

Tutorial: Poisson multi-Bernoulli mixtures for multiple target tracking

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Outline

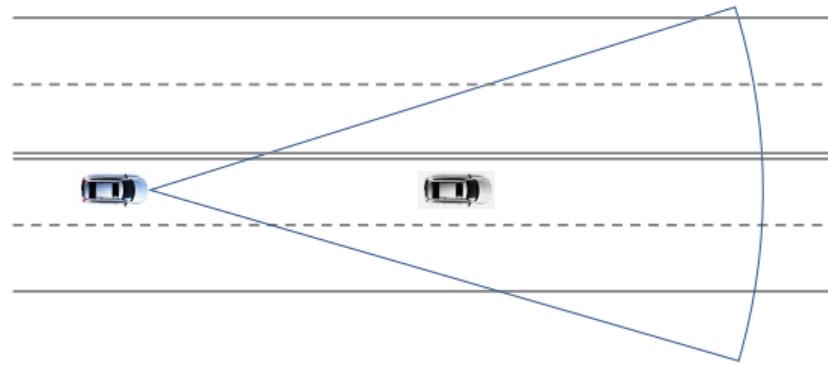
- 1 Overview of multiple target filtering
Introduction to random finite sets
- 2 Common random finite sets
Multi-target filtering recursion and models
- 3 PMBM density and structure
- 4 PMBM prediction and update
- 5 Practical aspects - pruning
- 6 Relation to other filters: MHT, δ -GLMB, PMB, JIPDA
- 7 Simulation example
Extension to sets of trajectories

Section 1

Overview of multiple target filtering
Introduction to random finite sets

Single target Bayesian filtering

- The sequential processing of noisy sensor measurements to determine the target state.



- In single target inference, we have a state $x_k \in \mathbb{R}^{n_x}$:
 - It evolves with transition probability $p(x_k|x_{k-1})$.
 - It is observed by a measurement with likelihood $p(z_k|x_k)$.

Single target Bayesian filtering

- Objective: compute the density $p(x_k|z_{1:k})$ of x_k given all past measurements $z_{1:k} = (z_1, \dots, z_k)$.
- Bayesian filtering recursions:
 - Chapman-Kolmogorov prediction

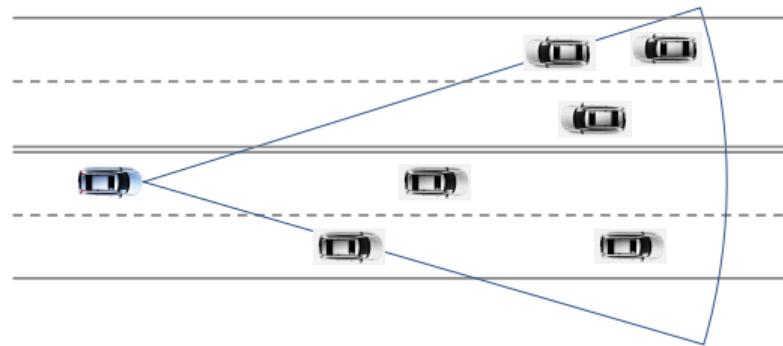
$$p(x_k|z_{1:k-1}) = \int p(x_k|x_{k-1})p(x_{k-1}|z_{1:k-1})dx_{k-1}$$

- Bayes update

$$p(x_k|z_{1:k}) = \frac{p(z_k|x_k)p(x_k|z_{1:k-1})}{\int p(z_k|x_k)p(x_k|z_{1:k-1})dx_k}$$

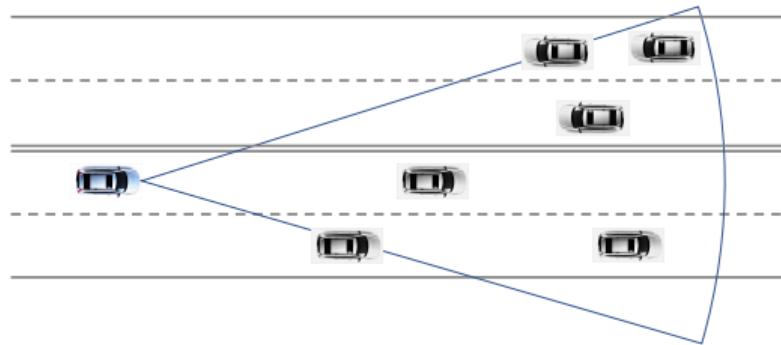
Multiple target Bayesian filtering

- In multiple target tracking, the number of targets is unknown and time-varying
 - Targets can appear and disappear.



Multiple target Bayesian filtering

- In multiple target tracking, the number of targets is unknown and time-varying
 - Targets can appear and disappear.



