1 Introduction

The aim of this section is to give the reader a feeling for the most popular methods, their assumptions and strong and weak properties as seen from an 2D maritime anti collision perspective.

1.1 Tracking

Tracking of an object object (target) is the process of estimating its state (i.e. position and velocity) based on discrete measurements from an observation system. An observation system can be a radar, sonar or any other sensor that passively or actively detects objects within a area or volume.

1.2 Tracking system

A tracking system can be interpreted as either the complete system from the signal processing level to the finished tracks, or as I will I this text: A system that associates consecutive measurements from an observation system, and initiate or assigns them to tracks. A track is a subset of all the measurements from the observation system that is believed to originate from the same target. The challenge with knowing which measurement originating from which (real) target is the core at any tracking system. This association problem is non-trivial even under ideal situations, and the addition of spurious measurements and missed targets only increases the complexity.

There has been developed a large variety of methods to overcome this association problem, and most of them have several sub-methods. In the following subsections, some of the most common and popular methods will be presented.

1.3 Definitions

Scan $\triangleq$ a procedure which measures the entire area of coverage of the system.
Measurement $\triangleq$ a point in the measurement space where something is detected.
Score $\triangleq$ a measure of the goodness of a measurement-to-track association.
Dummy measurement $\triangleq$ a self created measurement at the estimated position (with score 0).
Measurement list $\triangleq$ a set of measurement who originate from the same scan.
Target $\triangleq$ an actual object who the system is trying to track.
Track $\triangleq$ a list of measurement indices, one from each scan, who is believed to originate from the same target.
Gate $\triangleq$ an area in which a track expects and approves new measurement to associate with itself.

Track hypothesis $\triangleq$ a new measurement who is inside the gate for an existing track.

1.4   Nearest Neighbour Standard Filter

The Nearest Neighbour Standard Filter (NNSF)is the simplest approach in tracking where one always select the closes neighbour as the consecutive measurement in the track. This approach suffers from being very vulnerable from clutter and dense target scenarios, and can be somewhat improved by estimating an a-priori state through a Kalman Filter and selecting the nearest neighbour to the estimate. Even with this extension, it is a very primitive approach which does not yield good real world performance.

1.5   Probabilistic Data Association Filter

Probabilistic Data Association Filter (PDAF) is a *single target* Bayesian association filter which is based on single scan probabilistic analysis of measurements. At each scan the filter is calculating a most probable measurement based on a weighted sum on the measurement innovations inside a validation region.

$$\hat{\mathbf{y}} \triangleq \sum_{j=1}^{m} \beta_j \tilde{\mathbf{y}}_{\mathbf{j}} \tag{1}$$

where β_j is the probability of measurement j to be the correct one, and $\tilde{y}_j = y_j - \hat{y}_j$ is the j-th measurement innovation.

PDAF is computationally modest (approximate 50% more computationally demanding than a Kalman Filter [1] p.163) and have good results in an environment with up to about 5 false measurement in a 4σ validation region [1]. PDAF does not include track initialisation and assumes that at most one measurement can originate from an actual target. It also assumes that clutter is uniformly distributed in the measurement space and that the targets history is approximated by a Gaussian with a calculated mean and covariance (single scan).

PDAF can be used for multiple targets, but only as multiple copies of the single-target filter [2]. Since PDAF is generating a "best guess"-measurement from all the measurements inside its validation region, it can suffer from track coalescence. This coalescence occurs when two targets have similar paths, and the resulting tracks will be an "average" of the two (actual) tracks. PDAF is considered the simplest "state of the art" tracking algorithm.

1.6 Joint Probabilistic Data Association Filter

Joint Probabilistic Data Association Filter (JPDAF) is a *multi target* extension of the Probabilistic Data Association Filter in which joint posteriori association probabilities are calculated for every target at each scan. Both PDAF and JPDAF use the same weighted sum (1), the key difference is the way the weight β_j is calculated. Whereas PDAF treats all but one measurement inside its validation region as clutter, in JPDAF the targets who interacts (one cluster) are treated as connected and the connected β_js are computed jointly across the cluster set with a given set of active targets inside the cluster. The probability of a measurement j belonging to a target t is [2]

$$\beta_j^t = \sum_\chi P\{\chi|Y^k\}\hat{\omega}_{jt}(\chi)$$

$$\beta_0^t = 1 - \sum_{j=1}^m \beta_j^t \tag{2}$$

where

$$P\{\chi|Y^k\} = \frac{C^\phi}{c} \prod_{j:\tau_j=1} \frac{exp[-\frac{1}{2}(\tilde{\mathbf{y}}_\mathbf{j}^{\mathbf{t_j}})^T S_{t_j}^{-1}(\tilde{\mathbf{y}}^{\mathbf{t_j}})]}{(2\pi)^{M/2}|S_{t_j}|^{1/2}} \prod_{t:\delta_t=1} P_D^t \prod_{t:\delta_t=0} (1 - P_D^t) \tag{3}$$

Since the JPDAF is calculating joint probability for all the combinations of measurement associations in the cluster, the computation demand is growing exponentially with the numbers of tracks and measurements in the cluster. A real time implementation of the JPDAF has been developed and patented by QinetiQ [3], and an approach for avoiding track coalescence has been proposed by [4].

