Yun ZHU, Shuang LIANG, Xiaojun WU, Honghong YANG, 2021. A random finite set based joint probabilistic data association filter with non-homogeneous Markov chain. *Frontiers of Information Technology & Electronic Engineering,* 22(8):1114-1126. https://doi.org/10.1631/FITEE.2000209

A random finite set based joint probabilistic data association filter with non-homogeneous Markov chain

Key words: Target tracking; Filtering theory; Random finite set theory; Bayes methods; Markov chain

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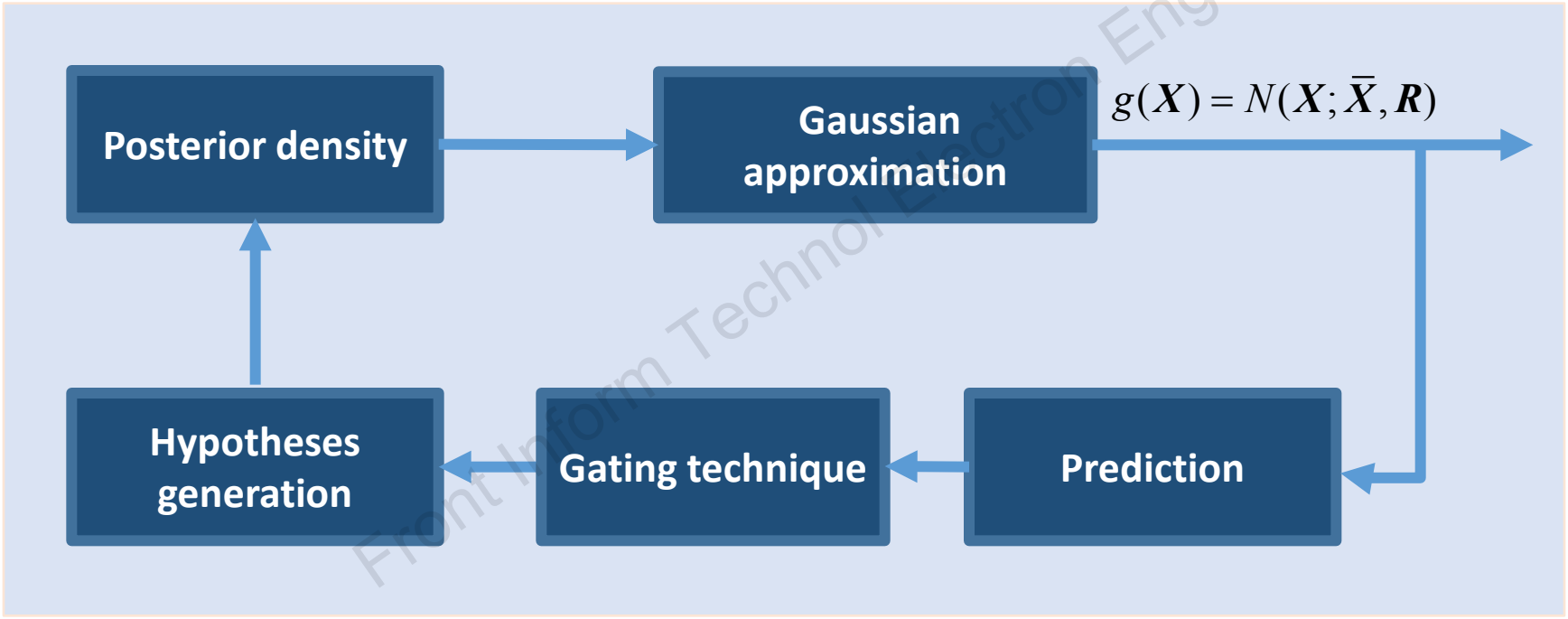
JPDA filter



