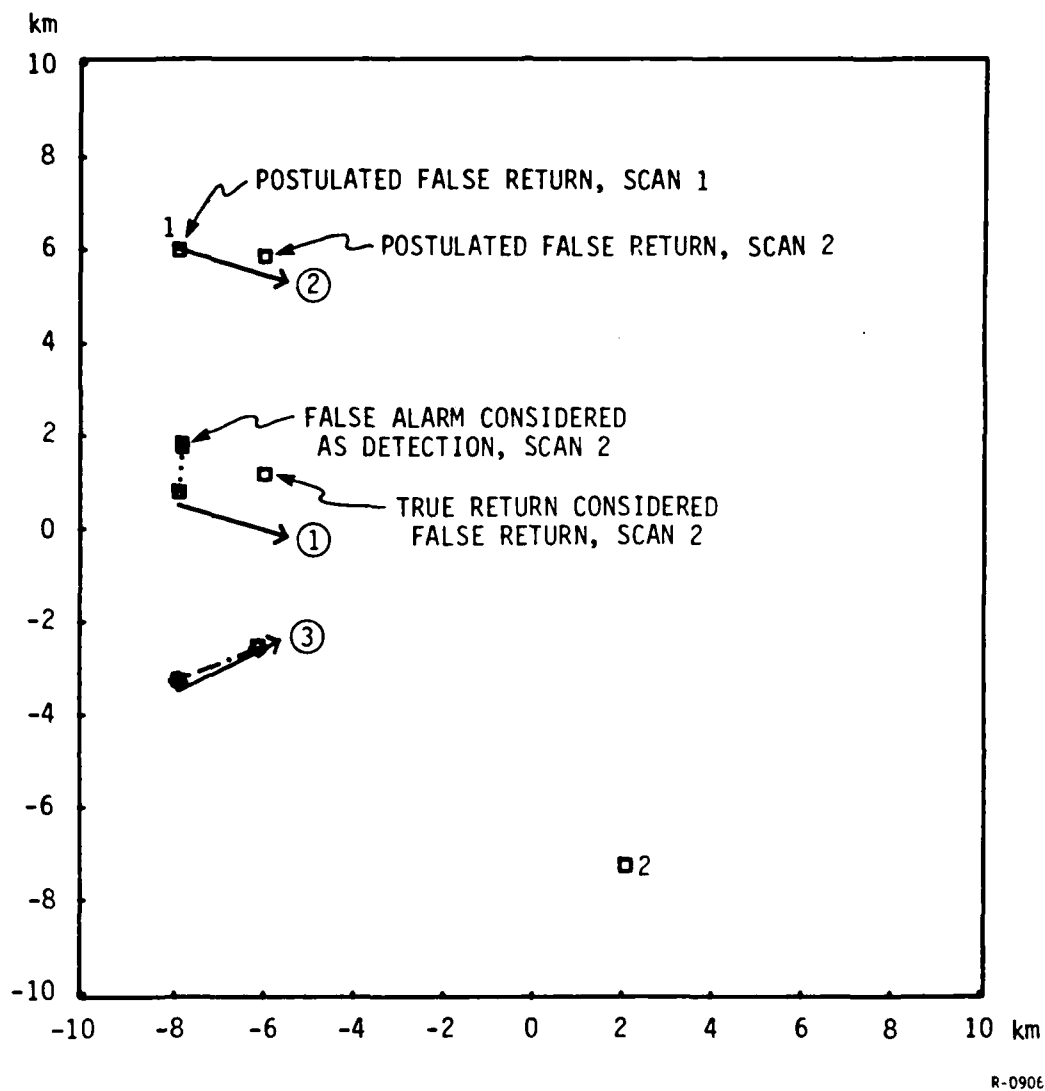
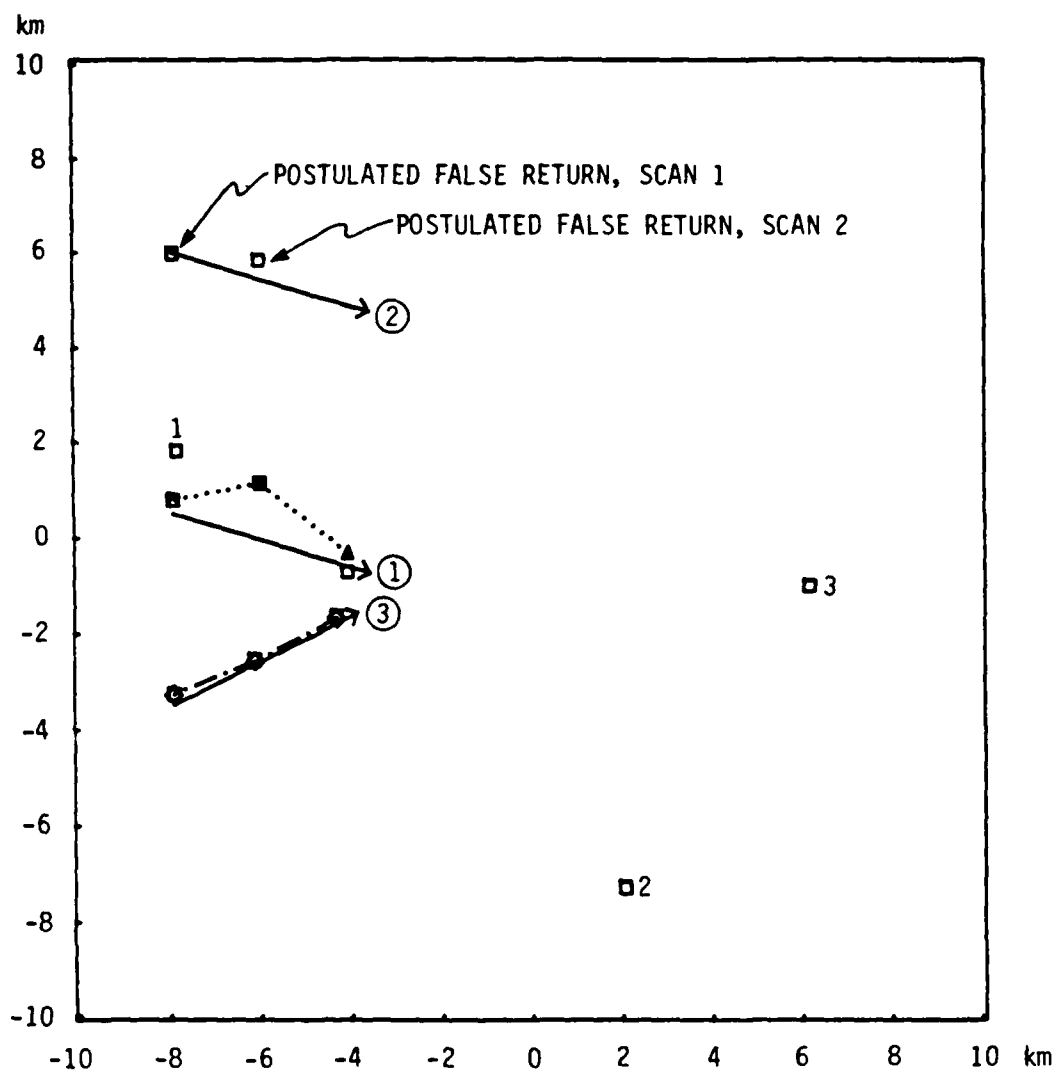


