Iterative Joint Integrated Probabilistic Data Association

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Abstract—In situations with a significant number of targets in mutual proximity (close to each other), optimal multi target data association approach suffers from the numerical explosion. This severely limits the applicability; i.e. the number of close targets that may be reliably tracked. We propose an iterative implementation of Joint Integrated Probabilistic Data Association (JIPDA). Starting level is Integrated Probabilistic Data Association (IPDA) for single target tracking, and each subsequent level improves the approximation towards JIPDA. The required number of iterations to achieve the performance of JIPDA is finite for tracking finite number of targets. Increasing the number of iterations also increases computational expenses. Thus we provide the possibility of trade off between the performance and the computational resources by adjusting the number of iterations.

I. INTRODUCTION

Target tracking in the presence of clutter measurements has to deal with the measurements without prior indication on the source of each measurement. Two problems typically need solving. One is the data association; i.e. association of measurements to tracks, and the other is the false track discrimination.

The false track discrimination involves recognizing and confirming true tracks (i.e. the tracks which follow targets) and recognizing and terminating false tracks. Target tracking algorithms which implement both data association and false track discrimination in a potentially optimal manner include the Multiple Hypotheses Tracking (MHT) [1], Integrated Track Splitting (ITS) [2] and Joint Integrated Track Splitting (JITS) [3]. The number of track components of MHT, ITS and JITS grows exponentially over time, and the Probabilistic Data Association (PDA) [4] approximation is often used, where all track components are merged into one trajectory estimate with a Gaussian probability density function. Joint Probabilistic Data Association (JPDA) [5] is used for multi-target tracking for cluttered environments with known numbers of targets. Applying the PDA approximation to ITS and JITS, we obtain Integrated Probabilistic Data Association (IPDA) [6] and Joint Integrated Probabilistic Data Association (JIPDA) [7] respectively with the false track discrimination capabilities.

Whilst the PDA approximation eliminates the increase of the numerical complexity in time per track, there are also the multi target tracking issues. ITS and IPDA are single target tracking algorithms, and they show poor results in an environment with multiple targets in close proximity. JITS and JIPDA are multi-target tracking algorithms which implement the optimal multi-target data association strategy of enumerating and evaluating all feasible joint measurement to track associations (feasible joint events).

This optimal strategy carries computational risks, as the number of feasible joint events grows combinatorially with the number of tracks and the number of measurements involved. Thus this approach becomes impractical for a relatively small number of close targets. To combat this problem, ad hoc and suboptimal approaches are published. Ad hoc approaches can be referred to the cheap JPDA [8], Roecker’s algorithm [9], while [10], [11] and references therein list further suboptimal multi target approaches. Besides these efforts to reduce computational cost, there have also been a few options to reduce track coalescence of near target tracks from which JPDA and JIPDA suffer [12][13].

Here we propose another approach to multi target tracking in clutter. The proposed iterative Joint IPDA (iJIPDA) algorithm approximates the JIPDA data association by chaining the tracks in a cluster. The chain has a number of levels. The first level is identical to the IPDA (i.e. no multi

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target capabilities), and the last one is identical to the JIPDA. The multi target data association monotonically improves with the number of levels, which also increases the computational complexity. This opens a number of practical possibilities. One is the trade off between the performance and the computational requirements. The other is the possibility of simply increasing the number of levels in each scan until we run out of processing time, when we simply use the currently available results. Thus we obtain best possible results given the constraints of real time processing.

The paper is organized as follows. Section II provides a top level overview of the IPDA tracking in clutter. The iJIPDA algorithm is presented in Section III, followed by the numerical results vindicating the approach in Section IV, followed by the concluding remarks. The Appendix provides the graphical demonstration of one scan one cluster iterations.

II. IPDA TRACKING OVERVIEW

The IPDA suite of target tracking algorithms in clutter consists of IPDA [6][10], JIPDA [7] and Linear Multitarget IPDA (LM-IPDA) [14][15]. They are well documented elsewhere, and here we provide just a brief overview.

