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Multitarget Tracking of Distributed Targets Using Histogram-PMHT

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The expectation-maximization method is applied to derive a stable tracking algorithm that uses the entire display (image) as its input data, completely avoiding peak picking and other data compression steps required to produce traditional point measurements. The algorithm links a histogram interpretation of the intensity data with the tracking method of probabilistic multihypothesis tracking (PMHT) and is thus referred to as H-PMHT. An example of H-PMHT applied to tracking in bearing on a passive sonar broadband display is provided.

Key Words: multitarget tracking; probabilistic multihypothesis tracking; distributed target signal; thresholding loss; azimuth tracking.

1. INTRODUCTION

The histogram probabilistic multihypothesis tracking (H-PMHT) algorithm [1] uses a synthetic histogram interpretation of the received power in the sensor cells to process all the sensor output data and thus avoids thresholding the data to produce point measurements. The PMHT [2, 3] methodology is used to model the superposition of target and noise components in the data, and to link these components across successive scans. In both the H-PMHT and the PMHT algorithms, parameter estimates are achieved using the expectation-maximization (EM) method.

In their seminal paper [4] on the EM method, Dempster *et al.* applied the method to fit a parametric probability density function (PDF) to histogram data. McLachlan and Jones [5] and Jones and McLachlan [6, 7] applied the EM method to estimate Gaussian mixtures from one-dimensional histogram data. Luginbuhl [8] and Luginbuhl and Willett [9] applied a histogram and mixture modeling methodology to intensity-modulated displays to estimate a

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general, discrete-time, frequency-modulated process using short-term, Fourier transform data. Among references [4–9], only Luginbuhl [8] and Luginbuhl and Willett [9] considered the important problem of linking successive histograms using a dynamical model.

This paper expands upon previous presentations of the H-PMHT algorithm [10, 11] and provides a complete description of the H-PMHT method. The incomplete- and complete-data densities are formulated in Sections 2 and 3, respectively. Application of the EM method is presented in Section 4. An azimuth tracking example is given in Section 5. Concluding remarks are given in Section 6.

2. INCOMPLETE-DATA DENSITY

Let $C = \{C_1, \ldots, C_S\}$, $S \geq 1$, denote the collection of all possible sensor cells. It is assumed that $C_i \cap C_j = \emptyset$ for all i and j and that $C_1 \cup \cdots \cup C_S = R^{\dim(C)}$, where $\dim(C)$ denotes the dimension of the sensor space. The cells C are intrinsically fixed; however, those cells in which measurements are collected and displayed may vary from scan to scan. The sensor display at time t is denoted by $B(t) = \{B_1(t), \ldots, B_{L(t)}(t)\} \subset C$, where $1 \leq L(t) \leq S$. The other sensor cells $B^c(t) = \{B_{L(t)+1}(t), \ldots, B_S(t)\} = C \setminus B(t)$ are not displayed and are said to be truncated. It is assumed that no measurements are collected for cells in $B^c(t)$.

Let $T \geq 1$ denote the number of scans in a batch of measurements, and let $Z_t = \{z_{t1}, \ldots, z_{tL(t)}\}$, $t = 1, \ldots, T$, denote the sensor measurement vector at time t, where $z_{t\ell}$ is the power output of the sensor at time t in the display cell $B_\ell(t)$. Let $\hbar^2 > 0$ be a specified quantization level, and let $N_t = \{n_{t1}, \ldots, n_{tL(t)}\}$ denote the quantized vector corresponding to Z_t, where

$$n_{t\ell} = \left\lfloor \frac{z_{t\ell}}{\hbar^2} \right\rfloor, \tag{1}$$

and $\lfloor x \rfloor$ denotes the greatest integer less than or equal to x. After deriving the auxiliary function of the H-PMHT algorithm using N_t, the measurements Z_t are recovered in the limit as $\hbar^2 \to 0$. Let $N_{t\Sigma} = \sum_{\ell=1}^{L(t)} n_{t\ell}$ denote the total count, or sample size, at time t.