Figure 6-11. Scenario 3, Scan 2, Rank 1 Hypothesis.



R-0907

Figure 6-12. Scenario 3, Scan 3, Rank 1 Hypothesis.

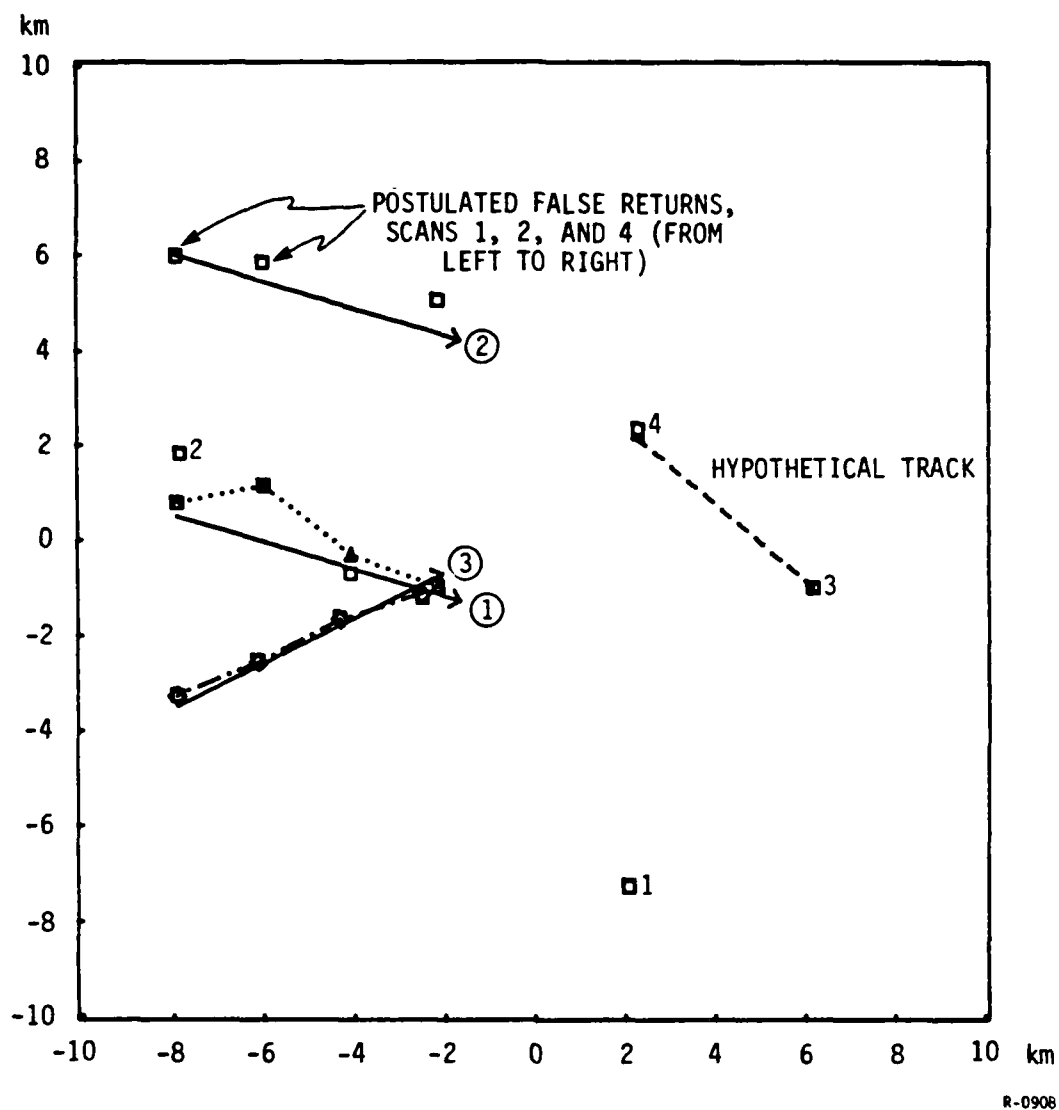
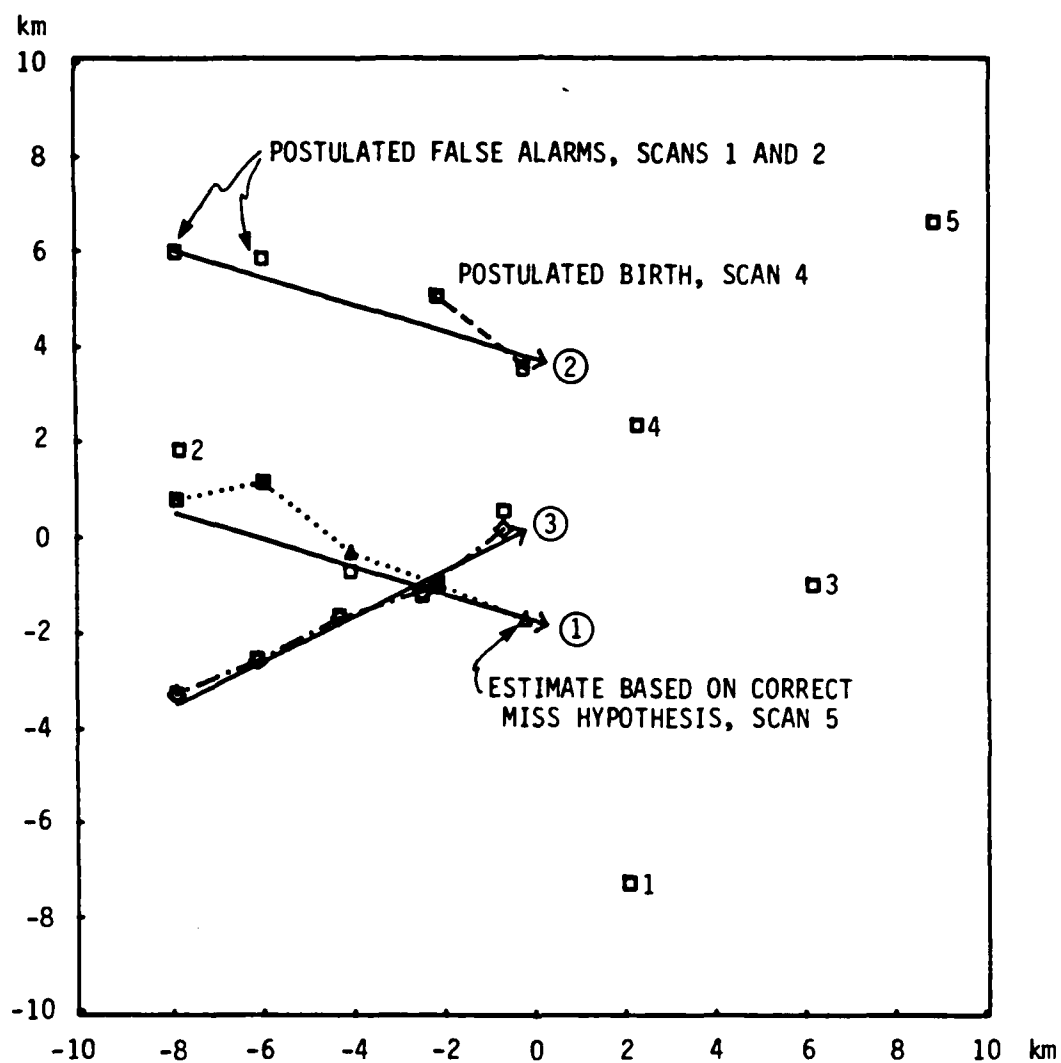