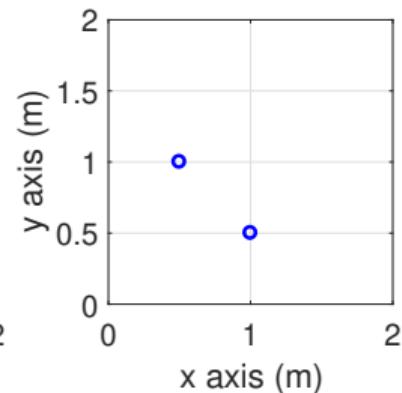
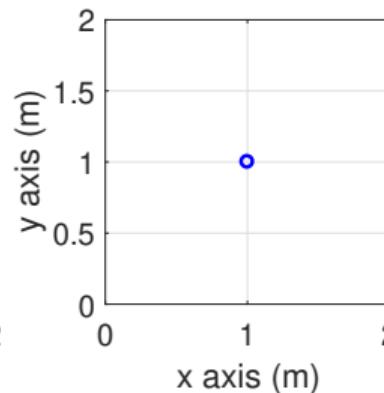
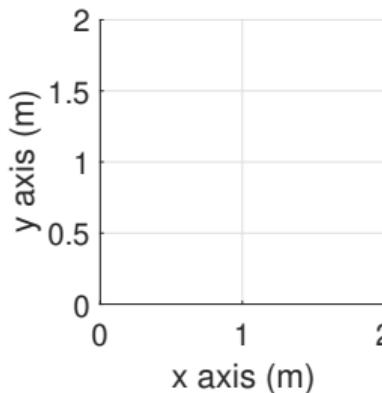
- It is suitable to use a set $X_k = \{x_k^1, \dots, x_k^{n_k}\}$ to represent the state. Why?
 - Set addition and subtraction are well understood operations.
 - Naturally accounts for invariance in target ordering.
 - It allows the development of mathematical metrics, e.g., OSPA [1] and GOSPA [2].

Sets of targets

- We use random finite sets (RFSs) [3, 4] to deal with uncertainty on sets of targets.
- In an RFS, both the number of elements and the elements themselves may be random.
- Given a single target space \mathbb{R}^{n_x} , $\mathcal{F}(\mathbb{R}^{n_x})$ denotes the set of all subsets of \mathbb{R}^{n_x}
 - Single target $x_k \in \mathbb{R}^{n_x}$.
 - Set of targets $X_k \in \mathcal{F}(\mathbb{R}^{n_x})$.

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 - Single target $x_k \in \mathbb{R}^{n_x}$.
 - Set of targets $X_k \in \mathcal{F}(\mathbb{R}^{n_x})$.
- $X_k = \emptyset$ (no target present), $X_k = \{x_k^1\}$ (one target present), $X_k = \{x_k^1, x_k^2\}$ (two targets present)



Random finite sets: definition and properties

Random finite set

A random variable whose possible outcomes are sets with a finite number of unique elements.

- A recap on set properties:

- Sets are **equal** if they contain the same elements.
- RFSs do not contain repeated elements, i.e., an RFS is never, e.g., $\{a, b, b, c\}$.
- A set that does not contain any elements is **empty**, denoted \emptyset .
- Two sets are **disjoint** if their intersection is empty, e.g., $X = \{1, 2, 3\}$ and $Y = \{4, 5, 6\}$ are disjoint since $X \cap Y = \emptyset$.
- The **cardinality** of a set X is denoted $|X|$. For a finite set, this is the number of unique elements in X , e.g., $X = \{4, 5, 6\} \Rightarrow |X| = 3$.

Multi-target densities

Probability Density Function(PDF)

Multi-target density

We use the multi-target density of an RFS, X , to describe its distribution.

- A multi-target density, $f(\{x_1, \dots, x_n\})$, is a non-negative function on sets that integrates to one.
- It captures both the distribution over cardinality and the distribution over the elements of the set (given the cardinality).

- Since sets are invariant to order so are multi-target densities, e.g.,

$$f(\{x_1, x_2\}) = f(\{x_2, x_1\}).$$

- Whenever we write $\{x_1, \dots, x_n\}$, we assume that $|\{x_1, \dots, x_n\}| = n$.

所以一个RFS的density function其实包括了两级(two levels)，一级是distribution over cardinality，相当于是一个宏观的整体的分布，这个是比如Possion分布的，Bernoulli分布的。另一级是每一个微观的single target自身的分布，这个还是用Gaussian建模的，和原来使用Kalman filter做single target tracking一样。

Multi-target densities: example

Example

- If $x_1 \sim \text{unif}(0, 1)$ and $x_2 \sim \text{unif}(1, 2)$ are independent and $X = \{x_1, x_2\}$, then

$$f(X) = \begin{cases} p_1(v_1)p_2(v_2) + p_1(v_2)p_2(v_1) & \text{if } X = \{v_1, v_2\} \\ 0 & \text{if } |X| \neq 2, \end{cases}$$

where

$$p_1(x) = \begin{cases} 1 & \text{if } 0 < x < 1 \\ 0 & \text{otherwise,} \end{cases} \quad p_2(x) = \begin{cases} 1 & \text{if } 1 < x < 2 \\ 0 & \text{otherwise.} \end{cases}$$

- For instance, $f(\{1.5, 0.5\}) = p_1(1.5)p_2(0.5) + p_1(0.5)p_2(1.5) = 0 + 1 = 1$.



Sums over mutually disjoint sets

Convolution formula for union of two RFSs

If X_1 and X_2 are independent RFSs, then $X = X_1 \cup X_2$ has the multiobject pdf

$$f(X) = \sum_{X_1 \subseteq X} f_1(X_1) f_2(X \setminus X_1).$$

- To generalize the formula to unions of n RFSs, let

$$\sum_{X_1 \uplus \dots \uplus X_n = X}$$

denote summation over all mutually disjoint (and possibly empty) sets X_1, \dots, X_n whose union is X . Recall: X_1 and X_2 are disjoint if $X_1 \cap X_2 = \emptyset$.