1.7 Multi Hypothesis Tracker

Multiple hypothesis tracking (MHT) is a category of methods that are based around the concept of evaluating multiple combinations of measurements to data association, and rank them with respect to their statistical properties. In contrast to PDA methods which in some cases will estimate an "average" of two tracks as the true on (coalesce), MHT methods split when in doubt. The original MHT algorithm was presented in [5], where a hypothesis oriented MHT was developed. Following this, a track oriented MHT was proposed in [6] and improved by [7].

1.7.1 Hypothesis Oriented MHT

Hypothesis Oriented Multiple Hypothesis Tracker (HOMHT) or Measurement Oriented Multiple Hypothesis Tracker (MOMHT) is on a fully Bayesian approach

where direct probabilities of global joint measurement to target association hypothesis are calculated. The algorithm initiates track and handles missing measurements, has a recursive nature and is allows for clustering for quicker calculations. One of the main benefits of MHT is the ability to utilize multiple scans to aid in the data association, in other words to use all the available data when taking decisions. TOMHT was developed under the assumption that no target can originate more than one measurement from each scan, and a target does not necessary show on every scan. When evaluating the probability of a hypothesis, the MHT takes into account the false-alarm statistics of the measurement system, the expected density of targets and clutter and the accuracy of the target estimates.

The probability of each data association hypothesis was developed by Reid in [5]

$$P_i^k = \frac{1}{c} P_D^{N_{DT}} (1 - P_D)^{(N_{TGT} - N_{DT})} \beta_{FT}^{N_{FT}} \beta_{NT}^{N_{NT}} \left[\prod_{m=1}^{N_{DT}} N(\mathbf{Z_m} - \boldsymbol{H}\bar{\mathbf{x}}, \boldsymbol{B}) \right] P_g^{k-1}$$

(4)

where P_i^k is the probability of hypothesis Ω_i^k given measurements up through time k. P_D is the probability of detection, β_{FT} is the density of targets, β_{NT} is the density of previously unknown targets that have been detected, N_{DT} is number of designated targets, N_{FT} is the number of false targets, N_{NT} is the number of new targets, N_{TGT} is the number of targets, $\mathbf{Z_m}$ is the m-th measurement in the current scan, $\boldsymbol{H}$ is the observation matrix and $\boldsymbol{B}$ is the measurement covariance.

1.7.2 Track Oriented MHT

Track Oriented Multiple Hypothesis Tracker (TOMHT) is a "bottom-up" approach where the tracks are assumed initialized, and for each scan the track split whenever there are more than one feasible measurement in the validation region. The new track hypothesis state is generated from the posteriori filtered estimate from a Kalman Filter, and a score/cost is calculated using (20) from [7]. Following the addition of a new track hypothesis, the tracks are divided into clusters where all tracks who share measurements from the latest scan are in one cluster. The clusters must then be analysed to find the beast possible combination of mutual exlucsivemeasurement associations. LP- and ILP-based methods as proposed by [8] can be used to find the best (nearest optimal) combinations of newly created track hypothesis in accordance to the assumption that a measurement only can be assigned to one target and that one target can maximally create one measurement.

To limit the size of the track hypothesis tree some sort of pruning/elimination

of unlikely hypothesis must be carried out. ""This step is, from a Bayesian point of view, the most problematic since ...""

2 Linear programming

The aim of this section is to elaborate the use of linear programming to solve the data association problem in MHT that arises when there are multiple (possible mutual exclusive) possibilities of measurement arrangements within the existing set of tracks. As with any optimization problem, we need an objective function which tells us how good or bad a given assignment is, and a set of constraints that limits the solution to the physical limits and our assumptions.