IPDA, JIPDA and LM-IPDA use the same track state, which consists of the target existence event and the trajectory state. Thus, each track probability density function (pdf) consists of the probability of target existence and the trajectory probability density function. As the trajectory pdf is approximated by a Gaussian pdf, this is parameterized by trajectory mean and covariance. They all use same parameters to calculate the data association probabilities and update the probability of target existence:

- The probability of detection \( P_d \) and the gating (selection) probability \( P_g \),
- Clutter measurement density \( \rho \), assumed known or estimated using the measurements, [17]
- Likelihoods \( p_{k,j} \) of each measurement \( z_{k,j} \), where \( k \) denotes the time (measurement scan) index,
- Propagated probability of target existence at time \( k \), \( \mathbf{\hat{\Psi}}_k \).

IPDA is a single target tracking algorithm, where each track ignores the other tracks as possible measurement sources.

JIPDA uses the optimal multi target data association approach, which enumerates and evaluates (calculates the posterior probabilities of) feasible joint events, i.e. of allocations of all measurements to all tracks. Although this multi target data association approach is optimal, JIPDA is still a suboptimal multi target tracker. This sub optimality stems from the single Gaussian trajectory pdf approximation. As the number of feasible joint events grows combinatorially with the number of tracks and the number of measurements involved, the JIPDA is simply not practical in situations with more than a few close targets. One example may be found in Section IV.

Linear Multitarget (LM) [14] is a suboptimal multi target tracking approach which effectively converts single target tracking algorithms into multi target tracking algorithms. The approach increases (modulates) the clutter measurement density to compensate for the possibility that the measurements are detections of targets being followed by other tracks. The number of operations are linear in the number of tracks and the number of measurements, thus it may be used with a large number of close targets. The LM-IPDA [14][15] is formed by applying the LM approach to the IPDA tracking.

III. ITERATIVE JIPDA

Iterative JIPDA (iJIPDA) utilizes the arithmetic structure of JIPDA [7] for calculation of data association probability and target existence probability, and transform it into a recursive form of the IPDA-like algorithm. It does not need to form a track-to-measurement assignment matrix for a cluster of multiple targets, and the data association probabilities can be calculated by a parallel computation architecture. Each target in a cluster is tracked as if it is in single target tracking environment. The JIPDA requires the enumeration and the evaluation of all possible joint measurement to track assignments. This becomes impractical even for tracking environments with a modest number of tracks and measurements. The gating and the clustering may reduce the number of feasible joint events, but this also has practical limitations. The proposed iJIPDA algorithm modifies clutter density with likelihood of the measurements in the upper level, and applies the same algorithm structure recursively until it reaches the final level which is determined by the number of tracks in the cluster. Other than no requirement of the assignment matrix and possible application of parallel computation architecture, the all-iterations iJIPDA algorithm has the JIPDA computational limitations. However, we can adjust the number of iterations in the algorithm to suit the complexities of the tracking environment and available computational resources to optimize the output given computational constraints. This sacrifices the multi target data association optimality of JIPDA; the trade off is illustrated in Section IV.

Denote by \( Z_{t} \) the set of measurements in a cluster of tracks, and by \( Z_{t}^c \) with cardinality \( m_t^c \) the set of the validated measurements of the track \( t \), such that \( Z_{t}^c = \{ z_{i,1}, z_{i,2}, \cdots, z_{i,m_t^c} \} \). Then \( Z_{c} = \bigcup Z_{t}^c \) and \( Z^c = \{ Z_{c1}, Z_{c2}, \cdots, Z_{cm} \} \). We assume a uniform clutter environment where the clutter spatial density is \( \rho \). The target \( t_i \) is detected with the prob-
ability of detection $P_o^r$ and the selection probability is denoted as $P_o^s$. The existence probability of target $\tau_i$ is defined as $\psi_i^s = P(X_i^s | Z^s)$ where $X_i^s$ is the event that the target $\tau_i$ exists. We assume that $\psi_i^s$ propagates by the Markov Chain One model [6]. The propagated existence probability is denoted by $\widetilde{\psi}_i^s = P(X_i^s | Z^{s-1})$.