It is assumed that the vector N_t has a multinomial distribution consisting of $N_{t\Sigma}$ independent draws (with replacement) on $L(t)$ "categories" with probabilities

$$\frac{P_\ell(\theta_t)}{P(\theta_t)}, \qquad \ell = 1, \ldots, L(t), \tag{2}$$

where $P(\theta_t) = \sum_{\ell=1}^{L(t)} P_\ell(\theta_t)$, and

$$P_\ell(\theta_t) = \int_{B_\ell(t)} f(\tau; \theta_t)\, d\tau, \qquad \ell = 1, \ldots, S, \tag{3}$$

where $f(\tau; \theta_t)$ denotes a "sample" PDF defined over all $\tau \in R^{\dim(C)}$ and where the vector θ_t denotes the parameter vector of the sample PDF at time t. In the

following, $f(\tau;\theta_t)$ is taken to be a Gaussian mixture in which, just as in PMHT, the mixture components correspond to targets.

Let $N=\{N_1,\ldots,N_T\}$ and $\theta=\{\theta_1,\ldots,\theta_T\}$. Then, assuming that the vectors making up N are independent, the so-called incomplete-data PDF of N is given by the product of the multinomial densities corresponding to the cell counts $N_t=\{n_{t1},\ldots,n_{tL(t)}\}$,

$$p_{inc}(N;\theta)=\prod_{t=1}^{T}p_{inc}(N_t;\theta_t)=\prod_{t=1}^{T}\frac{N_{t\Sigma}!}{n_{t1}!\cdots n_{tL(t)}!}\prod_{\ell=1}^{L(t)}\left[\frac{P_\ell(\theta_t)}{P(\theta_t)}\right]^{n_{t\ell}}. \tag{4}$$

If $p_\Theta(\theta)$ denotes the *a priori* density of θ, then the incomplete-data PDF is given by $p_{inc}(N,\theta)=p_{inc}(N|\theta)p_\Theta(\theta)$, where the density $p_{inc}(N|\theta)$ is essentially identical to (4), the only difference being its statistical interpretation.

3. COMPLETE-DATA DENSITY

3.1. Unobserved Cell Counts as Missing Data

In the development of the complete-data density, missing data are introduced in three stages. In the first stage, missing random variables are used to model the counts in the unobserved, or truncated, cells in $B^c(t)$. For $\ell=L(t)+1,\ldots,S$, let $n_{t\ell}$ denote the missing count for cell $B_\ell(t)$. It is assumed that the missing counts are distributed as a negative multinomial (see Johnson *et al.* [13, Chap. 36]).

Letting $N_t^c=\{n_{t,L(t)+1},\ldots,n_{tS}\}$ and $N_{t\Sigma}^c=\sum_{\ell=L(t)+1}^{S}n_{t\ell}$, the negative multinomial PDF on N_t^c is given by

$$p(N_t^c|N_t;\theta_t)=\frac{(N_{t\Sigma}+N_{t\Sigma}^c-1)!}{n_{t,L(t)+1}!\cdots n_{tS}!(N_{t\Sigma}-1)!}[P(\theta_t)]^{N_{t\Sigma}}\prod_{\ell=L(t)+1}^{S}[P_\ell(\theta_t)]^{n_{t\ell}}. \tag{5}$$

Letting $N^c=\{N_1^c,\ldots,N_T^c\}$ and using independence of the count vectors in N^c and Bayes' theorem gives the complete-data PDF at the end of the first stage as

$$p_{com}^{(1)}(N,N^c;\theta)=\prod_{t=1}^{T}p(N_t^c|N_t;\theta_t)p_{inc}(N_t;\theta_t). \tag{6}$$

Substituting (4) and (5) and simplifying the resulting expression gives

$$p_{com}^{(1)}(N,N^c;\theta)=\prod_{t=1}^{T}\gamma_t\prod_{\ell=1}^{S}[P_\ell(\theta_t)]^{n_{t\ell}}, \tag{7}$$

where

$$\gamma_t=\frac{N_{t\Sigma}!}{n_{t1}!\cdots n_{tL(t)}!}\,\frac{(N_{t\Sigma}+N_{t\Sigma}^c-1)!}{n_{t,L(t)+1}!\cdots n_{tS}!(N_{t\Sigma}-1)!}. \tag{8}$$

It is clear from (7) that the negative multinomial PDF cancels denominator terms of the form $P(\theta_t)$ in the multinomial PDF.