Figure 6-13. Scenario 3, Scan 4, Rank 1 Hypothesis.



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Figure 6-14. Scenario 3, Scan 5, Rank 1 Hypothesis.

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intersected by a third one. Three hypotheses are presented in Figs. 6-15 through 6-17. Figure 6-16 shows the truth hypothesis which, in the case at hand, ranks third. The Rank 1 hypothesis is shown in Fig. 6-15 which is practically identical to the truth hypothesis; only a minor crossing between the returns from target #1 and #2 occurs on the first scan. The most interesting case, however, is shown in Fig. 6-17, in which a total crossover between the two parallel targets occurs on the fourth scan. This hypothesis is ranked fifth. Clearly, with such congested returns a crossover of this type cannot be avoided.

6.4 PERFORMANCE OF THE GATING LOGIC

The final issue to be discussed in this section is the effectiveness of the gating algorithm. For the purpose of illustrating the performance of the gating logic consider Fig. 6-18, in which a simple tracking case, on the third scan, is shown. We assume a single target starting at $(-400, 0)$ and bearing 90° . We assume no missed returns but we simulate a uniformly distributed false return on the second and the third scans. All five returns are enumerated as shown. Next, examine Table 6-1 which lists all the possible data associations on the second and third scans, subject to our suboptimality assumptions. Clearly, only the reasonable hypotheses result with a small gating parameter value which will pass the gate of 10. For instance, the hypothesis which associates return 1-2-3 (on the third scan) results in 1.21. In contrast, the combination of 1-4-5 is given the value of 2730.34 which will be rejected by the gating logic. In this case, the large parameter value is effected by the tracking filter which limits the "allowable" distance between consecutive returns which may imply, in turn, an unreasonably high target velocity or position measurement error.

