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Probabilistic PCR6 fusion rule

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Abstract: *This chapter defines and implements a non-Bayesian fusion rule for combining densities of probabilities, derived from imprecise knowledge. This rule is the restriction to a strict probabilistic paradigm of the Proportional Conflict Redistribution rule no 6 (PCR6) developed in the DSmT framework for fusing basic belief assignments. A sampling method for probabilistic PCR6 (p-PCR6) is defined. It is shown that p-PCR6 allows to keep the modes of local densities and preserve as much as possible the whole information inherent to each densities to combine. In particular, p-PCR6 is able of maintaining multiple hypotheses/modes, when they are too distant for fusion, contrariwise to classical technique. The question of sequential filtering by p-PCR6 is addressed, thus implying the necessity to handle the redundancy of the information.*

Notations

- $\delta[x = y]$ is the Dirac distribution of variable x on value y ,
- $I[b]$, function of Boolean b, is defined by $I[\textbf{true}] = 1$ and $I[\textbf{false}] = 0$. In particular, $I[x = y]$ could be seen as a discrete counterpart of the Dirac $\delta[x = y]$.

4.1 Introduction

Bayesian inference is a powerful principle for modeling and manipulating probabilistic information. In many cases, Bayesian inference is considered as an optimal and legitimate rule for inferring such information. Bayesian filters for example, and their approximations by means of sequential Monte-Carlo, are typically regarded as optimal filters [1, 2, 7].

However, Bayesian methods need strong hypotheses, in particular about the information prior and the independence prior. A degradation of the performance of Bayesian filter occurs if the filter is not correctly initialized or updated, in accordance to the models in use. Being given a model of the system kinematic and of the measurement process, the main issue is to develop filtering methods which are sufficiently robust against the bias at the initialization as well as error in modeling. In this paper, a non-Bayesian rule for fusing the probabilistic information is proposed. This rule, denoted p-PCR6, is the restriction to the probabilistic paradigm of the Proportional Conflict redistribution rule no.6 (PCR6) which has been proposed in [12] for combining basic belief assignments. p-PCR6 is also an extension of discrete PCR6 version to its continuous probabilistic counterpart.

PCR6 has been first established for combining evidences (i.e. discrete belief assignments) in the DSmT framework. In particular, it has been designed in order to cope with highly conflicting and uncertain information. This rule could be considered in a probabilistic paradigm by restricting the basic belief assignment involved to only *probabilistic belief assignment*[1], and directly extended to densities of probabilities. This rule is non-Bayesian by nature. Although Bayesian techniques are widely well known and used in target tracking community (including authors works in tracking), it is interesting to see how such new approach can perform to estimate its real interest and potentiality.

[1]The denomination *probabilistic belief assignment* is preferred to *Bayesian belief assignment*, generally used in the literature, since we consider that Probability and Bayesian inference are distinguishable notions.

Surprisingly, it turns out through our works, that such approach is robust to an erroneous modeling: in particular, it is able of maintaining multiple hypotheses, when they are too distant for fusion. The resulting p-PCR6-based filter happens to be essentially non-linear, and has been implemented in our simulation using particle filtering techniques. In particular, the p-PCR6 multisensor filter developed here is based on a quite simple and direct implementation in terms of particles drawing and resampling. At the end of this chapter, the question of sequential filtering is addressed. In this case, it is necessary to take into account the redundancy of information over the time. Then, p-PCR6 is adapted in order to remove this redundancy.

Section 4.2 introduces the PCR6 rules, and establishes some results about probabilistic PCR6. A sampling method is deduced. Section 4.3 compares the results of the Bayesian rule and of probabilistic PCR6 on a simple example. On the basis of this comparison, some arguments about the robustness of PCR6 are given. Section 4.4 investigates the sequential filtering issue. Application of p-PCR6 to distributed filtering is provided as example. Section 4.5 concludes.

4.2 PCR6 formula for probabilities

4.2.1 Definition and justification of PCR6

The Proportional Conflict Redistribution rule no. 6 (PCR6) of combination [5] is an extension of rule PCR5 [10, 11]. These rules come from the necessity to manage precisely and efficiently the partial conflicts when combining conflicting and uncertain information expressed in terms of (quantitative) belief assignments. These rule have been proved useful and powerful in several applications where it has been used [12]. PCR5 and PCR6 are equivalent, when restricted to only two sources of information.

Let be given an universe of events Θ. A distribution of evidence over Θ is characterized by means of a basic belief assignment (bba) $m : \mathcal{P}(\Theta) \rightarrow \mathbb{R}^+$ such that:

$$m(\emptyset) = 0 \qquad \text{and} \qquad \sum_{X \subset \Theta} m(X) = 1 \ ,$$

where $\mathcal{P}(\Theta)$ is the set of subset of Θ.[2]

[2]In the general case, bba could also be defined over hyper-power sets (Dedekind's lattice) [12].

A bba typically represents the knowledge, which can be both uncertain and imprecise, that a sensor provides about its belief in the true state of the universe. The question then arising is *How to fuse the bba's related to multiple sensor responses?* The main idea is to corroborate the information of each sensor in a conjunctive way.

Example: Let's assume two sources with basic belief assignments m_1 and m_2 such that $m_1(A) = 0.6$, $m_1(A \cup B) = 0.4$ and $m_2(B) = 0.3$, $m_2(A \cup B) = 0.7$. The fused bba is then characterized in a conjunctive way by:

$$\begin{aligned} &m_\wedge(A \cap B) = m_1(A)m_2(B) = 0.18 \,, \\ &m_\wedge(A) = m_1(A)m_2(A \cup B) = 0.42 \,, \\ &m_\wedge(B) = m_1(A \cup B)m_2(B) = 0.12 \,, \\ &m_\wedge(A \cup B) = m_1(A \cup B)m_2(A \cup B) = 0.28 \,. \end{aligned}$$

The conjunctive consensus works well when there is no possibility of conflict. Now, make the hypothesis $A \cap B = \emptyset$. Then, it is obtained $m_\wedge(\emptyset) = 0.18$, which is not an acceptable result for a conventional interpretation of $\emptyset$ as a contradiction. Most existing rules solve this issue by redistributing the conflict $m_\wedge(\emptyset)$ over the other propositions. In PCR6, the partial conflicting mass $m_1(A)m_2(B)$ is redistributed to A and B only with the respective proportions $x_A = 0.12$ and $x_B = 0.06$, according to the proportionalization principle:

$$\frac{x_A}{m_1(A)} = \frac{x_B}{m_2(B)} = \frac{m_1(A)m_2(B)}{m_1(A) + m_2(B)} = \frac{0.18}{0.9} = 0.2 \,.$$

Basically, the idea of PCR6 is to transfer the conflicting mass only to the elements involved in the conflict and proportionally to their individual masses.