3.2. Sample Locations as Missing Data

In the second stage, missing random variables are used to represent the locations of the unobserved samples in all S cells. There are $n_{t\ell}$ samples at time t in cell $B_\ell(t)$, so let $\zeta_{t\ell} = \{\zeta_{t\ell 1}, \ldots, \zeta_{t\ell n_{t\ell}}\} \subset B_\ell(t)$ denote the locations of the samples within cell $B_\ell(t)$. The random variables in $\zeta_{t\ell}$ are assumed to be independent and identically distributed (IID) with PDF $f(z;\theta_t)/P_\ell(\theta_t)$, and their domain is restricted to $B_\ell(t)$. Let $\zeta_t = \{\zeta_{t1}, \ldots, \zeta_{tS}\}$ and $\zeta = \{\zeta_1, \ldots, \zeta_T\}$. The complete-data PDF for the second stage is thus

$$p^{(2)}_{com}(N, N^c, \zeta; \theta) = \prod_{t=1}^{T} \gamma_t \prod_{\ell=1}^{S} \prod_{r=1}^{n_{t\ell}} f(\zeta_{t\ell r}; \theta_t). \tag{9}$$

3.3. Mixture Component Assignments as Missing Data

The final stage of missing random variables is required by the particular sample PDF considered in this application. The sample PDF is a function of location in the sensor output space $R^{\dim(C)}$, and it is assumed to be the mixture density

$$f(\tau; \theta_t) = \sum_{k=0}^{M} \pi_{tk} G_k(\tau; X_t), \tag{10}$$

where $\theta_t = \{\pi_t, X_t\}$, $\pi_t = \{\pi_{tk}\}$ are the so-called mixing proportions, and $X_t = \{x_{tk}\}$ are the target states. The mixing proportions are such that $\pi_{tk} \geq 0$, and $\pi_{t0} + \pi_{t1} + \cdots + \pi_{tM} = 1$. $G_k(\tau; X_t)$ is a PDF for all k; i.e., it is nonnegative and its integral over τ is equal to 1 for all X_t.

A physical interpretation of component $\pi_{tk} G_k(\tau; X_t)$ is that π_{tk} represents the fraction of the total power due to the target k and $G_k(\tau; X_t)$ models the cell-to-cell variations of target k, where $k = 0$ corresponds to the background noise. The parametric form (10) assumes that a target's power level may be spread across more than one cell of the sensor display.

A missing variable $k_{t\ell r}$ is used to specify which component of the mixture generated the missing variable $\zeta_{t\ell r}$, so that $k_{t\ell r} \in \{0, 1, \ldots, M\}$. It is assumed that $k_{t\ell r}$ is a random variable with discrete PDF specified by $\{\pi_{t0}, \pi_{t1}, \ldots, \pi_{tM}\}$. Hence, if $K_{t\ell} = \{k_{t\ell 1}, \ldots, k_{t\ell n_{t\ell}}\}$ for $\ell = 1, \ldots, S$ and $t = 1, \ldots, T$, then all variables in $K_{t\ell}$ are IID. Let $K_t = \{K_{t1}, \ldots, K_{tS}\}$ and $K = \{K_1, \ldots, K_T\}$. Extending the density (9) to include K gives the complete-data PDF at the end of the third stage as

$$p^{(3)}_{com}(N, N^c, \zeta, K; \theta) = \prod_{t=1}^{T} \gamma_t \prod_{\ell=1}^{S} \prod_{r=1}^{n_{t\ell}} f_{k_{t\ell r}}(\zeta_{t\ell r}; \theta_t), \tag{11}$$

where $f_k(\tau|\theta_t) = \pi_{tk} G_k(\tau|X_t)$.

The derivation of the prior density for the target parameters θ is an important theoretical development in H-PMHT. In short, the prior needs to be sufficiently nondiffuse so that the synthetically generated histogram counts N, which depend on the arbitrary quantization level $\hbar^2$, do not overwhelm the prior as $\hbar^2 \to 0$. A resampled Bayesian formulation is adopted where the prior density

is resampled for each event that generates a count in a cell. Let Υ_t denote the location random variable with sample value $\zeta_{t\ell r}$, and let Θ_t denote the state random variable with sample value $\{\varpi_{t\ell r}, \xi_{t\ell r}\}$ consisting of the mixing parameter $\varpi_{t\ell r}$ and the target state $\xi_{t\ell r}$. The elements in the set