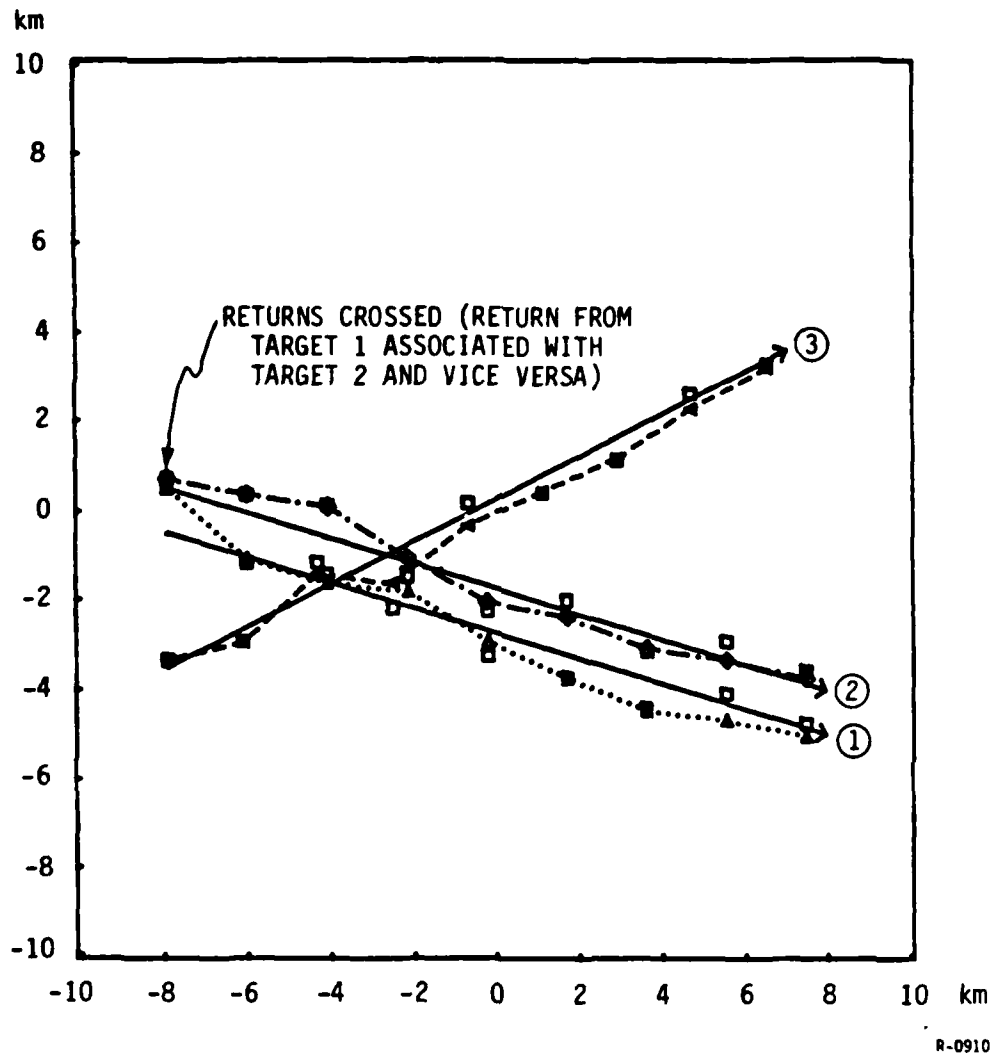


Figure 6-15. Scenario 4, Scan 9, Rank 1 Hypothesis.