Block diagram of JPDA

Motivation

The posterior density of JPDA can be modeled as a Gaussian mixture

$$f(\boldsymbol{X}) = \sum_{h=1}^{N_{\mathrm{H}}} P(\theta_h) N(\boldsymbol{X}; \boldsymbol{x}_h, \boldsymbol{P}_h)$$

where each Gaussian component corresponds to one of the possible hypotheses, $\boldsymbol{x}_h$ is the stacked vector of the updated target states in hypothesis θ_h and $\boldsymbol{P}_h$ is the state covariance of $\boldsymbol{x}_h$. Assuming that the targets are independent of each other, $\boldsymbol{P}_h$ can be denoted as

$$\boldsymbol{P}_h = \mathrm{diag}\{\boldsymbol{P}_h^1, \boldsymbol{P}_h^2, \cdots, \boldsymbol{P}_h^n\}$$

It is assumed that covariance matrices are strictly positive definite (not merely nonnegative definite). Then another description of the posterior density is

$$p(\boldsymbol{X}) = \sum_{h=1}^{N_{\mathrm{H}}} \frac{P(\theta_h)}{\sqrt{\det(2\pi \boldsymbol{P}_h)}} \exp\left[-\frac{1}{2} (\boldsymbol{X} - \boldsymbol{x}_h)^{\mathrm{T}} \boldsymbol{P}_h^{-1} (\boldsymbol{X} - \boldsymbol{x}_h) \right]$$

Motivation

Depending on the choice of the posterior density, the Gaussian approximation can be more or less accurate. It is assumed that the degenerate Gaussian mixture with a single component is given by

$$g(\boldsymbol{X}) = N(\boldsymbol{X}; \bar{\boldsymbol{X}}, \boldsymbol{R}) = \frac{1}{\sqrt{\det(2\pi \boldsymbol{R})}} \exp\left[-\frac{1}{2}(\boldsymbol{X} - \bar{\boldsymbol{X}})^{\mathrm{T}} \boldsymbol{R}^{-1} (\boldsymbol{X} - \bar{\boldsymbol{X}})\right]$$

where $\bar{\boldsymbol{X}}$ and $\boldsymbol{R}$ are computed as

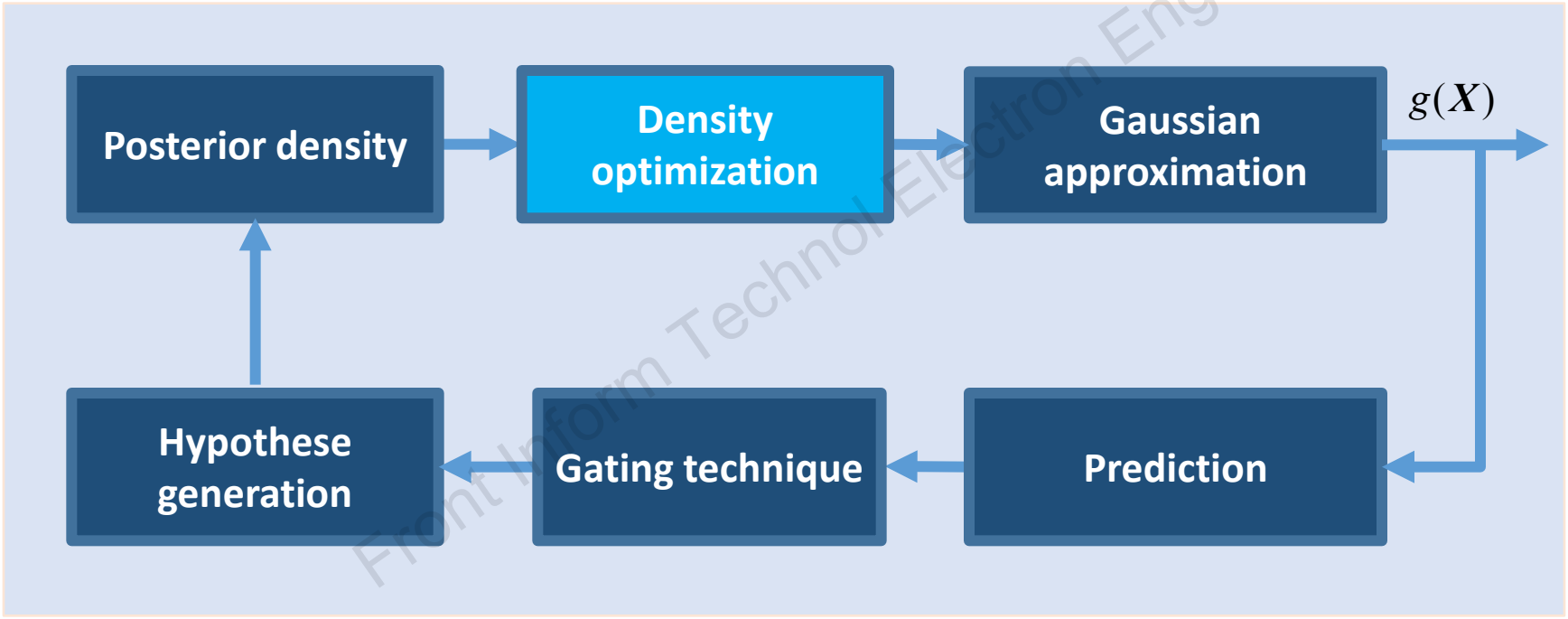
$$\bar{\boldsymbol{X}} = E_{p(\boldsymbol{X})}\{\boldsymbol{X}\}$$