$$\Omega_t = \bigcup_{\ell=1}^{S} \{(\varpi_{t\ell r}, \xi_{t\ell r}, \zeta_{t\ell r}) : r = 1, \ldots, n_{t\ell}\} \tag{12}$$

are assumed to be IID samples of a joint PDF given the state realization $\Theta_{t-1} = \theta_{t-1} = (\pi_{t-1}, X_{t-1})$ denoted by $p_{\Theta_t \Upsilon_t | \Theta_{t-1}}(\cdot, \cdot | \theta_{t-1})$. The resampled Bayesian assumption is that each measurement $\zeta_{t\ell r}$ is generated from a prior parameter specific to it, namely $\theta_{t\ell r}\{\varpi_{t\ell r}, \xi_{t\ell r}\}$; thus, the total number of prior parameters $\{\varpi_{t\ell r}, \xi_{t\ell r}\}$ equals, or balances, the total number of data points. Independence of mixing parameter and target state, as well as conditional independence, implies that the likelihood function is

$$p(\Omega_t | \theta_{t-1}) = \prod_{\ell=1}^{S} \prod_{r=1}^{n_{t\ell}} p_{\Xi_t | \Xi_{t-1}}(\xi_{t\ell r} | X_{t-1}) p_{\Pi_t | \Pi_{t-1}}(\varpi_{t\ell r} | \pi_{t-1}) \times p_{\Upsilon_t | \Theta_t}(\zeta_{t\ell r} | \varpi_{t\ell r}, \xi_{t\ell r}). \tag{13}$$

Substituting $p_{\Pi_t | \Pi_{t-1}}(\varpi_{t\ell r} | \pi_{t-1}) = 1$ (diffuse) and $p_{\Upsilon_t | \Theta_t}(\zeta_{t\ell r} | \varpi_{t\ell r} \xi_{t\ell r}) = f(\zeta_{t\ell r} | \varpi_{t\ell r} \theta_{t\ell r})$, and including the coefficient as in (8) and component assignments $k_{t\ell r}$, the complete data density is given by

$$p^{(3)}_{com}(N, N^c, \zeta, K, \xi, \theta) = p_{\Theta_0}(\theta_0) \prod_{t=1}^{T} \gamma_t \prod_{\ell=1}^{S} \prod_{r=1}^{n_{t\ell}} p_{\Xi_t | \Xi_{t-1}}(\xi_{t\ell r} | X_{t-1}) f_{k_{t\ell r}}(\zeta_{t\ell r} | \theta_{t\ell r}), \tag{14}$$

where $p_{\Theta_0}(\theta_0)$ is the Bayesian prior for the first scan. The parameter vector $\theta = \{\theta_0, \theta_1, \ldots, \theta_T\}$ defines a manifold $\mathcal{M}(\theta)$ on which the Bayesian parameters $\theta_{t\ell r}$ are restricted during the estimation process. Thus θ is neither a random variable nor the realization of a random variable. The random state variables are $\{\Theta_0, \Theta_1, \ldots, \Theta_T\}$, and their realizations are $\theta_{t\ell r}$. The manifold $\mathcal{M}(\theta)$ is defined by the system of linear equations

$$\mathcal{M}(\theta) = \{\theta_{t\ell r} : \varpi_{t\ell r} = \pi_t,\ \xi_{t\ell r} = X_t,\ r = 1, \ldots, n_{t\ell},\ \ell = 1, \ldots, L,\ t = 1, \ldots, T\}.$$

There are $N_\Sigma LT$ vectors in $\mathcal{M}(\theta)$, where $N_\Sigma = N_{1\Sigma} + \cdots + N_{T\Sigma}$. Conditioning on this manifold constraint leads to the standard prior; so we do not condition here: we constrain the estimate to the manifold to maintain the balance between prior and data.