Some theoretical considerations and justifications already briefly aforementioned led to the following PCR6 combination rule. Being given two bba's m_1 and m_2, the fused bba m_{PCR6} according to PCR6, or equivalently to PCR5 in this case, is defined for any $X \in \mathcal{P}(\Theta) \setminus \{\emptyset\}$ by:

$$\begin{aligned} m_{\text{PCR5/PCR6}}(X) = m_\wedge(X) \\ + \sum_{\substack{Y \in \mathcal{P}(\Theta) \\ X \cap Y = \emptyset}} \left(\frac{m_1(X)^2 m_2(Y)}{m_1(X) + m_2(Y)} + \frac{m_2(X)^2 m_1(Y)}{m_2(X) + m_1(Y)} \right) \end{aligned} \quad (4.1)$$

where $m_\wedge(\cdot)$ corresponds to the conjunctive consensus:

$$m_\wedge(X) \triangleq \sum_{\substack{Y_1 \cap Y_2 = X \\ Y_1, Y_2 \in \mathcal{P}(\Theta)}} m_1(Y_1)m_2(Y_2) \,.$$

When fusing $s \geq 2$ sources of informations, characterized by the bba's m_1 to m_s, the fused bba is defined in [5] by:

$$m_{\text{PCR6}}(X) = m_{\wedge}(X) + \sum_{i=1}^{s} m_i(X)^2 \sum_{\substack{\bigcap_{k=1}^{s-1} Y_{\sigma_i(k)} \cap X = \emptyset \\ Y_{\sigma_i(1)}, \cdots, Y_{\sigma_i(s-1)} \in \mathcal{P}(\Theta)}} \left(\frac{\prod_{j=1}^{s-1} m_{\sigma_i(j)}(Y_{\sigma_i(j)})}{m_i(X) + \sum_{j=1}^{s-1} m_{\sigma_i(j)}(Y_{\sigma_i(j)})} \right) , \quad (4.2)$$

where $m_{\wedge}(\cdot)$ corresponds to the conjunctive consensus:

$$m_{\wedge}(X) \triangleq \sum_{\substack{Y_1 \cap \cdots \cap Y_s = X \\ Y_1, \cdots, Y_s \in \mathcal{P}(\Theta)}} \prod_{i=1}^{s} m_i(Y_i) ,$$

and the function σ_i counts from 1 to s avoiding i :

$$\sigma_i(j) = j \times I[j < i] + (j+1) \times I[j \geq i] .$$

4.2.2 Reformulation of PCR6

Definition (4.2) could be reformulated into a more intuitive expression.

$$m_{\text{PCR6}}(X) = m_{\wedge}(X) + \sum_{i=1}^{s} \sum_{\substack{\bigcap_{k=1}^{s} Y_k = \emptyset \\ Y_1, \cdots, Y_s \in \mathcal{P}(\Theta)}} \left(\frac{I[X = Y_i] \; m_i(Y_i) \prod_{j=1}^{s} m_j(Y_j)}{\sum_{j=1}^{s} m_j(Y_j)} \right) ,$$

and then:

$$m_{\text{PCR6}}(X) = m_{\wedge}(X) + \sum_{\substack{\bigcap_{k=1}^{s} Y_k = \emptyset \\ Y_1, \cdots, Y_s \in \mathcal{P}(\Theta)}} \prod_{i=1}^{s} m_i(Y_i) \; \frac{\sum_{j=1}^{s} I[X = Y_j] \; m_j(Y_j)}{\sum_{j=1}^{s} m_j(Y_j)} . \quad (4.3)$$

At last, a new formulation of PCR6 is derived for $X \in \mathcal{P}(\Theta) \setminus \{\emptyset\}$:

$$m_{\mathrm{PCR6}}(X) = \sum_{Y_1,\cdots,Y_s \in \mathcal{P}(\Theta)} \left(\prod_{i=1}^{s} m_i(Y_i) \right) F_{\mathrm{PCR6}}(X|Y_{1:s}) \ ,$$

where the function F_{PCR6} is defined by:

$$\begin{aligned} F_{\mathrm{PCR6}}(X|Y_{1:s}) &= I\left[\bigcap_{k=1}^{s} Y_k = X\right] + I\left[\bigcap_{k=1}^{s} Y_k = \emptyset\right] \frac{\sum_{j=1}^{s} I[X = Y_j]\ m_j(Y_j)}{\sum_{j=1}^{s} m_j(Y_j)} \\ &= \frac{\sum_{j=1}^{s} \left(I\left[\bigcap_{k=1}^{s} Y_k = X\right] + I\left[\bigcap_{k=1}^{s} Y_k = \emptyset\right] I[X = Y_j] \right) m_j(Y_j)}{\sum_{j=1}^{s} m_j(Y_j)} \ . \end{aligned} \quad (4.4)$$

When considering probabilistic densities instead of belief functions, the components $\prod_{i=1}^{s} m_i(Y_i)$ and $\frac{\sum_{j=1}^{s}\left(I\left[\bigcap_{k=1}^{s} Y_k=X\right]+I\left[\bigcap_{k=1}^{s} Y_k=\emptyset\right] I[X=Y_j]\right)\, m_j(Y_j)}{\sum_{j=1}^{s} m_j(Y_j)}$ have a straightforward interpretation. The first is interpreted as an independent generation of answers by each source of information. The second is interpreted as a random choice among the answers *or* the consensus, weighted by the respective evidences.

4.2.3 Definition of probabilistic PCR6 (p-PCR6)

In [12], Dezert and Smarandache proposed a probabilistic version of the PCR5 / PCR6 rule (4.1) for two sources, by restricting the bba's m_1 and m_2 to discrete probabilities P_1 and P_2 which are called then *probabilistic belief assignments* (or masse[1]). Probabilistic belief masses are bba's, which focal elements[3] consist only in elements of the frame Θ, i.e. the singletons only. When dealing with probabilistic belief assignments $m_1 \equiv P_1$ and $m_2 \equiv P_2$, the conjunctive consensus is restricted to the same singleton, so that $m_\wedge(X) = P_1(X)P_2(X)$.

[3]Focal elements are elements of $\mathcal{P}(\Theta)$ having a strictly positive mass.