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Example

$$\sum_{X_1 \uplus X_2 \uplus X_3 = \{4\}} f(X_1, X_2, X_3) = f(\{4\}, \emptyset, \emptyset) + f(\emptyset, \{4\}, \emptyset) + f(\emptyset, \emptyset, \{4\})$$

Convolution formula for independent RFSs

Convolution theorem for independent RFSs

If X_1, \dots, X_n are independent RFSs, then $X = X_1 \cup \dots \cup X_n$ has the multi-target density

$$f(X) = \sum_{X_1 \cup \dots \cup X_n = X} \prod_{i=1}^n f_i(X_i),$$

where the summation is taken over all mutually disjoint (and possibly empty) sets X_1, \dots, X_n whose union is X .

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where the summation is taken over all mutually disjoint (and possibly empty) sets X_1, \dots, X_n whose union is X .

Example

!!!

- Suppose X_1, X_2, X_3 are independent RFSs with densities $f_1(\cdot)$, $f_2(\cdot)$ and $f_3(\cdot)$, respectively.
- The multi-target density of $X = X_1 \cup X_2 \cup X_3$ then satisfies

$$f(\{4\}) = f_1(\{4\})f_2(\emptyset)f_3(\emptyset) + f_1(\emptyset)f_2(\{4\})f_3(\emptyset) + f_1(\emptyset)f_2(\emptyset)f_3(\{4\}).$$

Convolution formula for independent RFSs: example

Example

!!!

- Suppose X_1 and X_2 are independent singletons, (for $i = 1, 2$)

$$f_i(X_i) = \begin{cases} p_i(x_i) & \text{if } X_i = \{x_i\} \\ 0 & \text{if } |X_i| \neq 1. \end{cases}$$

- If $X = X_1 \cup X_2$,

$$\begin{aligned} f(\{x_1, x_2\}) &= f_1(\emptyset)f_2(\{x_1, x_2\}) + f_1(\{x_1, x_2\})f_2(\emptyset) \\ &\quad + f_1(\{x_1\})f_2(\{x_2\}) + f_1(\{x_2\})f_2(\{x_1\}) \\ &= p_1(x_1)p_2(x_2) + p_1(x_2)p_2(x_1). \end{aligned}$$

- We also note that $f(X) = 0$ if $|X| \neq 2$.

Set integrals and expected values

Set integrals

Given a real-valued function $f(\cdot)$ on the space $\mathcal{F}(\mathbb{R}^{n_x})$, its set integral is defined as

$$\int f(X) \delta X = \sum_{i=0}^{\infty} \frac{1}{i!} \int f(\{x_1, \dots, x_i\}) dx_1 \cdots dx_i.$$

Set integrals and expected values

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Expected values

For $g : \mathcal{F}(\mathbb{R}^{n_x}) \rightarrow \mathbb{R}$, the expected value is

$$\mathbb{E}[g(X)] = \int g(X) f(X) \delta X = \sum_{i=0}^{\infty} \frac{1}{i!} \int g(\{x_1, \dots, x_i\}) f(\{x_1, \dots, x_i\}) dx_1 \cdots dx_i.$$

Set integrals: example

Example

- Consider the following multi-target density function

$$f(X) = \begin{cases} p_1(v_1)p_2(v_2) + p_1(v_2)p_2(v_1) & \text{if } X = \{v_1, v_2\} \\ 0 & \text{if } |X| \neq 2. \end{cases}$$

- Its corresponding set integral is

$$\begin{aligned} \int f(X) \delta X &= \sum_{i=0}^{\infty} \frac{1}{i!} \int f(\{v_1, v_2\}) dv_1 dv_2 = \frac{1}{2} \int f(\{v_1, v_2\}) dv_1 dv_2 \\ &= \frac{1}{2} \int (p_1(v_1)p_2(v_2) + p_1(v_2)p_2(v_1)) dv_1 dv_2 \\ &= \frac{2}{2} \int p_1(v_1) dv_1 \int p_2(v_2) dv_2 = 1 \end{aligned}$$

Cardinality distribution

Cardinality distribution

The cardinality distribution of an RFS, $X \sim f(\cdot)$, is

$$\rho(n) = \Pr [|X| = n] = \frac{1}{n!} \int f(\{x_1, \dots, x_n\}) dx_1 \cdots dx_n.$$

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Example

With $f(\cdot)$ from the previous example,

$$\rho(n) = \begin{cases} \frac{1}{2} \int f(\{v_1, v_2\}) dv_1 dv_2 & n = 2 \\ 0 & n \neq 2. \end{cases}$$

Probability hypothesis density

Probability hypothesis density

The probability hypothesis density (PHD) $D(\cdot)$ of an RFS with multi-target density $f(\cdot)$ is

$$D(x) = \int f(\{x\} \cup X) \delta X = \sum_{i=0}^{\infty} \frac{1}{i!} \int f(\{x, x_1, \dots, x_i\}) dx_1 \cdots dx_i.$$