$$\boldsymbol{R} = \mathrm{Cov}_{p(\boldsymbol{X})}\{\boldsymbol{X}\}$$

To make the posterior density be more accurately approximated by a Gaussian density, it is possible to switch the ordered posterior density in the corresponding RFS family, when target identity is irrelevant.

Svensson L, Svensson D, Guerriero M, Willett P, 2011. Set JPDA filter for multitarget tracking. *IEEE Trans Signal Process*, 59(10):4677-4691.

Method



Block diagram of NNSJPDA

Method

How to conduct the optimization?

First, all possible permutations of the joint target state in each hypothesis are enumerated. In hypothesis θ_h, the density for all possible permutations is denoted as

$$f_h(\boldsymbol{X}) = \sum_{\pi \in \Pi_n} N(\boldsymbol{x}_h^{\pi}, \boldsymbol{P}_h^{\pi})$$

where Π_n is the set of all possible permutations of the joint target and $n!$ means calculating the factorial of *n*, $\boldsymbol{x}_h^{\pi}$ is the joint state vector in permutation of π, and $\boldsymbol{P}_h^{\pi}$ is the covariance matrix for $\boldsymbol{x}_h^{\pi}$.

Method

How to conduct the optimization?

Second, the "nearness" between Gaussian components of $g(X)$ and $f(X)$ are measured in pairs. The component corresponding to the smallest dissimilarity with $g(X)$ is accepted and others are rejected. We require a suitable scalar measure to describe the dissimilarity and a possible one is the Euclidean distance.

The Euclidean distance between $f_h^{\pi}(\boldsymbol{X}) = N(\boldsymbol{x}_h^{\pi}, \boldsymbol{P}_h^{\pi})$ and $g(\boldsymbol{X}) = N(\boldsymbol{X}; \bar{\boldsymbol{X}}, \boldsymbol{R})$ is expressed as

$$L_{E\mathrm{uc}} = \sqrt{(\boldsymbol{x}_h^{\pi} - \bar{\boldsymbol{X}})^{\mathrm{T}} (\boldsymbol{x}_h^{\pi} - \bar{\boldsymbol{X}})}$$

This distance depends only on the means of the components, but not on their covariance matrices.

Method

How to conduct the optimization?