As a consequence, the PCR5/PCR6 formula (4.1) for two sources reduces to:

$$P_{\text{PCR5/PCR6}}(X) = P_1(X)P_2(X) + P_1(X)\sum_{Y\in\Theta\setminus\{X\}}\frac{P_1(X)P_2(Y)}{P_1(X)+P_2(Y)} + P_2(X)\sum_{Y\in\Theta\setminus\{X\}}\frac{P_2(X)P_1(Y)}{P_2(X)+P_1(Y)}\,.$$

Now, it happens that:

$$P_1(X)P_2(X) = P_1(X)\frac{P_1(X)P_2(X)}{P_1(X)+P_2(X)} + P_2(X)\frac{P_2(X)P_1(X)}{P_1(X)+P_2(X)}\,,$$

and finally:

$$P_{\text{PCR5/PCR6}}(X) = P_1(X)\sum_{Y\in\Theta}\frac{P_1(X)P_2(Y)}{P_1(X)+P_2(Y)} + P_2(X)\sum_{Y\in\Theta}\frac{P_2(X)P_1(Y)}{P_2(X)+P_1(Y)}\,. \tag{4.5}$$

Of course, this formula generalizes in the case of PCR6 for any number of sources. Since:

$$m_\wedge(X) = \prod_{i=1}^{s} P_i(X) = \sum_{i=1}^{s} P_i(X)\frac{\prod_{i=1}^{s} P_i(X)}{\sum_{i=1}^{s} P_i(X)}$$

and, for $X, Y_{\sigma_i(k)} \in \Theta$,

$$\bigcap_{k=1}^{s-1} Y_{\sigma_i(k)} \cap X \neq \emptyset \text{ if and only if } Y_{\sigma_i(1)} = \cdots = Y_{\sigma_i(s)} = X\,, \tag{4.6}$$

it comes:

$$P_{\text{PCR6}}(X) = \sum_{i=1}^{s} P_i(X)^2 \sum_{Y_{\sigma_i(1)},\cdots,Y_{\sigma_i(s-1)}\in\Theta} \left(\frac{\prod_{j=1}^{s-1} P_{\sigma_i(j)}(Y_{\sigma_i(j)})}{P_i(X) + \sum_{j=1}^{s-1} P_{\sigma_i(j)}(Y_{\sigma_i(j)})} \right)\,. \tag{4.7}$$

Equations (4.5) and (4.7) are however difficult to handle practically. The reformulated definition of p-PCR6 is introduced now.

4.2.4 Reformulation of p-PCR6

From (4.4), it is deduced:

$$P_{\mathrm{PCR6}}(X) = \sum_{Y_1,\cdots,Y_s\in\Theta} \prod_{i=1}^{s} P_i(Y_i) \frac{\displaystyle\sum_{j=1}^{s} \left(I[X=Y_1=\cdots=Y_s] + I\left[\bigcap_{k=1}^{s} Y_k = \emptyset\right] I[X=Y_j] \right) P_j(Y_j)}{\displaystyle\sum_{j=1}^{s} P_j(Y_j)} .$$

Now, the property (4.6) implies:

$$I[X=Y_1=\cdots=Y_s] + I\left[\bigcap_{k=1}^{s} Y_k = \emptyset\right] I[X=Y_j] = I[X=Y_j] .$$

As a consequence, the p-PCR6 rules is equivalently defined by:

$$P_{\mathrm{PCR6}}(X) = \sum_{Y_1,\cdots,Y_s\in\Theta} \prod_{i=1}^{s} P_i(Y_i) \frac{\displaystyle\sum_{j=1}^{s} I[X=Y_j]\, P_j(Y_j)}{\displaystyle\sum_{j=1}^{s} P_j(Y_j)} . \tag{4.8}$$

4.2.5 Extension of p-PCR6 on continuous propositions

The previous discrete p-PCR6 formula is now extended to densities of probabilities of random variables. Formula (4.7) is thus adapted for the fusion of continuous densities $p_1, \cdots, p_s$:

$$p_{\mathrm{PCR6}}(x) \triangleq \sum_{i=1}^{s} p_i(x) \int_{\Theta^{s-1}} \frac{p_i(x) \displaystyle\prod_{j=1}^{s-1} p_{\sigma_i(j)}(y_{\sigma_i(j)})}{p_i(x) + \displaystyle\sum_{j=1}^{s-1} p_{\sigma_i(j)}(y_{\sigma_i(j)})} \prod_{j=1}^{s-1} dy_{\sigma_i(j)} . \tag{4.9}$$

Notice that $p_i(x)$ is put inside the integration, so as to deal with possible singularities, when $p_i(x) = 0$. It is also necessary to prove that p_{PCR6} is a probabilistic density. And of course, it is possible to guess a reformulated definition of p-PCR6 for densities by means of (4.8). But, we establish now these results by calculus. First at all, a result is proved for computing the expectation based on p_{PCR6}.

4.2.5.1 Expectation

The expectation of a function according to the fused probability p_{PCR6} is expressed from the initial probabilities $p_1, \cdots, p_s$ by:

$$\int_{\Theta} p_{\mathrm{PCR6}}(y) f(y,z)\, dy = \int_{\Theta^s} \prod_{i=1}^{s} p_i(y_i) \frac{\sum_{i=1}^{s} p_i(y_i) f(y_i,z)}{\sum_{i=1}^{s} p_i(y_i)} \prod_{i=1}^{s} dy_i \,. \tag{4.10}$$

Proof.

$$\begin{aligned}
&\int_{\Theta} p_{\mathrm{PCR6}}(y) f(y,z)\, dy \\
&\quad = \sum_{i=1}^{s} \int_{\Theta} p_i(y) \int_{\Theta^{s-1}} \frac{p_i(y) \prod_{j=1}^{s-1} p_{\sigma_i(j)}(y_{\sigma_i(j)})}{p_i(y) + \sum_{j=1}^{s-1} p_{\sigma_i(j)}(y_{\sigma_i(j)})} f(y,z) \left(\prod_{j=1}^{s-1} dy_{\sigma_i(j)} \right) dy \\
&\quad = \sum_{i=1}^{s} \int_{\Theta^s} p_i(y_i) \frac{\prod_{j=1}^{s} p_j(y_j)}{\sum_{j=1}^{s} p_j(y_j)} f(y_i,z) \prod_{j=1}^{s} dy_j \\
&\quad = \int_{\Theta^s} \prod_{i=1}^{s} p_i(y_i) \frac{\sum_{i=1}^{s} p_i(y_i) f(y_i,z)}{\sum_{i=1}^{s} p_i(y_i)} \prod_{i=1}^{s} dy_i \,.
\end{aligned}$$

□□□

Corollary. The density p_{PCR6} is actually probabilistic, since it is derived:

$$\int_{\Theta} p_{\mathrm{PCR6}}(y)\, dy = 1 \,,$$

by taking $f = 1$.