As we want to obtain the track-to-measurement association probabilities of track $\tau_i$, $\tau_j$ is said to be in the root level (level 0), and the association probabilities are affected by other tracks in the upper level which share the measurement in common. All $m_i^s$ measurements inside the validation gate of $\tau_i$ used for the data association probabilities in the same form as IPDA [6] for single target tracking. Each measurement inside the validation gate of $\tau_i$ that is also a validated measurement of other tracks is used to form branches. The number of branches formed by the measurement is equal to the number of tracks that share the measurement excluding the root track $\tau_i$. If there are measurements that are not shared by other tracks, branches are not formed. The branches connected by the branches are said to be in the level 1. The measurement that connects the root track $\tau_i$ and a track in the level 1 is termed the chain measurement. The branches are extended to upper level by the chain measurements and the tracks selected to form a branch are no longer used in the extension of the branch so that the tracks involved in a branch are allocated only once in the branch extended from the root level to the final level.

The association probabilities of $\tau_i$ with validated measurements are obtained by

$$\beta_{k,j} = \frac{1}{\Delta} \left\{ \frac{1 - P_o^r P_o^s}{P_o^r \tilde{P}_i^s(z_{i,n})} \right\}, \quad j = 0, 1, 2, \cdots m_i^s, \quad (1)$$

$$\Delta = 1 - P_o^r P_o^s + P_o^r \sum_{l=0}^{m_i^s} P_i^l(z_{i,n}) / \tilde{P}_i^s(z_{i,n}), \quad (2)$$

where $P_i^l(z_{i,n})$ is the likelihood of track $\tau_i$ being the origin of $z_{i,n}$ such that

$$P_i^l(z_{i,n}) = \mathcal{N}(z_{i,n}; \tilde{z}_i^s, S_i^s), \quad (3)$$

is a Gaussian pdf with the mean equal to the predicted measurement $\tilde{z}_i^s$ of track $\tau_i$ and the innovation covariance $S_i^s$. In (1), $\tilde{P}_i^s(z_{i,n})$ is the modulated clutter measurement density that takes into account of the effect of tracks in the level 1 that share $z_{i,n}$ in common with the root track. The measurement $z_{i,n}$ is the chain measurement of $\tau_i$ and $\tau_j$. The effects of the tracks from level 1 to the root track $\tau_i$ through the chain measurements are expressed in the form of modulated clutter spatial density. The modulated clutter spatial density $\tilde{P}_i^s(z_{i,n})$ in (2) satisfies

$$\tilde{P}_i^s(z_{i,n}) = \rho \left\{ 1 + \sum_{l=0}^{m_i^s} R_{i,j}^s(z_{i,n}) \right\}, \quad (4)$$

where $T_i$ is the set of the indices of the tracks that share $z_{i,n}$ with the root track, and $R_{i,j}^s(z_{i,n})$ is the ratio of aposteriori probability that the chain measurement is from track $\tau_j$ and the sum of aposteriori probabilities that measurements other than $z_{i,n}$ are from $\tau_j$, and also including the probability that no measurement is a detection of $\tau_j$. A branch that connects the root track and a track in the level 1 is further extended to a track in level 2 by a new chain measurement. A measurement can be selected as the chain measurement only once in a branch. The chain measurements selected in a branch cannot be selected again to extend the branch to a track in the upper level. The chain measurement is used for calculation of the modulated clutter spatial density between the tracks in which it plays a role as the chain measurement, and it is no longer involved in any calculation executed in the extended branch thereafter. Note that if $z_{i,n} \notin Z^s$, then $R_{i,j}^s(z_{i,n}) = 0$. In (4) $R_{i,j}^s(z_{i,n})$ equals

$$R_{i,j}^s(z_{i,n}) = \frac{P_o^r \psi_i^s \tilde{P}_{i,j}^s}{(1 - P_o^r \psi_i^s) + \sum_{i=1}^{m_i^s} P_o^r \psi_i^s \tilde{P}_{i,j}^s / \tilde{P}_i^s(z_{i,n})}, \quad (5)$$

where $\tilde{P}_{i,j}^s(z_{i,n})$ is the modulated clutter spatial density that takes into account of the effect of tracks in the level 2 that share $z_{i,n}$ in common excluding the ancestor tracks, $\tau_i$ and $\tau_j$ for this branch. We denote the set of ancestor tracks as $\eta = \{ \tau, \tau_j \}$ and the collection of the track indices as $\alpha = \{ i, r \}$. The subscript $i$ stands for the collection of indices of the chain measurements of the branch such that $\xi = \{ n, l \}$. $\tilde{P}_{i,j}^s(z_{i,j})$ in (5) equals