It is necessary to find a measure of dissimilarity which not only considers the means of the components but also takes the covariance matrices into account. The measure of "nearness" used in the paper is given as

$$d_{\mathrm{KL}}[f_h^{\pi}(\boldsymbol{X}) \,\|\, g(\boldsymbol{X})] = \frac{1}{2}\left[2\log\left(\det(\boldsymbol{R}_h^{\pi})\right) - \log\left(\det(\boldsymbol{P}_h^{\pi})\right) - \log\left(\det(\boldsymbol{R})\right)\right]$$

where

$$\boldsymbol{R}_h^{\pi} = \boldsymbol{P}_h^{\pi} + \boldsymbol{R} + (\boldsymbol{x}_h^{\pi} - \bar{\boldsymbol{X}})(\boldsymbol{x}_h^{\pi} - \bar{\boldsymbol{X}})^{\mathrm{T}}$$

This formula has two important properties:

1) The function is symmetric;
2) The closer $f_h^{\pi}(\boldsymbol{X})$ is to $g(\boldsymbol{X})$, the smaller the distance $d_{\mathrm{KL}}[f_h^{\pi}(\boldsymbol{X}) \,\|\, g(\boldsymbol{X})]$ is.

Method

How to conduct the optimization?

In each hypothesis, the permutation with the smallest $d_{\mathrm{KL}}[f_h^{\pi}(\boldsymbol{X}) \| g(\boldsymbol{X})]$ is selected:

$$\boldsymbol{\pi} = \arg\min_{\boldsymbol{\pi}} d_{\mathrm{KL}}\left[f_h^{\pi}(\boldsymbol{X}) \| g(\boldsymbol{X}) \right], \ \boldsymbol{\pi} \in \Pi_n,$$

Once the permutations in all hypotheses are determined, the single Gaussian component is updated using the new Gaussian mixture.

The approximation should proceed until the algorithm converges; i.e., the single Gaussian component is fixed.

Method

The recursion of the probabilities of labels:

In the posterior density optimization procedure, the output is the best permutation of targets in each association event. Each event is associated with a posterior probability, and this probability also carries the information about the permutation of target labels. We define the probability of a target label at time *k* as the probability of a label vector $\boldsymbol{L}_j$, i.e.,

$$P_k^L(\boldsymbol{L}_j) \triangleq \Pr\{\boldsymbol{L}_k = \boldsymbol{\pi}_j \boldsymbol{L}_0 \mid \boldsymbol{Z}_k\},\ \ j = 1, 2, \cdots, n!$$

Assuming that all transition probabilities are known, the recursion of $P_k^L(\boldsymbol{L}_j)$ is

$$P_k^L(\boldsymbol{L}_j) = \sum_{i=1}^{n!} t_{k|k-1}^{ij} P_{k-1}^L(\boldsymbol{L}_i)$$

Method

The recursion of the probabilities of labels:

The vector $\boldsymbol{P}_k^L = [P_k^L(\boldsymbol{L}_1), P_k^L(\boldsymbol{L}_2), \ldots, P_k^L(\boldsymbol{L}_{n!})]^{\mathrm{T}}$ can be updated as a matrix product:

$$\boldsymbol{P}_k^L = \boldsymbol{T}_{k|k-1}\boldsymbol{P}_{k-1}^L$$

where

$$\boldsymbol{T}_{k|k-1} = \begin{bmatrix} t_{k|k-1}^{11} & t_{k|k-1}^{12} & \cdots & t_{k|k-1}^{1n!} \\ t_{k|k-1}^{21} & t_{k|k-1}^{22} & \cdots & t_{k|k-1}^{2n!} \\ \vdots & \vdots & & \vdots \\ t_{k|k-1}^{n!1} & t_{k|k-1}^{n!2} & \cdots & t_{k|k-1}^{n!n!} \end{bmatrix}$$

is an $n! \times n!$ transition matrix with element (i, j) being $t_{k|k-1}^{ij}$. With the propagation of $\boldsymbol{P}_k^L$ the approach has the ability to preserve the uncertainties of the target labels.

Method

The recursion of the probabilities of labels:

The information of the target label vectors can be preserved during the posterior density switching procedure. This information is used to propagate the distribution of the target label vectors, and the propagation is modeled as a non-homogeneous Markov chain. We prove that the chain is doubly stochastic and ergodic, and that it always converges to the equilibrium state whatever the initial distribution is.