4.2.5.2 Reformulated definition

$$p_{\mathrm{PCR6}}(z) = \int_{\Theta^s} \left(\prod_{i=1}^{s} p_i(y_i) \right) \pi(z|y_{1:s}) \prod_{i=1}^{s} dy_i \ ,$$

$$\text{where} \quad \pi(z|y_{1:s}) = \frac{\sum_{i=1}^{s} p_i(y_i)\delta[y_i = z]}{\sum_{i=1}^{s} p_i(y_i)} \ . \tag{4.11}$$

Proof.
Apply lemma 1 to the Dirac distribution $f(y, z) = \delta[y = z]$.
□□□

4.2.6 Sampling method

Being able to sample $p_1, \cdots, p_s$, it is possible to sample p_{PCR6} by applying the definition (4.11). The implied sampling process (let z be the sample to be generated) is sketched as follows:

1. For any $k \in \{1, \cdots, s\}$, generate y_k according to p_k, *together with its evaluation* $p_k(y_k)$,

2. Generate $\theta \in [0, 1]$ according to the uniform law,

3. Find j such that $\dfrac{\sum_{k=1}^{j-1} p_k(y_k)}{\sum_{k=1}^{s} p_k(y_k)} < \theta < \dfrac{\sum_{k=1}^{j} p_k(y_k)}{\sum_{k=1}^{s} p_k(y_k)}$,

4. Set $z = y_j$.

It is seen subsequently that p-PCR6 does not preserve the Gaussian distributions. As a consequence, its manipulation is essentially addressed by means of a Monte-Carlo method, and the previous sampling method is implemented in the applications.

The next section is devoted to a comparison of p-PCR6 and Bayesian rules on very simple examples.

4.3 Bayes versus p-PCR6

4.3.1 Bayesian fusion rule

In this section, we are interested in the fusion of two independent estimators by means of the Bayesian inference. Such fusion has to take into account the prior about the state of the system. Subsequently, this prior is chosen to be uniform. Although this is just a particular case of application, it is sufficient for our purpose, *i.e.* the illustration of essential differences between the Bayesian and PCR6 approaches.

4.3.1.1 General case

In Bayesian filter, the estimator is explained by means of the posterior probability $p(x|z_1, z_2)$ conditionally to the observation z_1 and z_2. Notice that this posterior estimation should not be confounded with the true state of the system. Now, our purpose here is to derive a rule for deriving the global estimator $p(x|z_1, z_2)$ from the partial estimators $p(x|z_1)$ and $p(x|z_2)$. Applying Bayes' rule, one gets $p(x|z_1, z_2) \propto p(z_1, z_2|x)p(x)$.[4] To go further in the derivation, one must assume the conditional independence between the two probabilistic sources/densities, *i.e.* $p(z_1, z_2|x) = p(z_1|x)p(z_2|x)$. As a consequence, $p(x|z_1, z_2) \propto p(z_1|x)p(z_2|x)p(x)$, and then:

$$p(x|z_1, z_2) \propto \frac{p(x|z_1)p(x|z_2)}{p(x)} \ . \tag{4.12}$$

So, in order to compute $p(x|z_1, z_2)$, it is needed both $p(x|z_1)$, $p(x|z_2)$ and the prior $p(x)$. If one assumes uniform prior for $p(x)$, and using notations $p_{\text{Bayes}} = p(\cdot|z_1, z_2)$, $p_1 = p(\cdot|z_1)$ and $p_2 = p(\cdot|z_2)$, the Bayes' fusion formula (4.12) becomes:

$$p_{\text{Bayes}}(x) \propto p_1(x)p_2(x) \ . \tag{4.13}$$

(It is noticed that a discrete counterpart of this result could also be obtained by applying Dempster Shafer rule to probabilistic belief masses)

4.3.1.2 Gaussian subcase

We investigate here the solution of the problem when p_1 and p_2 are Gaussian distributions. So assume for simplicity that $p_1(x)$ and $p_2(x)$ are monodimensional Gaussian distributions:

$$p_1(x) = \frac{1}{\sigma_1\sqrt{2\pi}} e^{-\frac{1}{2}\frac{(x-\bar{x}_1)^2}{{\sigma_1}^2}} \text{ and } p_2(x) = \frac{1}{\sigma_2\sqrt{2\pi}} e^{-\frac{1}{2}\frac{(x-\bar{x}_2)^2}{{\sigma_2}^2}}$$

[4] $p(\alpha|\beta) \propto \gamma$ means "$p(\alpha|\beta)$ is proportional to γ for β fixed".

In absence of prior information, one assumes $p(x)$ uniform. The Bayesian rule requires to compute (4.13). Then, it is easily shown that p_{Bayes} is Gaussian:

$$p_{\text{Bayes}}(x) = \frac{1}{\sigma_{\text{Bayes}}\sqrt{2\pi}} e^{-\frac{1}{2}\frac{(x-\bar{x}_{\text{Bayes}})^2}{\sigma_{\text{Bayes}}{}^2}} ,$$

with

$$\sigma^2_{\text{Bayes}} = \frac{\sigma_1^2\sigma_2^2}{\sigma_1^2+\sigma_2^2},$$

and

$$\bar{x}_{\text{Bayes}} = \sigma^2_{\text{Bayes}} \left(\frac{\bar{x}_1}{\sigma_1^2} + \frac{\bar{x}_2}{\sigma_2^2} \right) .$$

When $\sigma_1 = \sigma_2 = \sigma$, it is implied then:

$$\sigma^2_{\text{Bayes}}(x) = \frac{\sigma^2}{2} \text{ and } \bar{x}_{\text{Bayes}} = \frac{\bar{x}_1 + \bar{x}_2}{2} .$$

Hence, the resulting standard deviation σ_{Bayes} after Bayes fusion is equal to the initial standard deviation divided by the factor $\sqrt{2}$ and thus $\sigma_{\text{Bayes}} < \sigma$. This fusion process is optimal, when the model parameters are correct. Now, imagine that the difference $\bar{x}_2 - \bar{x}_1$ is obtained from a bias error of the model. For example, let us consider that the estimation of sensor 1 is correct but that the estimation of sensor 2 is erroneous, in regards to the deviation σ. Assuming x being the true state of the system, it comes most likely: $p_1(x) \gg p_{\text{Bayes}}(x) \gg p_2(x)$. Thus, the Bayesian fusion propagates the errors. This implies an irrelevant estimation. It is noticed however, that the bias is divided by two, each time a fusion with a good estimation occurs, while the deviation is only divided by $\sqrt{2}$. Then, good estimations will make the process converge correctly after some iteration.

The theoretical plots and those obtained with Monte Carlo simulation are given in figures 4.1, 4.2 and 4.3. These figures make the comparison with the p-PCR6 fused densities. This comparison will be discussed subsequently. It is yet confirmed that the Bayesian rule just concentrates the information, by reducing the deviation, even when the information are distant (that is putatively false).

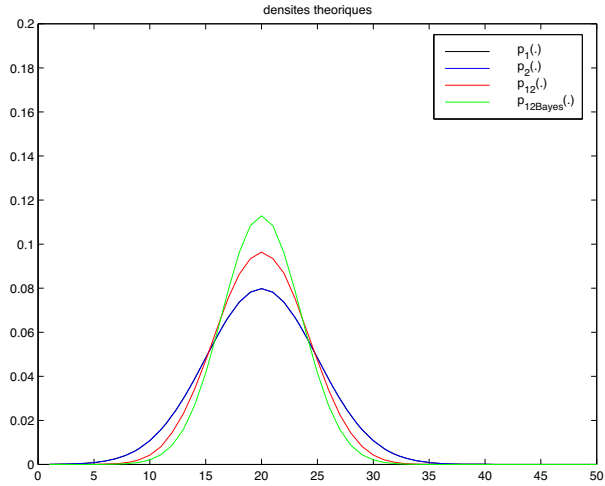


Figure 4.1: p-PCR6 fusion versus Bayesian fusion (theoretical).