$$\tilde{P}_{i,j}^s(z_{i,j}) = \rho \left\{ 1 + \sum_{a=1}^{T_i} \sum_{b=1}^{T_j} R_{i,a}^s(z_{i,j}) \right\}, \quad (6)$$

where $T_i$ is the set of indices of the tracks that share $z_{i,j}$ in common excluding the ancestor tracks $\tau_i$ and $\tau_j$. Note that if $z_{i,j} \notin Z^s$, then $R_{i,a}^s(z_{i,j}) = 0$. If $z_{i,j} \in Z^s$, then $z_{i,j}$ is the chain measurement between $\tau_i$ and $\tau_j$. Denote by $\xi' = \{ \xi, i' \}$ in this branch and $\eta' = \{ \eta, i' \}$ then $R_{i,a}^s(z_{i,j})$ of (6) equals
\[ R_{y_i}^{[2]}(z_{i,j}) = \left( 1 - P_{b}^{i} P_{c}^{i} \frac{P_{d}^{i}}{P_{e}^{i}} \right) \sum_{z_{i,k} \in \mathcal{Z}_{i}} \frac{P_{d}^{i}}{P_{e}^{i}} \left( \frac{\mathcal{G}_{i}^{j}}{\rho} \right) \left( \frac{\mathcal{G}_{i}^{j}}{\rho} \right) . \] (7)

This procedure continues until we can no longer find an upper level by the rule. The maximum achievable level of iJIPDA is at most \( N - 1 \) for a cluster of \( N \) targets so that JIPDA can be achieved by iJIPDA up to level \( N - 1 \) or less. The modulated clutter spatial densities at the final level become \( \rho \). The association probability of \( \beta_{i,j}^{o} \) in (1) contains all the branches from the root track \( \tau_{i} \) to the tracks in the final level. By disconnecting branches in the upper level, we can obtain approximate association probabilities. For example, if we disconnect the root track from the tracks in the level 1, the approximation is equivalent to IPDA, and this approximation is called iJIPDA up to level 0, iJIPDA-0. Disconnection can be done by letting \( \hat{\rho}_{i}^{j}(z_{i,j}) = \rho \) in (1) and (2). The iJIPDA-1 algorithm is obtained by disconnecting the branches between the level 1 and the level 2. This is equivalent to let \( \hat{\rho}_{i}^{j}(z_{i,j}) \) in (5) be \( \rho \). In a similar manner, we can obtain iterative approximations of JIPDA up to a designated level. Since the level of iJIPDA required to achieve JIPDA is finite, the number of iterative applications of the IPDA-like algorithm is finite to achieve the performance of JIPDA. The level for approximation can be determined according to tracking environments governed by number of targets, clutter spatial density and computational resources. An example of application of the proposed algorithm is listed in Appendix.

The target existence probability of \( \tau_{i} \) is updated by

\[ \psi_{i}^{j} = \frac{\left( 1 - \delta_{i}^{j} \mathcal{G}_{i}^{j} \right)}{1 - \delta_{i}^{j} \mathcal{G}_{i}^{j}} , \] (8)

where \( \delta_{i}^{j} \) is defined as

\[ \delta_{i}^{j} = \frac{P_{b}^{i} \left( P_{c}^{i} - \sum_{z_{i,k} \in \mathcal{Z}_{i}} \frac{P_{d}^{i}}{P_{e}^{i}} \left( \frac{\mathcal{G}_{i}^{j}}{\rho} \right) \left( \frac{\mathcal{G}_{i}^{j}}{\rho} \right) \right) . \] (9)

IV. SIMULATION RESULTS

We compare proposed iJIPDA algorithm with the IPDA [6], JIPDA [7] and LM-IPDA [14][15] algorithms with respect to the false track discrimination and the track retention performance in a cluttered environment with 8-target crossing trajectories. A 2-dimensional surveillance situation depicted in Fig. 1 in considered. The surveillance region is 1000m long and 1000m wide. The false measurements follow a Poisson distribution with a uniform clutter density \( \rho = 10^{-4}/\text{scan/m}^2 \) so that on the average 100 false measurements are taken per scan.