Results

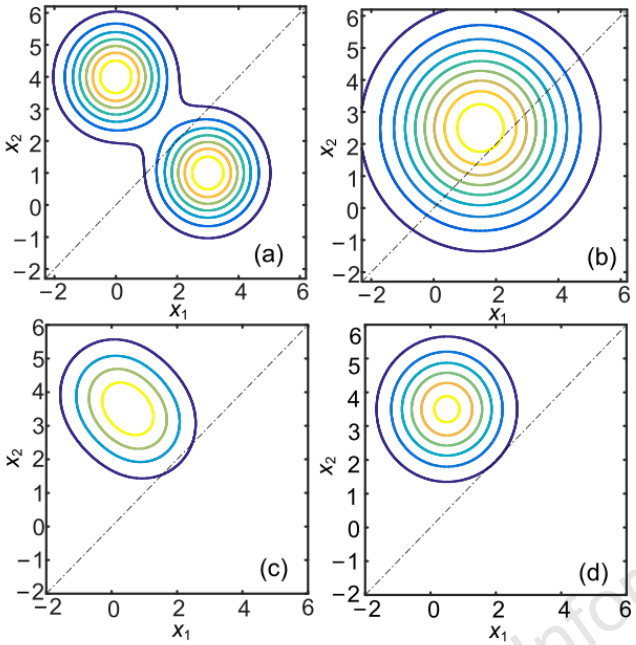


Fig. 1 Posterior density and its single Gaussian density: (a) posterior density of iteration 0; (b) single Gaussian of iteration 0; (c) posterior density of iteration 2; (d) single Gaussian of iteration 2

The example illustrates the posterior density optimization. It is assumed that there are two Gaussian distributed one-dimensional targets which generate two data association events. The initial posterior density $f^0(\boldsymbol{X})$ is

$$\begin{cases} P(\theta_1)=0.5, \\ \theta_1 \sim N\left(\boldsymbol{X};\begin{bmatrix}3\\1\end{bmatrix},\begin{bmatrix}1 & 0\\0 & 1\end{bmatrix}\right), \end{cases} \quad \begin{cases} P(\theta_2)=0.5, \\ \theta_2 \sim N\left(\boldsymbol{X};\begin{bmatrix}0\\4\end{bmatrix},\begin{bmatrix}1 & 0\\0 & 1\end{bmatrix}\right) \end{cases}$$

The single Gaussian approximation is

$$g^0(\boldsymbol{X}) = N\left(\boldsymbol{X};\begin{bmatrix}1.5\\2.5\end{bmatrix},\begin{bmatrix}3.25 & 0\\0 & 3.25\end{bmatrix}\right).$$

We plot $f^0(\boldsymbol{X})$ and $g^0(\boldsymbol{X})$ in Figs. 1a and 1b, respectively. The resulting densities are plotted in Figs. 1c and 1d, respectively. It is obvious that the initial densities are very different from each other, and that the similarity between the resulting densities becomes much higher than it was initially.