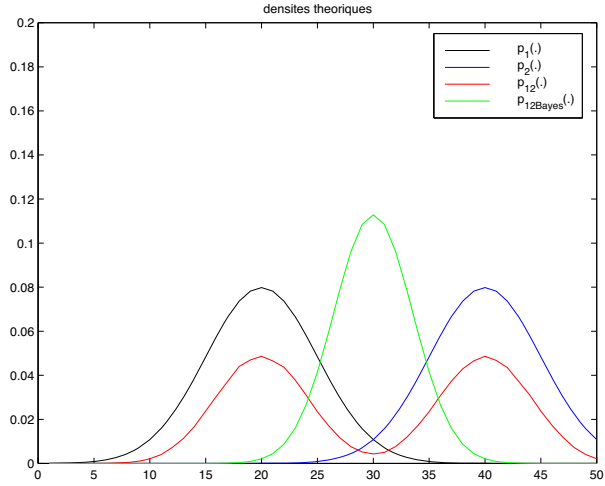


Figure 4.2: p-PCR6 fusion versus Bayesian fusion (theoretical).

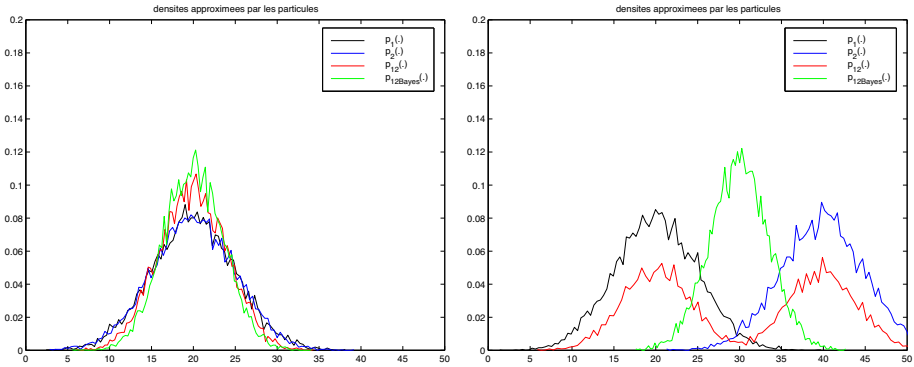


Figure 4.3: p-PCR6 fusion versus Bayesian fusion (based on 10000 samples).

4.3.2 Fusion based on p-PCR6 for Gaussian distributions

The same Gaussian distribution, p_1 and p_2, are considered, but are now fused by p-PCR6 rule (4.9), thus resulting in density p_{PCR6} . The fused densities are both computed, figures 4.1 and 4.2, and sampled, figure 4.3. Direct computations are expensive, and are obtained in two steps:

- Compute $I_s(x) = \int \frac{p_s(x)p_{\bar{s}}(y)}{p_s(x)+p_{\bar{s}}(y)}dy$, where $s \in \{1,2\}$ and $\bar{s} \in \{1,2\} \setminus \{s\}$,
- Then compute $p_{\mathrm{PCR6}}(x) = p_1(x)I_1(x) + p_2(x)I_2(x)$.

It appears clearly that computed and sampled densities match well, thus confirming the rightness of our sampling method. Now, contrariwise to the Bayesian rule, it is noticed two different behaviors (which are foreseeable mathematically):

- When the densities p_1 and p_2 are close, p_{PCR6} acts as an amplifier of the information by reducing the variance. However, this phenomena is weaker than for p_{Bayes}. p-PCR6 is thus able to amplify the fused information, but is less powerful than the Bayesian rule in this task.
- When the densities p_1 and p_2 are distant, p_{PCR6} keeps both modes present in each density and preserves the richness of information by not merging both densities into only one (unimodal) Gaussian density. This is a very interesting and new property from a theoretical point of view, which presents advantages for practical applications.

In regards to these differences, it is thus foreseeable that the p-PCR6 should be more robust to potential errors.

4.4 A distributed sequential filtering application

4.4.1 Whitened p-PCR6 rule

It has been seen that the p-PCR6 fusion of the same densities $p_1 = p_2$ will result in an amplified density p_{PCR6}. Of course, this is not practicable when the densities p_1 and p_2 are related to correlated variables. Consider for example that the state y are measured by z^1 and z^2. The (distributed) posterior probabilities are $p_s(y) = p(y|z^s) \propto p(y)p(z^s|y)$ for $s = 1, 2$. It happens that p_1 and p_2 are correlated, so that p-PCR6 should not be applied directly. In particular, the fusion of p_1 and p_2 by means of p-PCR6 results in a density p_{PCR6} stronger than the prior p over y, even when there is no informative measure, *i.e.* $p(z^s|y) = p(z^s)$! In order to handle this difficulty, we propose a *whitened* p-PCR6 rule, producing a fused density $p_{\text{whitePCR6}}$ from the updated information only:

$$\begin{aligned} p_{\text{whitePCR6}}(y) &= \iint_{\Theta^2} p_1(y_1)p_2(y_2)\pi(y|y_1,y_2)\,dy_1dy_2\ , \\ \text{where } \pi(y|y_1,y_2) &= \frac{\frac{p(y_1|z^1)}{p(y_1)}\delta[y_1=y] + \frac{p(y_2|z^2)}{p(y_2)}\delta[y_2=y]}{\frac{p(y_1|z^1)}{p(y_1)} + \frac{p(y_2|z^2)}{p(y_2)}}\ . \end{aligned} \tag{4.14}$$

In (4.14), the proportion $\frac{p(y|z^s)}{p(y)}$ should be considered as the information intrinsically obtained from sensor s. It happens that the whitened p-PCR6 does not change the prior when there is no informative measure, *i.e.* $p_{\text{whitePCR6}}(y) = p(y)$ when $p(z^s|y) = p(z^s)$ for $s = 1, 2$.