4. APPLICATION OF EM METHOD

4.1. E-step

In the E-step of the EM method, the so-called auxiliary function $Q_\hbar$ is evaluated as a conditional expectation of the logarithm of the complete-data

density (11). The required expectation is with respect to the missing data $\{N^c, \zeta, K\}$, and it is conditioned on N and a current value of θ, denoted by θ'. Explicitly,

$$Q_\hbar = E_{N^c \zeta K}\left[\log p^{(3)}_{com}(\theta, N, N^c, \zeta, K)|N, \theta'\right], \tag{15}$$

where $E_{N^c \zeta K}$ denotes the expectation with respect to the missing data. The mechanics of the E-step for H-PMHT are tedious but straightforward. The final result in terms of the counts N is

$$\begin{aligned} Q_\hbar = {} & \log p_{\Theta_0}(\theta_0) + \sum_{t=1}^{T} \frac{N_{t\Sigma}}{P(\theta_t)} \log p_{\Xi_t|\Xi_{t-1}}(X_t|X_{t-1}) \\ & + \sum_{k=0}^{M} \sum_{t=1}^{T} \sum_{\ell=1}^{S} \frac{\bar{n}_{t\ell}}{P_\ell(\theta_t)} \int_{B_\ell(t)} f_k(\tau|\theta_t) \log f_k(\tau|\theta_t)\, d\tau, \end{aligned} \tag{16}$$

where

$$\bar{n}_{t\ell} = \begin{cases} n_{t\ell}, & 1 \le \ell \le L(t), \\ N_{t\Sigma} \dfrac{P_\ell(\theta'_t)}{P(\theta'_t)}, & L(t)+1 \le \ell \le S. \end{cases} \tag{17}$$

Truncated cells are seen from (17) to contribute to $Q_\hbar$ in proportion to the expected number of measurements in those cells; thus, the negative multinomial PDF is a kind of extrapolation procedure to compensate for truncated data.

It can be shown that the synthetic histogram is eliminated by taking the limit

$$Q^\sharp = \lim_{\hbar^2 \to 0} \hbar^2 Q_\hbar. \tag{18}$$

The result is

$$\begin{aligned} Q^\sharp = {} & \sum_{t=1}^{T} \frac{\|Z_t\|}{P(\theta'_t)} \log p_{\Xi_t|\Xi_{t-1}}(X_t|X_{t-1}) \\ & + \sum_{k=0}^{M} \sum_{t=1}^{T} \sum_{\ell=1}^{S} \frac{\bar{z}_{t\ell}}{P_\ell(\theta'_t)} \int_{B_\ell(t)} f_k(\tau|\theta'_t) \log f_k(\tau|\theta_t)\, d\tau, \end{aligned} \tag{19}$$

where the expected measurement $\bar{z}_{t\ell}$ is defined as

$$\bar{z}_{t\ell} = \lim_{\hbar^2 \to 0} \hbar^2 \bar{n}_{t\ell} = \begin{cases} z_{t\ell}, & 1 \le \ell \le L(t), \\ \|Z_t\| \dfrac{P_\ell(\theta'_t)}{P(\theta'_t)}, & L(t)+1 \le \ell \le S, \end{cases} \tag{20}$$

and $\|\cdot\|$ denotes the so-called L_1-norm. Note that the quantity $\hbar^2 \log p_{\Theta_0}(\theta_0)$ goes to 0 in the limit and that the limiting form $Q^\sharp$ uses measured sensor output data, not the synthetic histogram data.

4.2. M-step

The objective of the M-step is to maximize the auxiliary function $Q^\sharp$ with respect to the unknown signal parameters θ. To proceed, application-specific

terms in the auxiliary function (19) must be defined. For the linear Gauss–Markov target models,

$$p_{\Xi_t|\Xi_{t-1}}(X_t|X_{t-1}) = \prod_{k=1}^{M} \mathcal{N}(x_{tk};\, F_{t-1,k}x_{t-1,k},\, Q_{t-1,k}), \tag{21}$$

where F_{tk} and Q_{tk} represent known process and process covariance matrices, respectively. It is easily shown that $Q^\sharp = \sum_{t=1}^{T} Q_{t\pi} + \sum_{k=0}^{M} Q_{kX}$, where

$$Q_{t\pi} = \sum_{k=0}^{M} \left[\sum_{\ell=1}^{S} \frac{\bar{z}_{t\ell}}{P_\ell(\theta_t')} \int_{B_\ell(t)} G_k(\tau|x_{tk}')\, d\tau \right] \pi_{tk}' \log \pi_{tk}, \tag{22}$$

and

$$\begin{aligned} Q_{kX} = &\sum_{t=1}^{T} \|Z_t\| \log p_{\Xi_{tk}|\Xi_{t-1,k}}(x_{tk}|x_{t-1,k}) \\ &+ \sum_{t=1}^{T} \sum_{\ell=1}^{S} \frac{\pi_{tk}' \bar{z}_{t\ell}}{P_\ell(\theta_t')} \int_{B_\ell(t)} G_k(\tau|x_{tk}') \log G(\tau|x_{tk})\, d\tau. \end{aligned} \tag{23}$$