2.1 Objective function

Storms and Spieksma [8] are suggesting an Integer Linear Programming (ILP) scheme with Linear Programming (LP) relaxation and Greedy Rounding Procedure (GRP) as solvers.

$$
\begin{aligned}
\underset{f}{\text{minimize}} \quad & f = \sum_{z \in \mathbf{Z}^*} c_z x_z \\
\text{subject to} \quad & \sum_{z \in \mathbf{Z}^*, z(k)=z_{i_k}^k} x_z = 1, \forall k = 1, \ldots, N \text{ and } i_k = 1, \ldots, M_k \quad (5) \\
& x_z \in \{0, 1\}
\end{aligned}
$$

where, $c_z = -lnQ_z$ and the likelihood for a track is

$$
Q(z) = \prod_{k=1}^{N} (P_\phi^k)^{\Delta_{i_k}} \left\{ \left[\frac{P_d f_\delta^k(z_{i_k}^k|z)}{\lambda_\varphi f_\varphi^k(z_{i_k}^k)} \right]^{\delta_{i_k}^k} \left[\frac{\lambda_\nu f_\nu^k(z_{i_k}^k|z)}{\lambda_\varphi f_\varphi^k(z_{i_k}^k)} \right]^{\nu_{i_k}^k} \right\}^{(1-\Delta_{i_k})} \quad (6)
$$

where,

$$\Delta_{i_k} = \begin{cases} 1, i_k = 0 \, (\text{dummy report}) \\ 0, \text{otherwise} \end{cases}$$

$$P_\phi^k = \begin{cases} 1 - P_d, z_{i_k}^k \, \text{is a missing report} \\ 0, \text{otherwise} \end{cases}$$

$$\nu_{i_k}^k = \begin{cases} 1, z_{i_k}^k \, \text{initiates a track} \\ 0, \text{otherwise} \end{cases}$$

$$\delta_{i_k}^k = \begin{cases} 1, z_{i_k}^k \, \text{proceeds as a track} \\ 0, \text{otherwise} \end{cases}$$

$$P_d = \text{probability of detection}$$

$$\lambda_\varphi = \text{expexted number of false alarms (Poisson distr.)}$$

$$\lambda_\nu = \text{expected number of new targets (Poisson distr.)}$$

$$f_\nu^k = f_\varphi^k = \frac{1}{\pi r^2}, \text{where r is the sensor range}$$

$$f_\delta^k = \frac{e^{-\frac{1}{2}[z_{i_k}^k - h(\bar{s}(t_k))]^T B^{-1}[z_{i_k} - h(\bar{s}(t_k))]}}{\sqrt{(2\pi)^n |B|}}$$

$$n = \text{dimension of measurement vector}$$

$$h(\cdot) = \text{transformation of Cartesian to polar}$$

$$\bar{s} = \text{predicted state vector}$$

$$B = \text{covariance of } z_{i_k}^k - h(\bar{s}(t_k))$$

This approach uses a rather inelegant summation notation which is not on a standard (I)LP format.

A more compact formulation of the data association problem is proposed on a ILP standard form

$$\text{maximize} \quad \mathbf{c}^T \mathbf{x}$$

$$\text{s.t.} \quad \begin{aligned} \boldsymbol{A_1}\mathbf{x} &= \mathbf{b_1} \\ \boldsymbol{A_2}\mathbf{x} &= \mathbf{b_2} \\ \mathbf{x} &\in \{0,1\} \end{aligned} \tag{7}$$

where $\boldsymbol{A_1}$ is a $N_1 \times M$ matrix with N_1 real measurements and M track hypotheses (all leaf nodes), where $\boldsymbol{A_1}(i,j) = 1$ if hypothesis j are utilizing measurement i, 0 otherwise. $\boldsymbol{A_2}$ is a $N_2 \times M$ binary matrix where $N_2 1$ is the number of targets in the cluster and $\boldsymbol{A_2}(i,j) = 1$ if hypothesis j belongs to target i. $\mathbf{b_1}$ is a N_1 long vector with ones, $\mathbf{b_2}$ is a N_2 long vector with ones. $\mathbf{c}$ is a N long vector with

a measure of the goodness of the track hypotheses. For example in figure **??** at time step 2, the A matrix and C vector would be

$$A_1 = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 \end{bmatrix} A_2 = \begin{bmatrix} 1 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 \end{bmatrix} c = \begin{bmatrix} \lambda_1 \\ \lambda_2 \\ \lambda_3 \\ \lambda_4 \end{bmatrix} \tag{8}$$

2.2 Score function

An alternative score function was proposed in [7] was the Negative Logarithmic Likelihood Ratio (NLLR) for each hypothesis assignment.

$$NLLR_{t,j}(k) = \frac{1}{2}\left[\tilde{y}_k^T S_{tj}(k)^{-1}\tilde{y}_k\right] + \ln\frac{\lambda_{ex}|2\pi S_{tj}(k)|^{1/2}}{P_{D_t}(k)} \tag{9}$$

$$\tilde{y}_k = z_j(k) - \hat{z}_t(k|k-1)$$

where the cumulative NLLR is

$$l_t^k \triangleq \sum_{l=0}^{k} NLLR_{t,j(t,l)}(l) \tag{10}$$

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References

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