4.4.2 Theoretical setting

A target is moving according to a known Markov prior law. Let y_t be the state of the target at time t. It is assumed:

$$p(y_{1:t+1}) = p(y_{t+1}|y_t)p(y_{1:t})\ .$$

In order to estimate the state of the target, S sensors are providing some measurements. Denote z_t^s the measurement of the state y_t by sensor s. The measure is characterized by the law $p(z_t^s|y_t)$, which is known. It is assumed

that the measure are made independently, conditionally to the state:

$$p(z_t^{1:S}|y_t) = \prod_{s=1}^{S} p(z_t^s|y_t) \ .$$

Our purpose is to derive or approximate the optimal estimator, $p(y_{t+1}|z_{1:t+1}^{1:S})$, from the distributed retroacted estimators, $p(y_{t+1}|z_{1:t}^{1:S}, z_{t+1}^s)$, related to sensors s. There is a Bayesian approach to this problem, and we propose some comparison with a p-PCR6 approach and a whitened p-PCR6 approach.

4.4.2.1 Distributed Bayesian filter

This filter is derived from:

$$p(y_{t+1}|z_{1:t}^{1:S}) = \int_{y_t} p(y_{t+1}|y_t)p(y_t|z_{1:t}^{1:S})\, dy_t \ , \tag{4.15}$$

$$p(y_{t+1}|z_{1:t}^{1:S}, z_{t+1}^s) \propto p(z_{t+1}^s|y_{t+1})p(y_{t+1}|z_{1:t}^{1:S}) \ , \tag{4.16}$$

$$p(y_{t+1}|z_{1:t+1}^{1:S}) \propto \left(\prod_{s=1}^{S} \frac{p(y_{t+1}|z_{1:t}^{1:S}, z_{t+1}^s)}{p(y_{t+1}|z_{1:t}^{1:S})}\right) p(y_{t+1}|z_{1:t}^{1:S}) \ . \tag{4.17}$$

This approach is unstable, when some components of the target state are non-observable; for example, adaptations of the method are necessary [2] for bearing only sensors. However, the method will be applied as it is here to bearing only sensors, in order to compare to the robustness of the PCR6 approach.

4.4.2.2 p-PCR6 filter

This filter is derived from (4.15), (4.16) and:

$$\begin{aligned} &p(y_{t+1}|z_{1:t+1}^{1:S}) = \int_{y_{t+1}^{1:S}} \left(\prod_{s=1}^{S} p(y_{t+1}^s|z_{1:t}^{1:S}, z_{t+1}^s)\right) \pi(y_{t+1}|y_{t+1}^{1:S}) dy_{t+1}^{1:S} \\ &\text{where } \pi(y_{t+1}|y_{t+1}^{1:S}) = \frac{\sum_{s=1}^{S} p(y_{t+1}^s|z_{1:t}^{1:S}, z_{t+1}^s)\delta[y_{t+1} = y_{t+1}^s]}{\sum_{s=1}^{S} p(y_{t+1}^s|z_{1:t}^{1:S}, z_{t+1}^s)} \ , \end{aligned} \tag{4.18}$$

and $p(y_{t+1}^s|z_{1:t}^{1:S}, z_{t+1}^s)$ is an instance of $p(y_{t+1}|z_{1:t}^{1:S}, z_{t+1}^s)$, obtained by just replacing y_{t+1} by y_{t+1}^s.
It is noticed that this filter is necessary suboptimal, since it makes use of the p-PCR6 rule on correlated variables. The whitened p-PCR6 filter will resolve this difficulty. However, it is seen that the p-PCR6 filter still works experimentally on the considered examples.

4.4.2.3 Whitened p-PCR6 filter

This filter is derived from (4.15), (4.16) and:

$$\begin{aligned} p(y_{t+1}|z_{1:t+1}^{1:S}) &= \int_{y_{t+1}^{1:S}} \left(\prod_{s=1}^{S} p(y_{t+1}^{s}|z_{1:t}^{1:S}, z_{t+1}^{s}) \right) \pi(y_{t+1}|y_{t+1}^{1:S}) dy_{t+1}^{1:S} \\ \text{where } \pi(y_{t+1}|y_{t+1}^{1:S}) &= \frac{\sum_{s=1}^{S} \frac{p(y_{t+1}^{s}|z_{1:t}^{1:S}, z_{t+1}^{s})}{p(y_{t+1}^{s}|z_{1:t}^{1:S})} \delta[y_{t+1} = y_{t+1}^{s}]}{\sum_{s=1}^{S} \frac{p(y_{t+1}^{s}|z_{1:t}^{1:S}, z_{t+1}^{s})}{p(y_{t+1}^{s}|z_{1:t}^{1:S})}} . \end{aligned} \tag{4.19}$$

Again, y_{t+1}^{s} is just an instance of y_{t+1} for sensor s .

These filters have been implemented by means of particles. The sampling of p-PCR6 has been explained yet, but it is not the purpose of this paper to explain all the theory of particle filtering; a consultation of the literature, *e.g.* [9], is expected.

4.4.3 Scenario and tests

These examples are retrieved from [4]. This work has been implemented by *Aloïs Kirchner* during his internship in our team.

4.4.3.1 Scenario for passive multi-sensor target tracking

In order to test the p-PCR6 fusion rule, we simulate the following scenario: in a 2-dimensional space, two independent passive sensors are located in (0,100) and (100,0) in Cartesian coordinates. These sensors provide a noisy azimuth measurement (*0.01 rad.* normal noise) on the position of a moving target. We associate a tracking particle filter to each sensor. The motion model is the following :

$$\begin{aligned} \dot{x}_{t+1} &= \dot{x}_t + 0.1 * N(0,1) \\ \dot{y}_{t+1} &= \dot{y}_t + 0.1 * N(0,1) \\ x_{t+1} &= x_t + dt * \dot{x}_t + 0.3 * N(0,1) \\ y_{t+1} &= y_t + dt * \dot{y}_t + 0.3 * N(0,1) \end{aligned} \tag{4.20}$$

where dt = 1 time unit and N(0,1) is the normal distribution.

In our simulations, each local particle filter is implemented by means of 200 particles. At each time step, we proceed to the fusion of the local posterior densities and then re-inject the fused state density into each local filter (feedback loop). Three different paradigms are considered for the fusion: Bayesian, p-PCR6 and whitened p-PCR6 rules. These filters try to estimate both the position and speed of the target which is assumed to follow a quasi-constant velocity model. It is noticed that we are dealing directly with both the observable and non-observable components of the target state.

4.4.3.2 A simple example

In this first example, the filters are well initialized (we give them good starting speed and position). The mobile follows a non-linear trajectory (figure 4.4), in order to show the capability of this distributed filter to converge. On this example, the Bayesian filter manages to track the target with some difficulties during the last curve in figure 4.4. On the same example, p-PCR6 and whitened p-PCR6 rules have been tested with success. While both filters have to reestimate the speed direction at each turn, it appears that this reestimation is more difficult for p-PCR6. This difference is also particularly apparent during the last curve.