The updated mixing proportions π_t are obtained at each time t by maximizing with respect to π_t the Lagrangian equation involving $Q_{t\pi}$ and the constraint $\pi_{t0} + \pi_{t1} + \cdots + \pi_{tM} = 1$.

It is now assumed that the target components in the mixture distribution are Gaussian and that the means of these Gaussians are linearly related to the states of the targets $k = 1, \ldots, M$ at times $t = 1, \ldots, T$, so that

$$G_k(\tau|x_{tk}) = \mathcal{N}(\tau;\, H_{tk}x_{tk},\, R_{tk}), \tag{24}$$

where the H_{tk} are known measurement matrices and the R_{tk} are the measurement covariance matrices. The noise component $G_k(\tau)$ is assumed known.

With these assumptions, it can be shown [1] that for $X(k) = \{x_{0k}, x_{1k}, \ldots, x_{Tk}\}$, the value of $X(k)$ that maximizes the auxiliary function Q_{kX} for each target k is efficiently solved by a recursive Kalman smoothing filter, even when there are truncated cells and the measurement covariance matrices $R = \{R_{tk}\}$ are to be estimated. The details of this result are omitted here, but the filter steps are listed explicitly in [1, 10, 11] for the linear Gaussian case and constant background noise.

4.3. Measurement Covariance Estimates

Here the measurement covariance matrices are assumed unknown, and an estimation algorithm is derived by the generalized EM (GEM) method. The E-step of the GEM method is the same as the E-step of the EM method. Consequently, the mixing proportions π are estimated in exactly the same way as before.

The terms in $Q^\sharp$ not involving π constitute a function of the form $Q^\sharp(X, R)$. The M-step of the EM method requires solving the problem $\max_{X,R} Q^\sharp(X, R)$.

Unfortunately, the necessary equations are coupled, so the EM method is difficult to use. By replacing the maximization with a nested maximization

$$\max_R \{ \max_X Q^\sharp(X, R) \}, \tag{25}$$

it is readily verified that $Q^\sharp$ is necessarily increased, even though it is not maximized. Any increase is sufficient to ensure convergence of a GEM sequence [4].

Let $\{\hat{x}_{0k}, \hat{x}_{1k}, \ldots, \hat{x}_{Tk}\}$ denote the updated state estimates obtained for current estimates of mixing proportions, states, and covariances. The notation of (24) must be adjusted slightly for the present context, that is, $\mathcal{N}(\tau; H_{tk}x_{tk}, R_{tk})$ must be replaced by $\mathcal{N}(\tau; H_{tk}x'_{tk}, R'_{tk})$, as is easily seen from the derivation of Q_{kX}. Also, x_{tk} in (23) must be replaced by $\hat{x}_{tk}$ because of the nested maximization (25). Substituting (24) into (23), taking the gradient of (23) with respect to R_{tk}, and solving for R_{tk} gives the estimator

$$\widehat{R}_{tk} = \frac{\sum_{\ell=1}^{S} [(\bar{z}_{t\ell}/P_\ell(X'_t)) \int_{B_\ell(t)} \mathcal{N}(\tau; H_{tk}x'_{tk}, R'_{tk})\, d\tau] \widehat{R}_{tk\ell}}{\sum_{\ell=1}^{S} [(\bar{z}_{t\ell}/P_\ell(X'_t)) \int_{B_\ell(t)} \mathcal{N}(\tau; H_{tk}x'_{tk}, R'_{tk})\, d\tau]}, \tag{26}$$

where the cell-level measurement covariance matrix contributions are defined by

$$\widehat{R}_{tk\ell} = \frac{\int_{B_\ell(t)} \mathcal{N}(\tau; H_{tk}x'_{tk}, R'_k)(\tau - H_{tk}\hat{x}_{tk})(\tau - H_{tk}\hat{x}_{tk})^{\mathrm{T}}\, d\tau}{\int_{B_\ell(t)} \mathcal{N}(\tau; H_{tk}x'_{tk}, R'_{tk})\, d\tau}. \tag{27}$$

The estimator (26) cannot be full rank unless $S > \dim(C)$.