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- The PHD is
 - ✖ • a first-order statistical moment of the RFS,
 - ✖ • a function that is defined on the single target space \mathbb{R}^{n_x} .
- The expected number \hat{N}_A of targets in a region $A \subseteq \mathbb{R}^{n_x}$ is

$$\hat{N}_A = \int_A D(x) dx.$$

- If X is the union of the independent RFSs X_1, \dots, X_N , then

$$D(x) = D_1(x) + \cdots + D_N(x).$$

Tutorial: Poisson multi-Bernoulli mixtures for multiple target tracking

End of video

Section 2

Common random finite sets
Multi-target filtering recursion and models

Poisson RFS/Poisson point process



Poisson随机有限Set的基数符合
Poisson分布

- Cardinality is Poisson distributed.
- For each cardinality, its elements are independently and identically distributed (IID).
- It is commonly used to model
 - clutter measurements,
 - appearing targets.
- Its multi-target density is given by

$$f(\{x_1, \dots, x_n\}) = e^{-\lambda} \lambda^n \prod_{i=1}^n p(x_i)$$

where $\lambda \geq 0$ is the parameter of the Poisson distribution of the cardinality, also referred to as Poisson rate, and $p(\cdot)$ is a single target density.

- Its intensity function is $\lambda p(x)$.

Poisson RFS/Poisson point process

- The PHD of a Poisson RFS is equal to its intensity $\lambda p(x)$. !!
- A Poisson RFS is characterised by either its PHD/intensity function $D(x) = \lambda p(x)$ or by λ and $p(x)$

$$f(\{x_1, \dots, x_n\}) = e^{-\int D(x)dx} \prod_{i=1}^n D(x_i).$$

- We can also use multi-target exponential notation to express the Poisson RFS density

$$f(X) = e^{-\int D(x)dx} [D(\cdot)]^X$$

where $[h(\cdot)]^X = \prod_{x \in X} h(x)$ with $h(\cdot)$ a real-valued function and $h^\emptyset = 1$ by convention.

Sampling a Poisson RFS

Algorithm 1 Sampling a Poisson RFS

Input: Intensity $D(\cdot)$ or, parameter λ and single target density $p(\cdot)$.

Output: Sample X .

Set $X = \emptyset$

Sample n from a Poisson distribution with parameter λ .

for $j = 1$ to n **do**

 Sample $x \sim p(\cdot)$.

 Set $X = X \cup \{x\}$

end for

Example

Suppose

$$D(x) = 4\mathcal{N}\left(x; \begin{bmatrix} 3 \\ 3 \end{bmatrix}, I_2\right) + \mathcal{N}\left(x; \begin{bmatrix} -3 \\ -3 \end{bmatrix}, I_2\right).$$

Bernoulli RFS

!!!

Bernoulli 随机有限Set的基数符合the Bernoulli distribution, 又名两点分布或者0-1分布

换言之, 就是表示: 有($\text{number of measurement} / \text{number of target} = 1$)或者没有($\text{number of measurement} / \text{number of target} = 0$)。

- Cardinality is Bernoulli distributed.
- It is used to model
 - measurement from a single target,
 - a potential target.
- Its multi-target density is given by

$$f(X) = \begin{cases} 1 - r & X = \emptyset \\ rp(x) & X = \{x\} \\ 0 & \text{otherwise} \end{cases}$$

where r is the existence probability and $p(\cdot)$ is a single target density.

- The PHD of a Bernoulli RFS $X \sim f(X)$ is $rp(x)$.

Sampling a Bernoulli RFS

Algorithm 2 Sampling a Bernoulli RFS

Input: Existence probability r and single target density $p(\cdot)$.

Output: Sample X .

Sample i , where $i = 0$ with probability $1 - r$ and $i = 1$ with probability r .

if $i = 0$ **then**

 Set $X = \emptyset$.

else

 Sample $x \sim p(\cdot)$.

 Set $X = \{x\}$.

end if

Example

Suppose $r = 0.7$ and $p(x) = \mathcal{N}(x; 0_2, I_2)$.

Multi-Bernoulli RFS



- A multi-Bernoulli (MB) RFS is the union of n independent Bernoulli RFS X_1, \dots, X_n .
- MB RFSs are used to model potential targets.
- Its multi-target density can be obtained by applying the convolution formula

$$f(X) = \sum_{X_1 \uplus \dots \uplus X_n = X} \prod_{i=1}^n f_i(X_i)$$

where $f_i(\cdot)$ is the i th Bernoulli component, characterised by a probability r_i of existence and a single target density $p_i(\cdot)$.

- The PHD of multi-Bernoulli RFS $X \sim f(X)$ is $\sum_{i=1}^n r_i p_i(x)$.