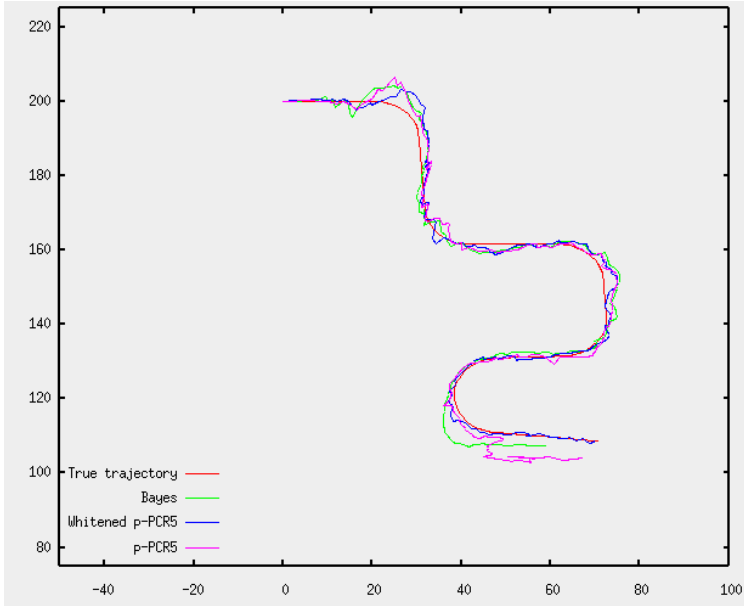
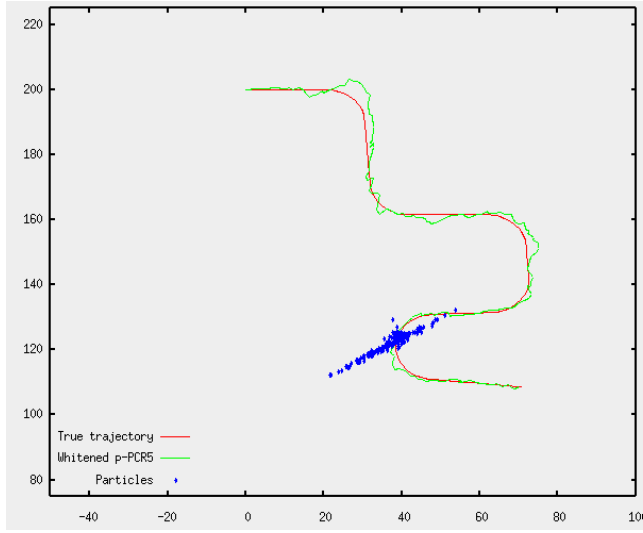
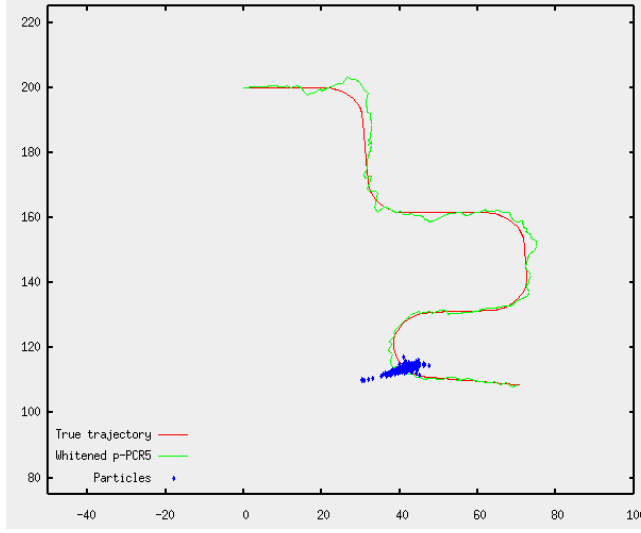


Figure 4.4: Estimated trajectories using different tracking methods.

Figure 4.5 displays the particle cloud of the whitened PCR6 filter during and after the last curve. The variance rises along the curve, resulting in the cross-like cloud of sub-figure 4.5(a), which is characteristic to the p-PCR6 fusion: *the branches correspond to the direction the sensors are looking at.* Then, the p-PCR6, by amplifying the zone where the filters are according to see the object, allows the process to converge again toward the object real position in an expansion-contraction pattern (figure 4.5(b)).



(a) Time step 160.



(b) Time step 170.

Figure 4.5: Particle clouds for whitened p-PCR6 in the last curve.

In more difficult cases, with poor initialization for instance (see figure 4.6), both p-PCR6 and whitened p-PCR6 manage to follow the target, while the Bayesian filter diverges in about one third of the cases and give mitigate results otherwise.

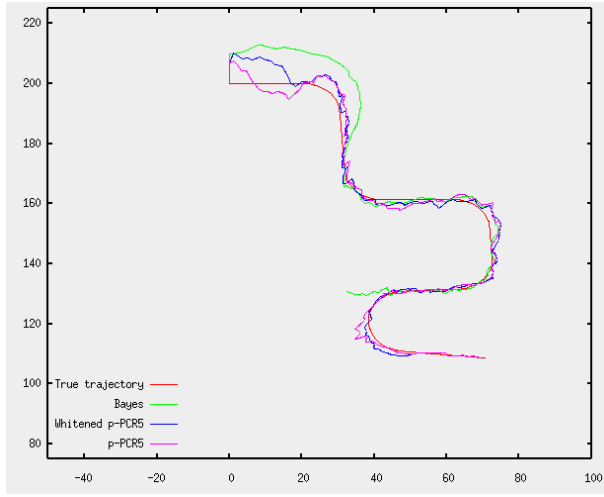


Figure 4.6: Estimated trajectories using different tracking methods. Poor initialization: null speed and 10 units away starting position.

Next sections investigate more thoroughly the properties of the whitened p-PCR6 filtering.

4.4.3.3 Whitened p-PCR6 robustness against poor initialization

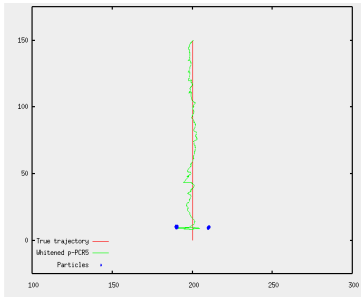
In order to test the capability of (whitened) p-PCR6 to recover from erroneous measurements or from a total contradiction of the local estimations, we considered two scenarios in which the filters are badly initialized at various degrees. In these scenarios, the real trajectory of the object is the same: it starts from $(200, 0)$ and moves toward $(200, 150)$ at a constant speed $(0, 1)$.