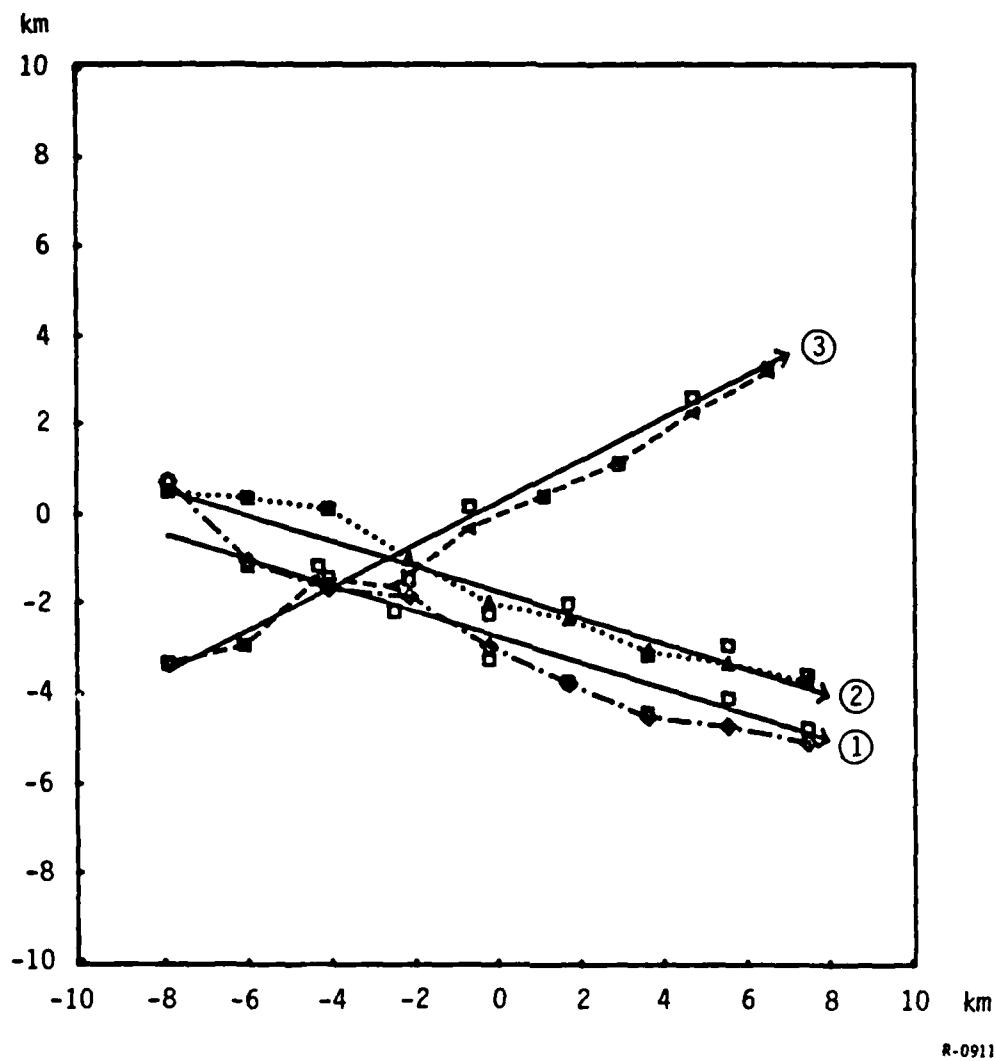
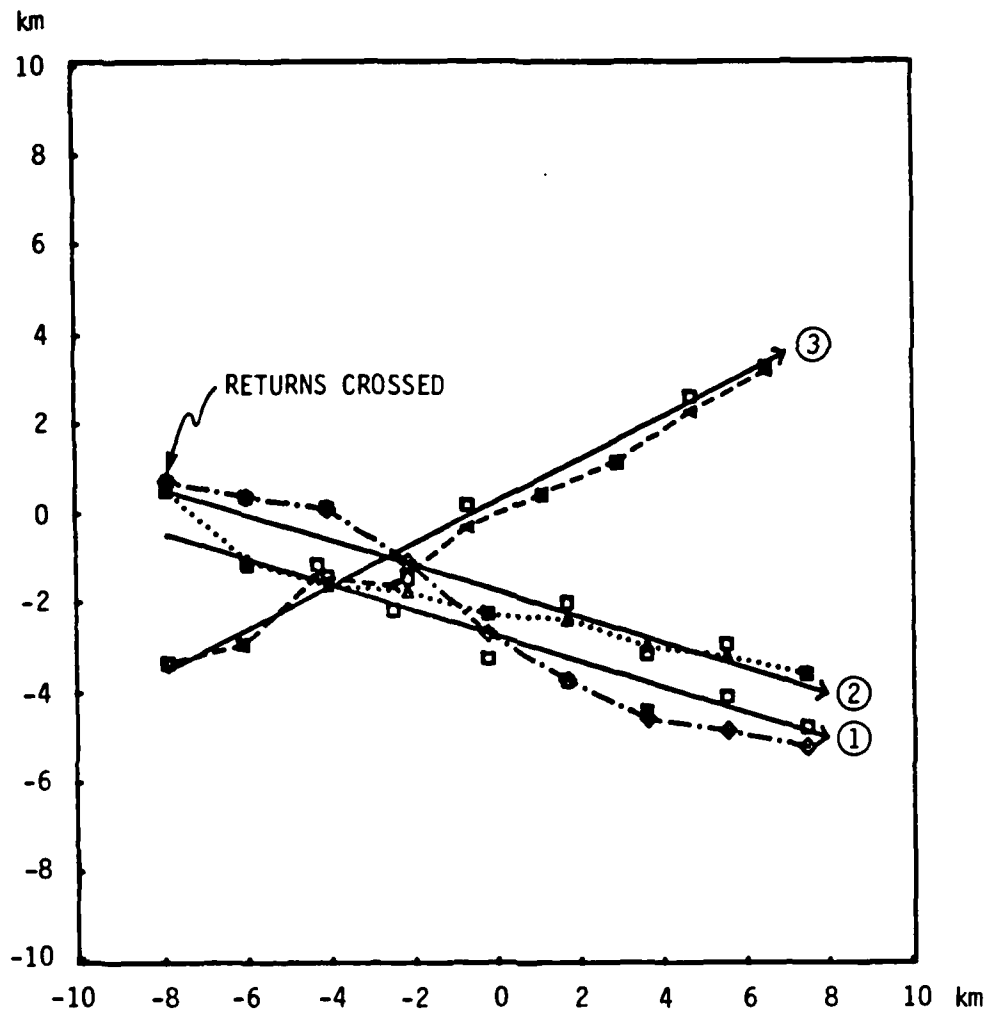