5. AZIMUTH TRACKING EXAMPLE

For one-dimensional azimuth tracking, the target parameters of interest are the azimuthal angle β_t and the instantaneous rate $\dot{\beta}_t$ at time t; therefore, for target k, $x_{tk} = [\beta_{tk} \quad \dot{\beta}_{tk}]^{\mathrm{T}}$. For this two-state linear Markov model, the state matrices $F_{t-1,k}$ and the process covariance matrices $Q_{t-1,k}$ have simple forms (see [12]),

$$F_{t-1,k} = \begin{bmatrix} 1 & \Delta_{t-1} \\ 0 & 1 \end{bmatrix} \qquad \text{and} \qquad Q_{t-1,k} = q_{t-1,k} \begin{bmatrix} \frac{1}{3}\Delta_{t-1}^3 & \frac{1}{2}\Delta_{t-1}^2 \\ \frac{1}{2}\Delta_{t-1}^2 & \Delta_{t-1} \end{bmatrix}, \tag{28}$$

where Δ_t is the time between time t and time $t-1$ and where the $q_{t-1,k}$ are scale factors. The measurement matrices H_{tk} and the measurement covariance matrices R_{tk} also have simple forms: $H_{tk} = [1 \;\; 0]$ and $R_{tk} = \rho_{tk}^2$, where ρ_{tk} is the target spread, or beam extent, of target k at time t.

In this example, the H-PMHT algorithm was applied to the beamformed data from an acoustic line array to form bearing tracks. Simulated data were generated for an observer with a set of 51 equal width beams spanning 180° of azimuth that receive energy from two targets (plus uniform background noise).

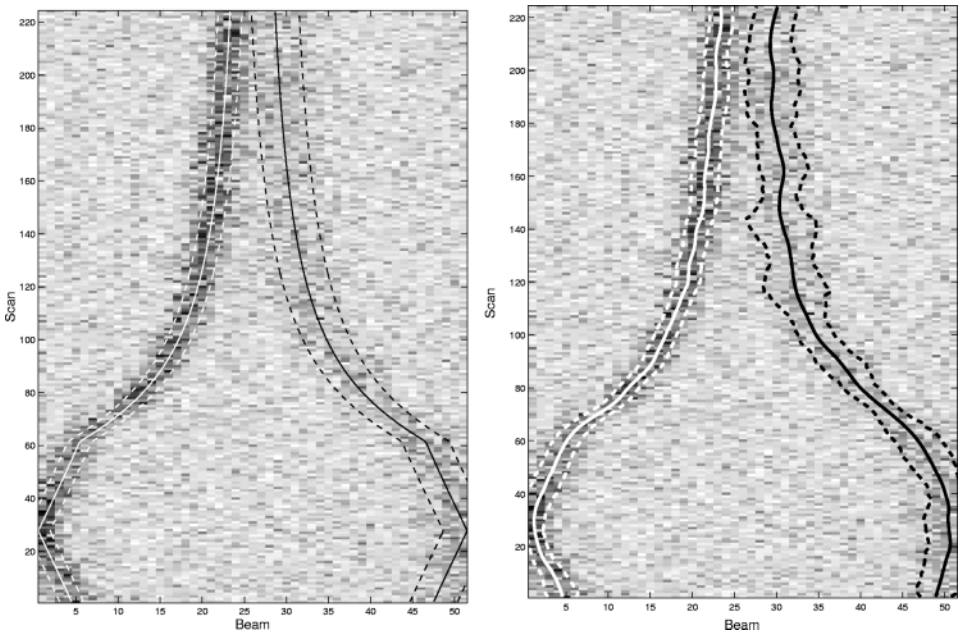

FIG. 1. Intensity data (left). Two-component model with truncated cells (right).