所以对于一个MB RFS可以理解为2个level的关系：最内一级就是每个single target state还是以Gaussian distribution表示。向外一级是个Multi-Bernoulli来表示n个target的state over Cardinality的一个宏观分布(该MB用existenc probability r和每个Gaussian distribution的pdf函数p表示)。

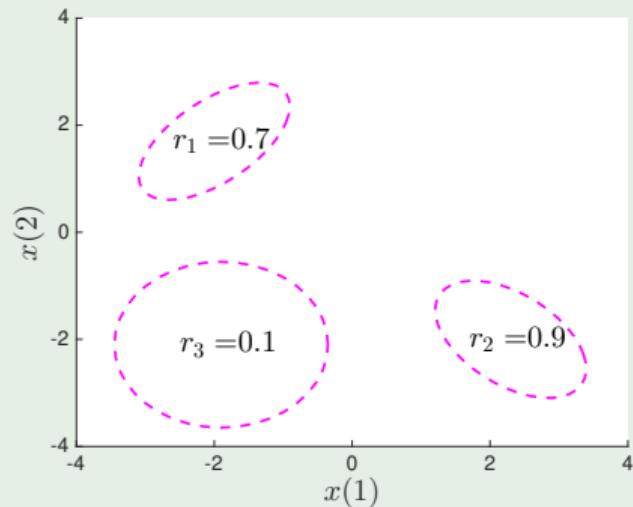
Multi-Bernoulli RFS: example

- Suppose $f_i(X_i)$ is parameterised by r_i and $p_i(\cdot)$.

Example

- Suppose $n = 3$, $r_1 = 0.7$, $r_2 = 0.9$ and $r_3 = 0.1$.
- Also, let $p_1(x)$, $p_2(x)$ and $p_3(x)$ be Gaussian, see figure.
- The MB RFS X represents that there are three potential targets.

即第二级的每一个 target 的 state 的“微观分布”还是用 Gaussian 建模。



Sampling a multi-Bernoulli RFS

Algorithm 3 Sampling a multi-Bernoulli RFS

Input: Set $\{(r_1, p_1(\cdot)), \dots, (r_n, p_n(\cdot))\}$.

Output: Sample X .

for $i = 1$ to n **do**

 Sample X_i from a Bernoulli RFS density
 with parameter r_i and $p_i(\cdot)$.

end for

Set $X = X_1 \cup \dots \cup X_n$.

Example

Suppose $n = 2$, $r_1 = r_2 = 0.8$,
 $p_1(x) = \mathcal{N}\left(x; \begin{bmatrix} 2 \\ 2 \end{bmatrix}, 0.3I_2\right)$ and
 $p_2(x) = \mathcal{N}\left(x; \begin{bmatrix} -2 \\ -2 \end{bmatrix}, 0.3I_2\right)$.

Multi-Bernoulli vs. Poisson

MB RFS \approx Poisson RFS?

- A Bernoulli RFS with $r < 0.1$ is approximately a Poisson RFS.
 - \Rightarrow an MB RFS with $r_1, \dots, r_n < 0.1$ is approximately a Poisson RFS.
 - Any Poisson RFS can be approximated by an MB RFS, but it may require a large n .
-
- Often computationally efficient to use a Poisson RFS.

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- Any Poisson RFS can be approximated by an MB RFS, but it may require a large n .
- Often computationally efficient to use a Poisson RFS.

Why use MB RFS instead of Poisson RFS?

- If X is Poisson RFS, the mean and variance of $|X|$ are equal.
- Problematic if we are certain that there are, say, 10 targets present.
- The MB density is better at expressing the posterior in such situations.
- MB RFSs are not restricted to IID states.

Multi-Bernoulli mixture RFS

- An MB mixture (MBM) RFS is a weighted sum of MB RFSs.
- It is used to model posterior distribution of potential targets.
- Suppose $f_i^h(X_i)$ are Bernoulli RFS densities for $i = 1, \dots, n$ and $h = 1, \dots, \mathcal{H}$.
- Then X is an MBM RFS if it has the multi-target density

$$f(X) = \sum_{h=1}^{\mathcal{H}} w_h \sum_{X_1 \uplus \dots \uplus X_n = X} \prod_{i=1}^n f_i^h(X_i)$$

where $w_1, \dots, w_{\mathcal{H}}$ are non-negative weights such that $\sum_{h=1}^{\mathcal{H}} w_h = 1$.

- Sampling an MBM RFS
 - sample h from a categorical distribution parameterised by $w_1, \dots, w_{\mathcal{H}}$,
 - sample X from the h -th MB RFS.

代表不同的Hypotheses。

所以对于一个MBM可以理解为3个level的结构关系，最外两层为树状：
最内一级就是每个single target state还是以Gaussian distribution(如同single target state Bayesian filter一样，如果系统的noise符合Gaussian分布的话)表示。
向外一级是个Multi-Bernoulli来表示n个target的state over Cardinality的一个宏观分布(该MB用existence probability r和每个Gaussian distribution的pdf函数p表示)。
最外面一级是个Multi-Bernoulli Mixture，即任意第i个Bernoulli component都有 h^i 个hypotheses，每个hypothesis都有其对应的weight。

Multi-target filtering recursion

- The set of targets at time step k is X_k .
- It evolves with a transition density $f_{k|k-1}(\cdot|X_{k-1})$.
- It is observed at time step k by measurements Z_k with conditional density $f(\cdot|X_k)$.
- All information about X_k is included in the posterior $f_{k|k}(X_k)$.
- The objective is to recursively compute $f_{k|k}(X_k)$ via
 - Chapman-Kolmogorov prediction

$$f_{k|k-1}(X_k) = \int f_{k|k-1}(X_k|X_{k-1}) f_{k-1|k-1}(X_{k-1}) \delta X_{k-1}$$

- Bayes update

$$f_{k|k}(X_k) = \frac{f(Z_k|X_k) f_{k|k-1}(X_k)}{\int f(Z_k|Y) f_{k|k-1}(Y) \delta Y}$$

- We need models for motion $f_{k|k-1}(X_k|X_{k-1})$ and measurements $f(Z_k|X_k)$.