Results

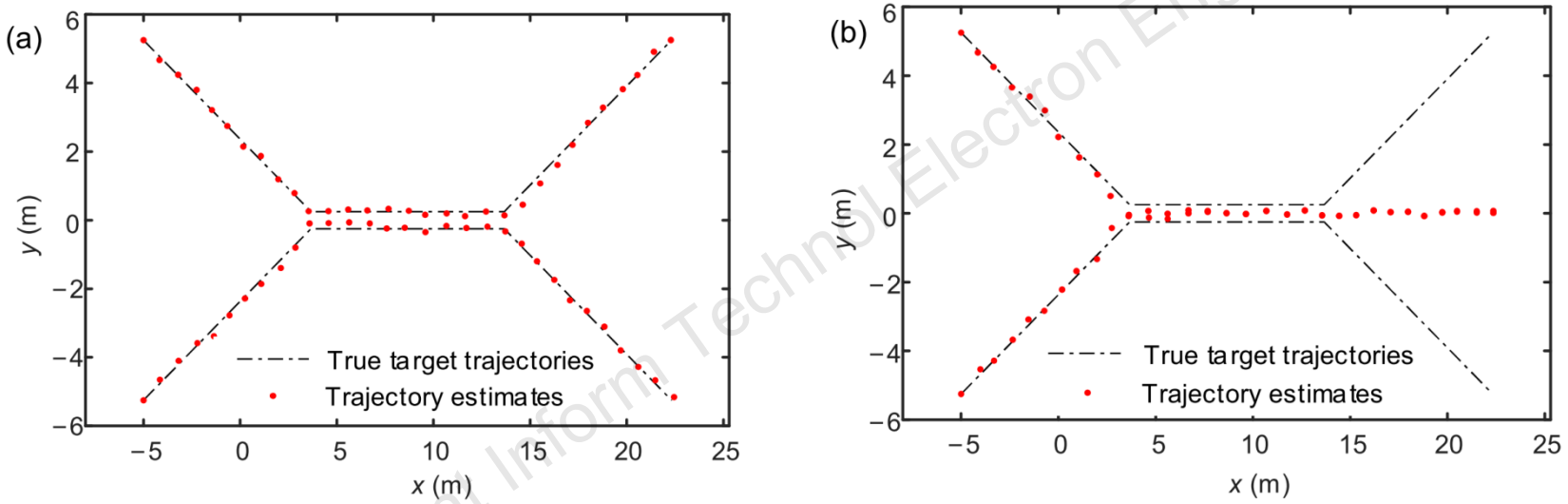


Fig. 2 True and estimated target trajectories: (a) output of NNSJPDA; (b) output of JPDA