In the first scenario (figure 4.7), the first filter, which sensor is placed at $(0, 100)$, is initialized at position $(190, 10)$ and at speed $(0, 0)$. The second filter, which sensor is at $(100, 0)$, is initialized at position $(210, 10)$ and at the same speed (figure 4.7(a)). As the estimated positions are far from the real one and both sensors are looking at the object from a remote position, the particle cloud quickly spread horizontally (figure 4.7(b)). Then the (whitened) PCR6 begins to find zones where both filters estimate a non-negligible probability of presence and amplifies them until convergence (figure 4.7(c)). Though the particle cloud still seems to be fairly spread (because of

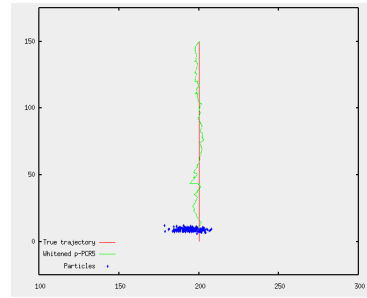
sensors remote position), the global estimate is very close from the real position and speed, and will remain so until the last time step (figure 4.7(d)).

		x	y	x speed	y speed
First example	Filter 1	190	10	0	0
	Filter 2	210	10	0	0
Second example	Filter 1	190	10	0.1	-1
	Filter 2	210	10	0.5	1.5

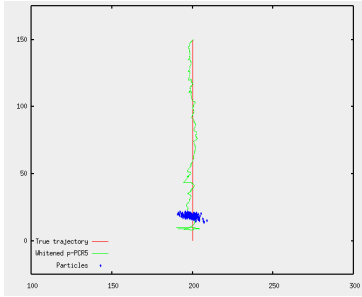
Table 4.1: Initialization data.



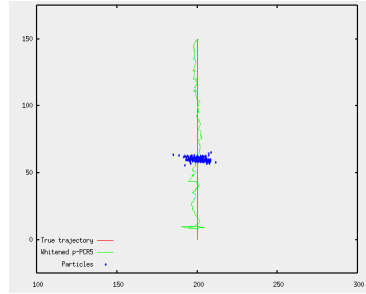
(a) Time step 1.



(b) Time step 10.



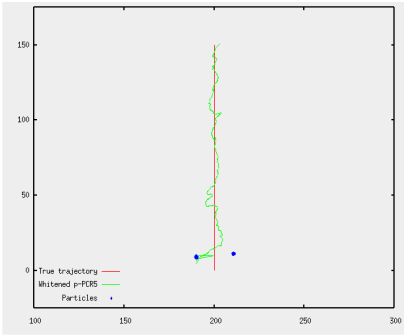
(c) Time step 20.



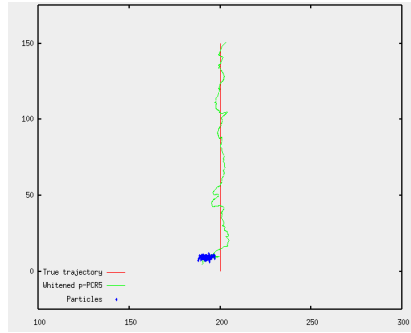
(d) Time step 60.

Figure 4.7: The real mobile starts at $(200, 0)$ and moves upward at constant speed $(0, 1)$; poor filters initialization.

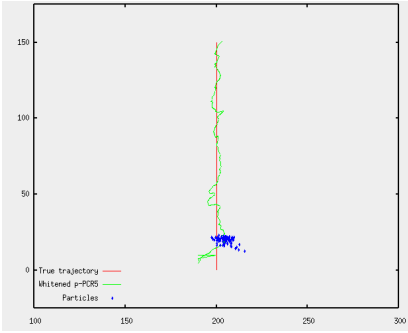
Our second example (figure 4.8) is an extreme case: the initialization is quite worse (see table 4.1), since our motion model assumes nearly constant speed and therefore makes it hard to recover from such erroneous and contradictory speed initialization. An interesting point is that, for a tight prediction noise, p-PCR6 sometimes does not converge on this example, while whitened p-PCR6 usually does. Artificially raising the prediction noise solves this problem for 'standard' p-PCR6, showing its trend to over-concentrate the particle cloud.



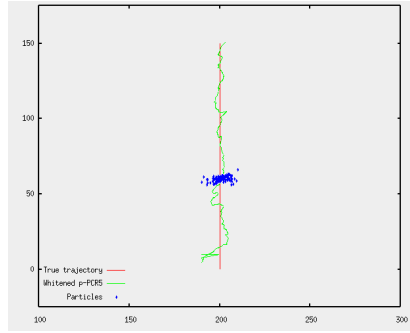
(a) Time step 1.



(b) Time step 10.



(c) Time step 20.

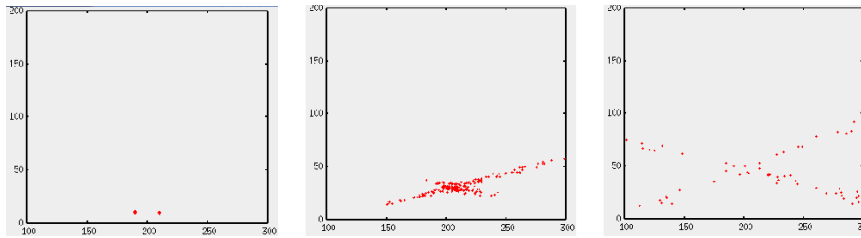


(d) Time step 60.

Figure 4.8: The real mobile starts at $(200, 0)$ and moves upward at constant speed $(0, 1)$; *bad* filters initialization.

4.4.3.4 Whitened p-PCR6 versus mean

As seen before, the PCR6-fusion of two probabilistic densities amplifies the areas where both densities have a non-negligible value. Otherwise, it usually works like just averaging the two densities. In order to measure the impact of the amplification, we reprocessed the first example of previous subsection while using the mean, $p_{\text{mean}} = \frac{p_1+p_2}{2}$, instead of p-PCR6. The result (figure 4.9) is self explanatory: the same expansion as with p-PCR6 occurs (figure 4.7), but contraction never happens.



(a) Time step 1. (b) Time step 30. (c) Time step 45.

Figure 4.9: Using mean instead of p-PCR6. Red dots are the positions of the particles after fusion. The real mobile starts from (200,0) at time step 0 and moves at the constant speed (0,1).

4.4.3.5 Concluding remarks

The results presented here have clearly shown that p-PCR6, and especially whitened p-PCR6, filters are more robust than the Bayesian filter against bad initialization. However, it is clear that Bayesian filters are the best, when the priors are correctly defined. The real interest of p-PCR6 is that it does not need a precise prior knowledge about the antedating local particle filters.

4.5 Conclusions

This paper has investigated a new fusion rule, p-PCR6, for fusing probabilistic densities. This rule is derived from the PCR6 rule for fusing evidences. It has a simple interpretation from a sampling point of view. p-PRC6 has been compared to the Bayesian rule on a simple fusion example. Then, it has been shown that p-PCR6 was able to maintain multiple hypothesis in the fusion process, by generating multiple modes. Thus, more robustness of p-PCR6 were foreseeable in comparison to Bayes' rule. This robustness has been tested successfully on examples of distributed target

tracking. It is expected that this new rule will have many applications, in particular in case of ill-posed filtering problems.

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