Multi-target measurement model

Single target measurement model

- A target with state x is detected with probability $p^D(x)$.
- If detected, it generates a measurement from the single target measurement density $l(\cdot|x)$.

Multi-target measurement model



Single target measurement model

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- If detected, it generates a measurement from the single target measurement density $l(\cdot|x)$.

In the presence of other targets:

- Conditioned on the target states, each target measurement is independent of all other targets and measurements (including clutter measurements).
- Each target-generated measurement is the result of at most one target.
- The measurement Z_k is the union of the target-generated measurements and Poisson clutter with intensity $\lambda^C(\cdot)$.

Multi-target dynamic model

Single target dynamic model (for already present targets)

- A target with state x survives with probability $p^S(x)$.
- If it survives, it moves to a new state with a transition density $g(\cdot|x)$.

Multi-target dynamic model

!!!

Single target dynamic model (for already present targets)

- An target with state x survives with probability $p^s(x)$.
- If it survives, it moves to a new state with a transition density $g(\cdot|x)$.

In the presence of other targets:

- Conditioned on its state, each target moves independently of all other targets.
- Two common birth models for new appearing targets:
 - Poisson RFS with intensity $\lambda^B(\cdot)$.
 - MB RFS parameterised by set $\{(r^{b,1}, p^{b,1}(\cdot)), \dots, (r^{b,n^b}, p^{b,n^b}(\cdot))\}$.

Poisson birth vs. multi-Bernoulli birth

MB birth

- Suitable when number of newborn targets per time is known a priori and the targets appear around some known locations.
- \Rightarrow e.g., tracking of people in a room with several doors where only one person can pass each door at a time.
- Number of newborn targets per time $>$ number of Bernoullis \Rightarrow modelling error.

Poisson birth vs. multi-Bernoulli birth

!!!

MB birth



- Suitable when number of newborn targets per time is known a priori and the targets appear around some known locations.
- ⇒ e.g., tracking of people in a room with several doors where only one person can pass each door at a time.
- Number of newborn targets per time > number of Bernoullis ⇒ modelling error.

Poisson birth



- Model target births at known points sources and also cover large areas of potential births.
- ⇒ e.g., radar surveillance applications in broad areas and robotic applications.
- Does not set a maximum to the number of newborn targets per time.
- Measurement-driven, beneficial when prior birth information is vague.
- ⇒ Bernoulli components initialisation in PMB(M) filtering.

Tutorial: Poisson multi-Bernoulli mixtures for multiple target tracking

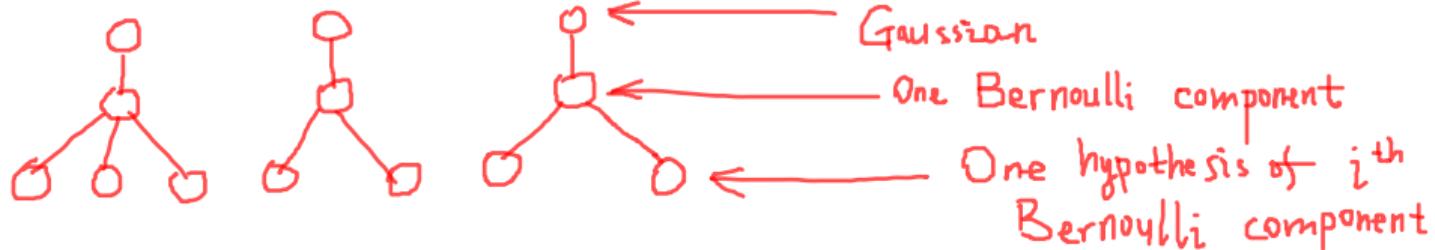
End of video

Section 3

PMBM density and structure

开始PMBM(Poisson Multi-Bernoulli Mixture) density and structure这一节内容前，再强调一次：

对于一个MBM(Multi-Bernoulli Mixture) RFS可以理解为3个level的结构关系，最外两层为树状。最内一级就是每个single target state还是以 Gaussian distribution表示(如果noise符合高斯分布的话)。向外一级是个Multi-Bernoulli来表示n个target的state over Cardinality的一个宏观分布(该MB用existence probability r 和每个Gaussian distribution的pdf函数 p 表示)。最外面一级是个Multi-Bernoulli Mixture，即对于MB中的n个Bernoulli component，对任意第 i 个Bernoulli component都有 h^i 个不同的hypothesis，每个Bernoulli component都有对应的在这个hypothesis的weight。



Poisson multi-Bernoulli mixture (PMBM) density !!!