![Figure 1. Target Trajectories](image)

In this 8-target scenario, each target has a uniform straight line trajectory with a constant speed of 22.5m/s. At each simulation run, a small random velocity is added to the initial velocity of each target so that they do not cross at the same point but are still close enough to create a cluster. Targets cross this point at scan time 20. The probability of detection \( P_{d} = 0.9 \) for each target. The simulation consists of 300 Monte Carlo runs, 40 scans each and sampling time \( T = 1\text{s} \). The gating probability \( P_{e} = 0.99 \). The process noise covariance is

\[ Q = 0.75 I_{2} \otimes \begin{bmatrix} T^{4}/4 & T^{3}/2 \\ T^{3}/2 & T^{2} \end{bmatrix} \text{m}^2/\text{s}^4 \] (10)

Where \( \otimes \) denotes the tensor (Kronecker) matrix product, and \( I_{2} \) denotes the two-dimensional identity matrix. The measurement noise covariance \( R = 25I_{m} \text{m}^2 \). Tracks are initialized by the two point differencing [16] with initial probability of target existence equal to 0.1. The termination threshold is set to be 0.006.

The target retention statistics are obtained by identifying the confirmed true tracks at scan 14. This identification is checked again at scan 35, and the following statistics are obtained and accumulated with the following measures:

- \( n \text{Cases} \): total number of cases of target being followed by a confirmed track at scan 14.
• nOK: total number of tracks counted in nCases and still following the original target at scan 35.
• nSwitched: total number of tracks counted in nCases and which end up following a different target at scan 35.
• nLost: total number of tracks counted in nCases and not following any target at scan 35.
• nMerged: total number of tracks lost due to merging among tracks counted in nCases between scans 14 and 35.
• nResult[CT]: total number of targets being followed by a confirmed track at the last scan.
• C/F Track: total number of confirmed false tracks during the simulation experiment

The target retention statistics are summarized in Table I.

<table>
<thead>
<tr>
<th>Confirmed Threshold</th>
<th>IPDA</th>
<th>LM-IPDA</th>
<th>JIPDA-1</th>
<th>JIPDA-2</th>
<th>JIPDA-3</th>
<th>JIPDA</th>
</tr>
</thead>
<tbody>
<tr>
<td>nCases</td>
<td>895</td>
<td>2073</td>
<td>1904</td>
<td>2204</td>
<td>2204</td>
<td>2205</td>
</tr>
<tr>
<td>nOK</td>
<td>648</td>
<td>2015</td>
<td>1789</td>
<td>2163</td>
<td>2176</td>
<td>2172</td>
</tr>
<tr>
<td>nSwitched</td>
<td>154</td>
<td>32</td>
<td>40</td>
<td>18</td>
<td>10</td>
<td>11</td>
</tr>
<tr>
<td>nLost</td>
<td>13</td>
<td>22</td>
<td>60</td>
<td>20</td>
<td>15</td>
<td>15</td>
</tr>
<tr>
<td>nMerged</td>
<td>80</td>
<td>4</td>
<td>15</td>
<td>3</td>
<td>3</td>
<td>7</td>
</tr>
<tr>
<td>nResult[CT]</td>
<td>1954</td>
<td>2381</td>
<td>2372</td>
<td>2385</td>
<td>2387</td>
<td>2385</td>
</tr>
<tr>
<td>C/F Track</td>
<td>59</td>
<td>55</td>
<td>54</td>
<td>56</td>
<td>56</td>
<td>56</td>
</tr>
</tbody>
</table>

The confirmation thresholds for each algorithm are adjusted to have almost the same number of confirmed false tracks across the algorithms.

True track confirmation rates over time are presented in Fig. 2. Together with the number of confirmed false tracks they illustrate each tracker’s ability to correctly distinguish between true and false tracks.

The average CPU times per track in ms used to calculate 1 recursion cycle \( T = 1s \) for each algorithm on a standard platform (3.2GHz Intel PC, running Windows XP, C++ Program) are summarized in Table II.