Figure 6-16. Scenario 4, Scan 9, Rank 3 Hypothesis (Truth Hypothesis).



R-0912

Figure 6-17. Scenario 4, Scan 9, Rank 5 Hypothesis (Total Crossover at Scan 4).

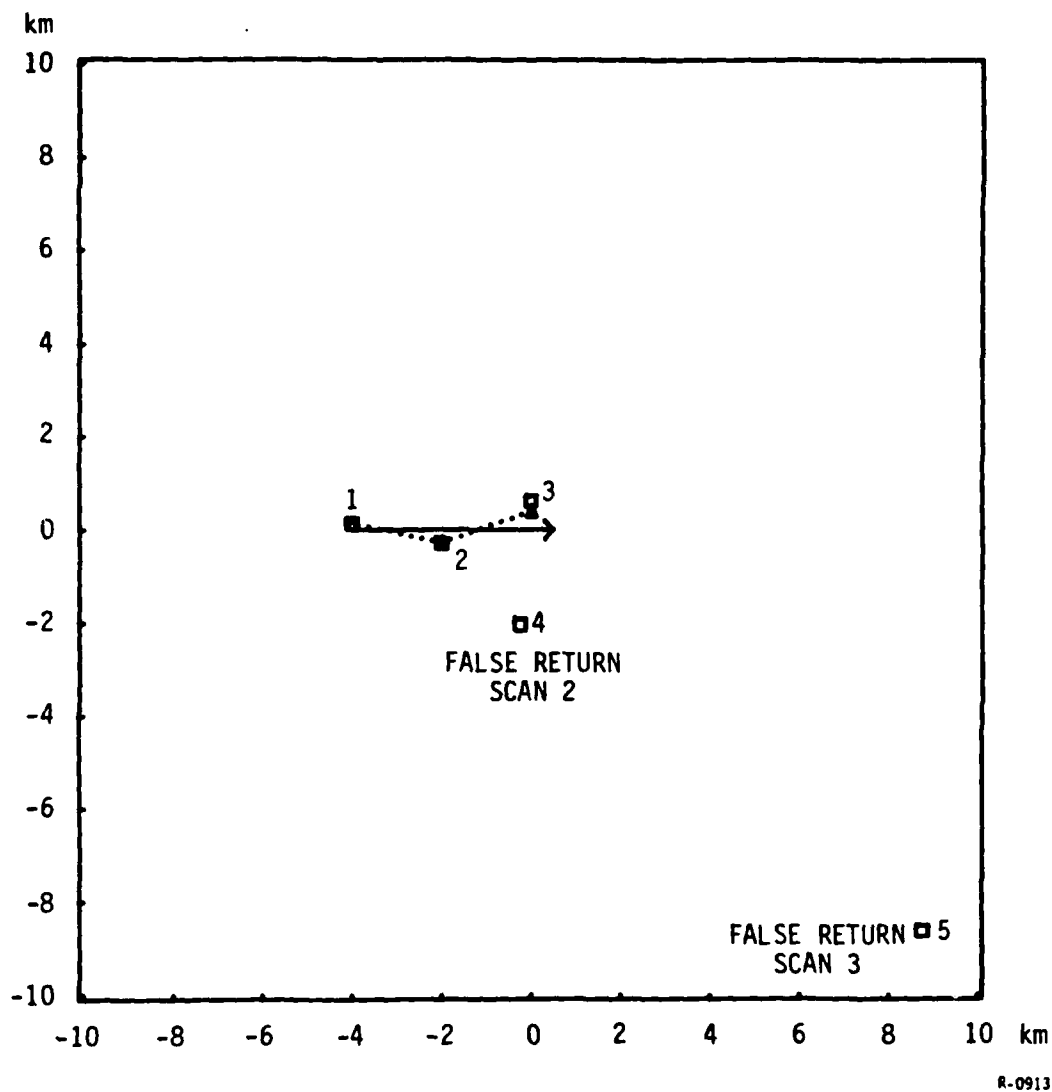


Figure 6-18. Auxiliary Figure to Table 6-1.