- For the standard multi-target models with Poisson birth [4], the posterior and the predicted density are PMBM [5, 6]



$$f_{k'|k}(X_{k'}) = \sum_{Y \uplus W = X_{k'}} f_{k'|k}^P(Y) f_{k'|k}^{mbm}(W)$$



$$f_{k'|k}^P(X_{k'}) = e^{-\int \lambda_{k'|k}(x) dx} [\lambda_{k'|k}(\cdot)]^{X_{k'}}$$

$$f_{k'|k}^{mbm}(X_{k'}) \propto \sum_{a \in \mathcal{A}_{k'|k}} \sum_{\substack{n_{k'|k} \\ \uplus_{i=1}^{n_{k'|k}} X^i = X_{k'}}} \prod_{i=1}^{n_{k'|k}} \left[w_{k'|k}^{i,a^i} f_{k'|k}^{i,a^i}(X^i) \right].$$

where $k' \in \{k, k+1\}$ and $f_{k'|k}^{i,a^i}(\cdot)$ is a Bernoulli density:

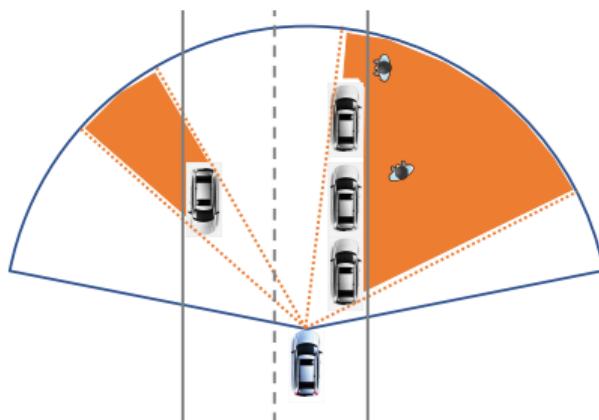
- Existence probability $r_{k'|k}^{i,a^i}$.
- Single target density $p_{k'|k}^{i,a^i}(\cdot)$.

该Bernoulli RFS用existence probability和(高斯分布的)single target density描述。

PMBM density (II) !!!

PMBM RFS is

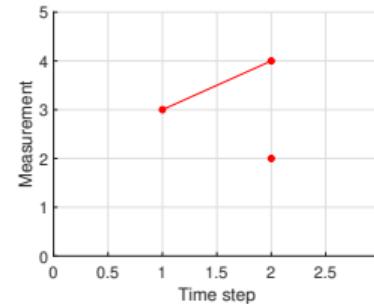
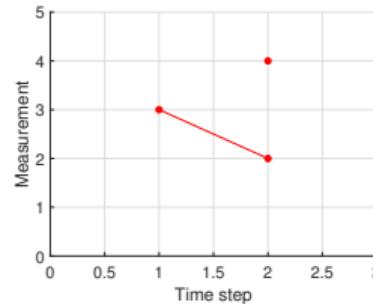
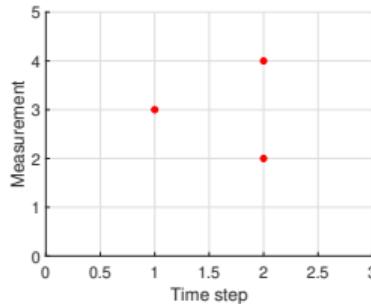
- Union of an independent Poisson RFS/Poisson point process (PPP) $f_{k'|k}^p(\cdot)$ and a multi-Bernoulli mixture RFS $f_{k'|k}^{mbm}(\cdot)$.
 - Poisson RFS includes information on existing targets that have never been detected.
 - Key information: we can account for undetected objects in occluded areas.
 - Multi-Bernoulli mixture (MBM) includes information on existing targets that have been detected at some point.



- One Bernoulli per vehicle.
- Intensity of the PPP mainly covering occluded areas.

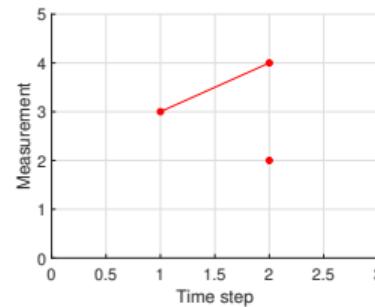
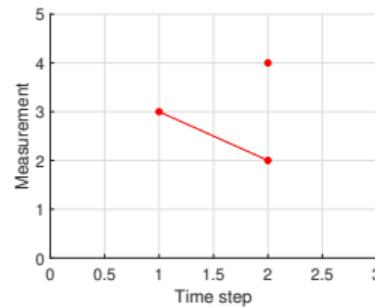
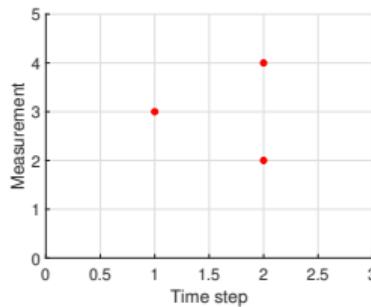
Interpretation MBM

- Each measurement at each time step gives rise to a new potentially detected target (Bernoulli)
 - A measurement can be the first detection of a target, or clutter.
 - It can also correspond to a previously detected target: probability of existence 0.



Interpretation MBM

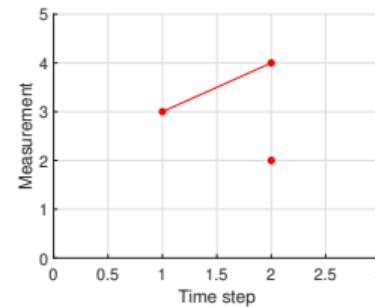
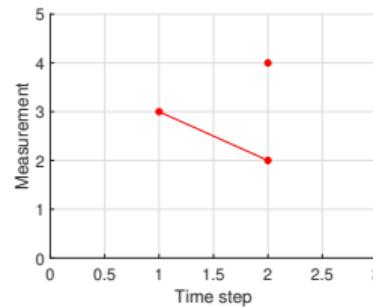
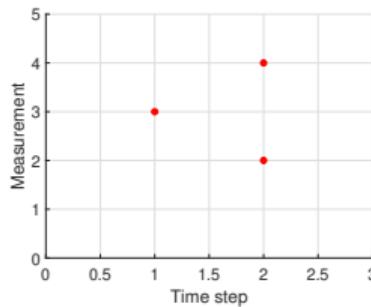
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- For each Bernoulli component, there are single target association history hypotheses (local hypotheses), which are data-to-data.