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>CPU Time per Track for 1 cycle</th>
</tr>
</thead>
<tbody>
<tr>
<td>IPDA</td>
<td>0.0508</td>
</tr>
<tr>
<td>LM-IPDA</td>
<td>0.0814</td>
</tr>
<tr>
<td>JIPDA-1</td>
<td>0.0594</td>
</tr>
<tr>
<td>JIPDA-2</td>
<td>0.0894</td>
</tr>
<tr>
<td>JIPDA-3</td>
<td>0.6836</td>
</tr>
<tr>
<td>JIPDA</td>
<td>46251.292</td>
</tr>
</tbody>
</table>

In this application the JIPDA cannot be used in real-time. Increasing the level of JIPDA from zero, we improve the track discrimination and the track retention performance. For the simulation environment described in this section iJIPDA-2 and iJIPDA-3 have similar performance to JIPDA and may be used in real time on the host system. Their performances significantly improve upon IPDA and LM-IPDA.

V. CONCLUSIONS

This paper presents an iterative implementation of the JIPDA algorithm which results in a recursive form of the IPDA-like algorithm for single target tracking. Unlike JIPDA, the proposed algorithm can be used in parallel computation architecture without forming the track-to-measurement assignment matrix generated by enumeration of all possible joint events. By adjusting the level, the proposed algorithm adjusts its performance. The algorithm can be made as simple as the IPDA algorithm and as complete as the JIPDA algorithm. In between these two extremes, the application may adjust the number of levels to suit the situation and the available computation resources.

The simulation study of 8-target crossing in clutter indicates that the proposed algorithm with the level 2 or 3 is shown to be compatible with JIPDA in track discrimination and retention performance but with much less computational load. JIPDA in this scenario is shown to be computationally not feasible due to exorbitant computational cost.

APPENDIX

In this Appendix we detail the iJIPDA data association calculation using a cluster in a 2-dimensional multi-target tracking situation that consists of 3 tracks and 3 measurements as shown in Fig. 3. For this cluster, there are 22 feasible joint events. For the cluster, the branches of iJIPDA for
calculation of the data association probabilities of the track $\tau_i$ are formed as Fig. 4. This tree picture at Fig. 4 is repeated for every track in the cluster at the root.

Figure 3. Example cluster

$\tau_i$ is in the root level and selects 2 measurements, $z_{k,1}$ and $z_{k,2}$, is the chain measurement between $\tau_i$, $\tau_1$, and $\tau_2$, while $z_{k,3}$ is the chain measurement between $\tau_i$ and $\tau_3$. Each chain measurement connects $\tau_i$ to a track in the level 1 by forming a branch. Every measurement of a track in the level 1 is tested for eligibility of a chain measurement that connects the track to the tracks to be located in the level 2. In the eligibility test, one should apply the rules that the chain measurements selected in a branch cannot be selected again to extend the branch to a track in the upper level, and that the tracks involved in a branch are allocated only once in the branch extended from the root level to the final level.

Figure 4. Branches for association probability calculation

The data association probability of $\tau_i$ to $z_{k,1}$ and $z_{k,2}$ are obtained by (1) as

$$\beta_{z_{k,1}}^i = \frac{P_0^i p_{k,1}^i / \bar{R}_i^i (z_{k,1})}{\Delta} , \quad \text{(A-1)}$$

$$\beta_{z_{k,2}}^i = \frac{P_0^i p_{k,2}^i / \bar{R}_i^i (z_{k,2})}{\Delta} , \quad \text{(A-2)}$$

where

$$\Delta = 1 - P_0^i p_{k,1}^i + P_0^i p_{k,2}^i / \bar{R}_i^i (z_{k,1}) + P_0^i p_{k,2}^i / \bar{R}_i^i (z_{k,2}) , \quad \text{(A-3)}$$

and

$$\bar{R}_i^i (z_{k,1}) = \rho \left( 1 + R_{z_{k,1}}^i (z_{k,1}) + R_{z_{k,1}}^i (z_{k,1}) \right) , \quad \text{(A-4)}$$

$$\bar{R}_i^i (z_{k,2}) = \rho \left( 1 + R_{z_{k,2}}^i (z_{k,2}) \right) , \quad \text{(A-5)}$$