The resulting beam intensity history is shown in Fig. 1a. The strong target has an SNR (peak signal to nominal noise power, in a beam) of +4.5 dB, while the weak target has an SNR of −1.5 dB. These SNRs reflect the use of an exponentially distributed beam intensity with mean value determined by the mixture model (10). The simulated mixture assumed a uniform noise distribution and Gaussian target distributions with means given by the true target bearings and standard deviations $\rho_{tk} = \rho_k = 5°$ for the strong target and $\rho_{tk} = \rho_k = 10°$ for the weak target. The H-PMHT algorithm was applied using a sliding batch of 15 scans with the mixing proportions π_{tk} and the target spreads R_{tk} constrained to be constant over the batch. The estimate for the earliest scan in the batch serves as a prior for the subsequent batch that has been slid forward by one scan.

When H-PMHT is implemented with truncated cells on either side of the sensor display, as in right part of Fig. 1, the beam spread estimates (represented by the dashed lines) do a good job of modeling the intensity fluctuation on the display. In contrast, Fig. 2 (left) shows the effect of not using the truncated cells. In this case, the beam spread estimates "pinch" near the edges of the display, resulting in biased beam spread and bearing estimates. Figure 2 (right) shows the effect of undermodeling the target energy on the display. In this case, one component (with truncated cells) was initialized on the weak target and was subsequently "seduced" by the strong target when the tracks are in close proximity. Overlayed on the same plot is the corresponding single component track initialized on the strong target, showing a slight bias toward the end of the scenario when compared to the track in Fig. 1 (right) due to the presence of the weak target's energy. The seduction phenomenon underscores the necessity

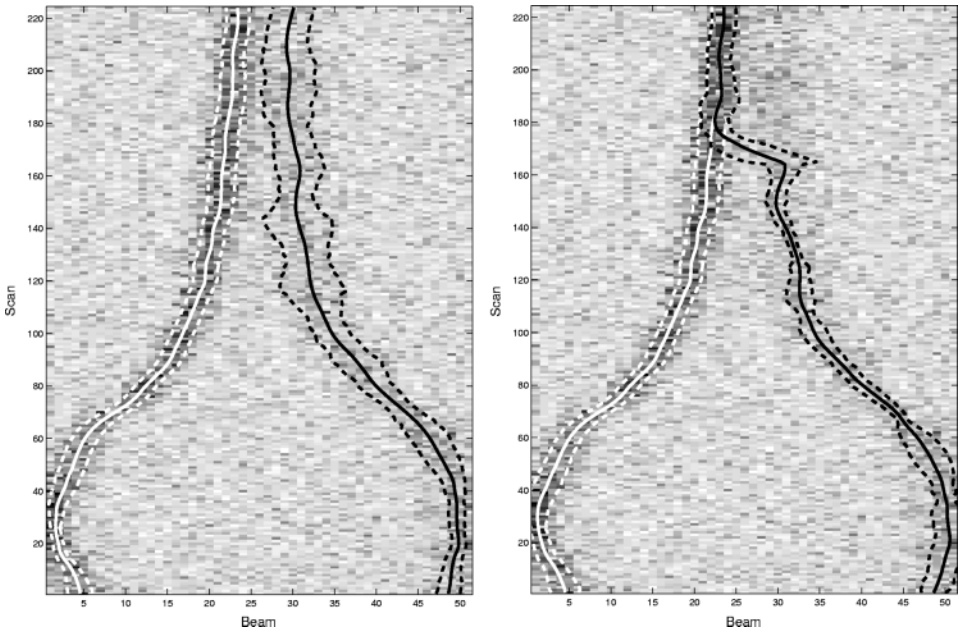

FIG. 2. Two-component model without truncated cells (left). Two independent one-component models with truncated cells (right).

of an integrated approach to the tracking problem rather than using a set of independent, single-target trackers to track multiple targets.

6. CONCLUDING REMARKS

The H-PMHT algorithm is a multitarget tracking algorithm designed to be used with the entire sensor output data stream. It completely avoids thresholding losses incurred by the traditional methods of generating point measurements by peak-picking, three-point interpolation, etc. The theoretical development of the H-PMHT algorithm has a mathematically sound foundation based on the framework of PMHT.

The negative multinomial model compensates for missing data by extrapolating the given data into truncated cells; hence, it may reduce parameter estimation bias and other undesirable edge effects induced by cell truncation. Joint estimation of multiple targets yields a higher fidelity signal model and hence improved tracking.

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