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TABLE 6-1. AN EXAMPLE OF GATING EFFECTIVENESS
(SEE FIG. 6-18)

Scan	Return
1	1
2	2, 4 (false return)
3	3, 5 (false return)

Scan 2 Associations

Scan 1	Scan 2	Gating Parameter
1	2	1.05
1	4	4.60

Scan 3 Associations

Scan 1	Scan 2	Scan 3	Gating Parameter
1	2	3	1.21
1	2	5	7614.61
1	4	3	1236.19
1	4	5	2730.34
1	Miss	3	1.01
1	Miss	5	14.85
	2	3	1.19
	2	5	44.40
	4	3	1.59
	4	5	39.93

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SECTION 7

CONCLUSIONS

In this effort, an advanced algorithm for surveillance radars has been developed and demonstrated. The algorithm can track multiple tracks, identifying false alarms, accepting missed detections of targets in track, initiating tracking of new detected targets, and terminating tracking of targets which are no longer detected. It is based on the statistical estimation theoretic concept called multiple model adaptive estimation and, in the absence of limitations on data storage and processing rate, it is optimal. Such limitations forced an implementation which is suboptimal in theory, but which closely approximates the performance of the optimal algorithm due to the resiliency of the multiple model approach to adaptive estimation.

In the course of developing the algorithm, two models were developed of the multitarget radar environment, one suitable for algorithm design and the other suitable for simulating inputs to a tracking algorithm. Both models stand on their own as well as serving in the development and evaluation of the tracking algorithm. The development of the model is firmly grounded in the existing body of theoretical results on multiple model adaptive estimation and serves as a good example of the application of these results in its progression through cases of increasingly complex environments. The reorganization of the optimal tracking algorithm for the most complex case is particularly

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significant since it sets the stage for practically implementing the algorithm without, at that state, compromising its theoretical optimality.

The impossibility of implementing the optimal algorithm with finite limitation on data storage and processing was clearly demonstrated; for quite reasonable scenarios, the storage and processing requirements grow exponentially or faster with the number of scans. But by starting from a complete optimal algorithm and proceeding systematically to develop rules for ignoring, pruning, and merging hypotheses, we have begun to develop a suboptimal tracking algorithm which avoids such problems while maintaining performance which is approximately optimal. The rules resemble the ad hoc rules incorporated for common sense reasons into many practical tracking algorithms in use today and suggest how one might profitably proceed to improve upon the presently used rules; common sense does not.

The tracking algorithm was implemented in a flexible and general manner to allow experimentation with various rules for keeping the algorithm's data storage and processing requirements within reasonable limits or even to use the full implementation of the optimal algorithm for a limited number of scans. A consequence was the development of a pair of data structures of great utility for organizing the data storage and processing of a multitarget tracking algorithm: the association list and the global hypothesis list. While not exploited in the actual implementation due to the inherently serial nature of the computer use (VAX-11/780), there are ample opportunities for parallel computation provided by these data structures and the procedures manipulating them.

The power of the tracking algorithm was well illustrated by the examples of tracking performance provided in Section 6. Target tracks can be picked

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out of an environment so high in false alarms that the eye cannot discern the number of targets appearing in 10 scans of tracker input data, let alone their tracks. The resiliency of the algorithm is demonstrated by the inclusion of the truth hypothesis at or near the head of the global hypothesis list in every case despite their stressing natures. Usually, the other hypotheses are trivially or transiently different from the truth hypothesis. Sometimes a false track was hypothesized, but these tracks are distinguished by being based on few and recent detections; potentially spurious tracks can be recognized by using that criterion. The only notable exception occurs with the transposition of tracks in Fig. 6-17. In such a congested environment, such crossovers are possible (e.g., a fighter-on-fighter engagement) and measured radar positions do not by themselves provide the information needed to recognize them. Knowledge about typical multi-aircraft flight patterns under varying circumstances (engagements versus patrolling) are needed; such knowledge is not readily captured in an automated target tracker.

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