As an approximation, if we equate $R_{z_{k,1}}^i (z_{k,1})$, $R_{z_{k,1}}^i (z_{k,1})$, and $R_{z_{k,1}}^i (z_{k,1})$ to zero, then the data association probabilities in (A-1) and (A-2) are equal the IPDA ones; we term this approximation of JIPDA by jIPDA-0. The probability ratios in the above equations are

$$R_{z_{k,1}}^i (z_{k,1}) =$$

$$\frac{P_0^i \bar{R}_i^i p_{k,1}^i}{\rho \left( 1 - P_0^i p_{k,1}^i + P_0^i \bar{R}_i^i p_{k,2}^i / \bar{R}_i^i (z_{k,1}) + P_0^i \bar{R}_i^i p_{k,2}^i / \bar{R}_i^i (z_{k,1}) \right) , \quad \text{(A-6)}$$

$$R_{z_{k,2}}^i (z_{k,2}) =$$

$$\frac{P_0^i \bar{R}_i^i p_{k,2}^i}{\rho \left( 1 - P_0^i p_{k,2}^i + P_0^i \bar{R}_i^i p_{k,2}^i / \bar{R}_i^i (z_{k,2}) \right) , \quad \text{(A-7)}$$

$$R_{z_{k,1}}^i (z_{k,1}) =$$

$$\frac{P_0^i \bar{R}_i^i p_{k,1}^i}{\rho \left( 1 - P_0^i p_{k,1}^i + P_0^i \bar{R}_i^i p_{k,2}^i / \bar{R}_i^i (z_{k,1}) + P_0^i \bar{R}_i^i p_{k,2}^i / \bar{R}_i^i (z_{k,1}) \right) , \quad \text{(A-8)}$$
where
\[
\hat{P}_{1,2}^{z_1} (z_{1,2}) = \rho, \quad (A-9)
\]
\[
\hat{P}_{2,3}^{z_2} (z_{1,3}) = \rho \left( 1 + R_{2,1}^{z_2} (z_{1,2}) \right), \quad (A-10)
\]
\[
\hat{P}_{3,2}^{z_3} (z_{1,3}) = \rho \left( 1 + R_{3,1}^{z_3} (z_{1,2}) \right), \quad (A-11)
\]
\[
\hat{P}_{1,3}^{z_1} (z_{1,3}) = \rho \left( 1 + R_{1,2}^{z_1} (z_{1,2}) \right), \quad (A-12)
\]
\[
\hat{P}_{2,1}^{z_2} (z_{1,3}) = \rho \left( 1 + R_{2,1}^{z_2} (z_{1,2}) \right). \quad (A-13)
\]

Note that if we equate the probability ratios in (A-10)–(A-13) to zero, the algorithm becomes iJPDA-1. The probability ratios in (A-10)–(A-13) become

\[
R_{1,3}^{z_1} (z_{1,3}) = \frac{P_D^{z_1} \varphi_{1,3} p_{1,3}}{\rho \left( 1 - P_D^{z_1} P_D^{z_2} \varphi_{1,2} \right)}, \quad (A-14)
\]
\[
R_{2,3}^{z_2} (z_{1,3}) = \frac{P_D^{z_2} \varphi_{1,3} p_{1,3}}{\rho \left( 1 - P_D^{z_1} P_D^{z_2} \varphi_{1,2} \right) + P_D^{z_2} \varphi_{2,3} p_{2,3}}, \quad (A-15)
\]
\[
R_{3,2}^{z_3} (z_{1,3}) = \frac{P_D^{z_3} \varphi_{1,3} p_{1,3}}{\rho \left( 1 - P_D^{z_1} P_D^{z_2} \varphi_{1,2} \right) + P_D^{z_2} \varphi_{2,3} p_{2,3}}, \quad (A-16)
\]
\[
R_{2,1}^{z_2} (z_{1,3}) = \frac{P_D^{z_2} \varphi_{1,3} p_{1,3}}{\rho \left( 1 - P_D^{z_1} P_D^{z_2} \varphi_{1,2} \right) + P_D^{z_2} \varphi_{2,3} p_{2,3}}, \quad (A-17)
\]

Now we have iJPDA-2 which is equivalent to JIPDA for \( r_1 \).

REFERENCES