Results

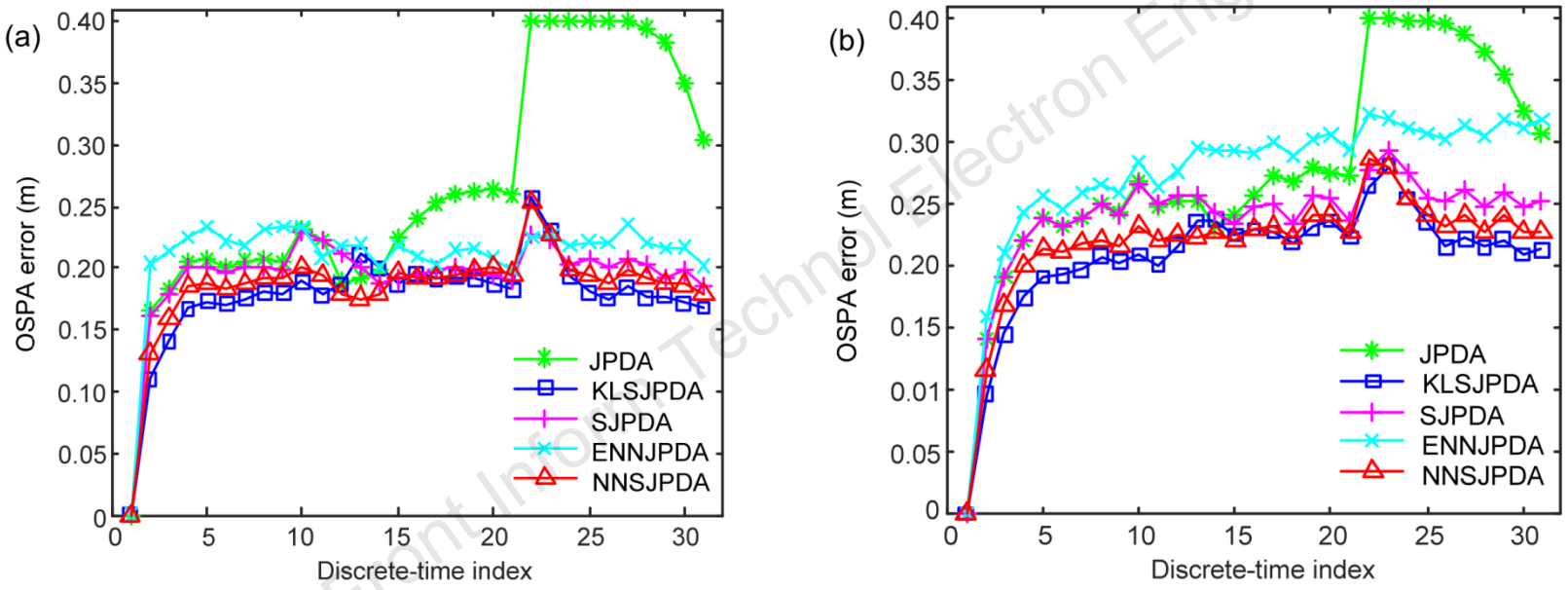


Fig. 3 Evaluation of the JPDA, ENNJPDA, SJPDA, KLSJPDA, and NNSJPDA filters for different detection probabilities: (a) P_d=1; (b) P_d=0.75

Results

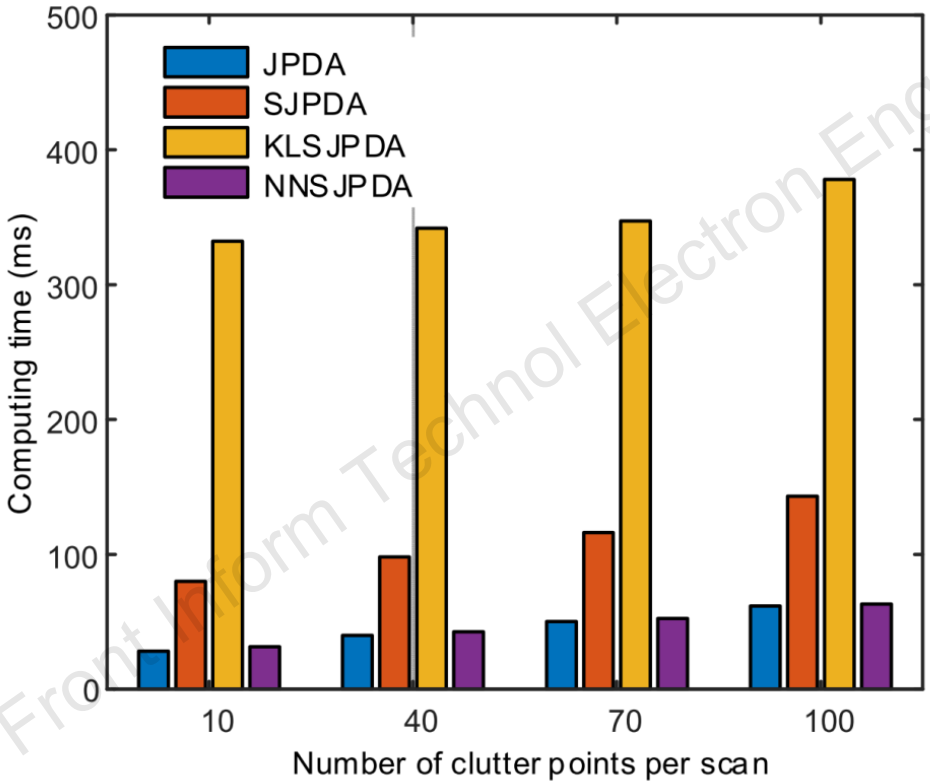


Fig. 4 Averaged computing time against the averaged number of clutter points per scan

Conclusions

To accurately approximate the posterior density of the NNSJPDA filter with a single Gaussian density, the posterior density is optimized by switching within its RFS family. Specifically, posterior density optimization is accomplished by switching the posterior densities of all possible data association events in parallel, aiming to minimize the KL divergence between the posterior density and the single Gaussian density. It is further shown that the information of the target label vectors can be pre-served during the posterior density switching procedure. This information is used to propagate the distribution of the target label vectors, and the propagation is modeled as a non-homogeneous Markov chain. The chain is doubly stochastic and ergodic, and always converges to the equilibrium state whatever the initial distribution is.