Interpretation MBM

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- For each Bernoulli component, there are single target association history hypotheses (local hypotheses), which are data-to-data.
- A global hypothesis is represented by one of the multi-Bernoulli RFSs in the mixture.

Structure of the multi-Bernoulli mixture (MBM)

- We can also write



$$f_{k'|k}^{mbm}(X_{k'}) = \sum_{a \in \mathcal{A}_{k'|k}} w_{k'|k}^a \underbrace{\sum_{\substack{n_{k'|k} \\ \bigcup_{i=1}^{n_{k'|k}} X^i = X_{k'}}} \prod_{i=1}^{n_{k'|k}} f_{k'|k}^{i,a^i}(X^i)}_{\text{Multi-Bernoulli}}$$



$$w_{k'|k}^a = \frac{\prod_{i=1}^{n_{k'|k}} w_{k'|k}^{i,a^i}}{\sum_{a \in \mathcal{A}_{k'|k}} \prod_{i=1}^{n_{k'|k}} w_{k'|k}^{i,a^i}}$$



- $n_{k'|k}$ number of Bernoulli components.

- Equal to the number of measurements received so far.



- i is an index over Bernoulli components



- A global hypothesis $a = (a^1, \dots, a^{n_{k'|k}})$ where $a^i \in \{1, \dots, h_{k'|k}^i\}$ is the index to the single-target hypothesis for the i -th Bernoulli component.



- The weight of global hypothesis a is $w_{k'|k}^a$.

PMBM global hypotheses (I)

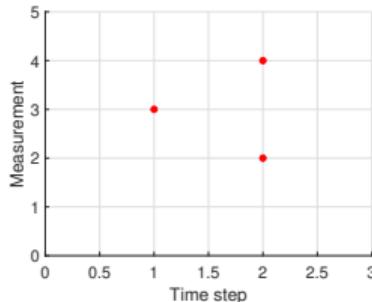
- We refer to measurement z_k^j using the pair (k, j) .
- Set of all these measurement pairs up to time step k is \mathcal{M}_k .
- A single target hypothesis a^i for the i -th Bernoulli has a set of measurement pairs $\mathcal{M}_k^{i,a^i} \subseteq \mathcal{M}_k$.
 - At most one measurement index per each time step in \mathcal{M}_k^{i,a^i} .
- In a global hypothesis, each measurement must belong to only one single target hypothesis.

Example 1

k i j

- We have $\mathcal{M}_2 = \{(1, 1), (2, 1), (2, 2)\}$.
- We consider a global hypothesis

注意: \mathcal{M}_k 表示所有测量对直到时间 k 。



k i a^i

- This global hypothesis: $\mathcal{M}_2^{1,1} = \{(1, 2)\}$, $\mathcal{M}_2^{2,1} = \{(2, 1)\}$, $\mathcal{M}_2^{3,1} = \{(2, 2)\}$.
- We can represent global hypothesis with a look-up table.

Illustrative example

!!!

这个例子很重要！！认真理解其意义！！

- Three time steps, measurement sets:
 - $Z_1 = \{z_1^1, z_1^2\}$.
 - $Z_2 = \emptyset$.
 - $Z_3 = \{z_3^1\}$.
- At time $k = 0$, the prior is a Poisson RFS.

Illustrative example: local hypotheses

Time

0

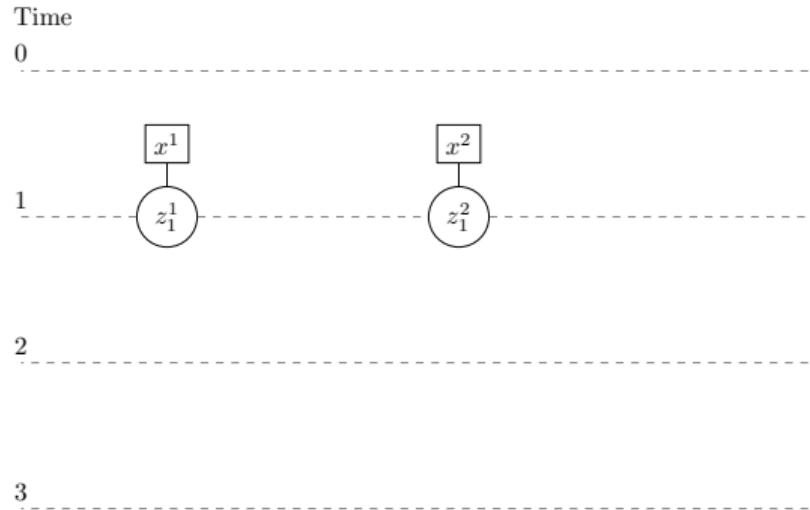
1

2

3

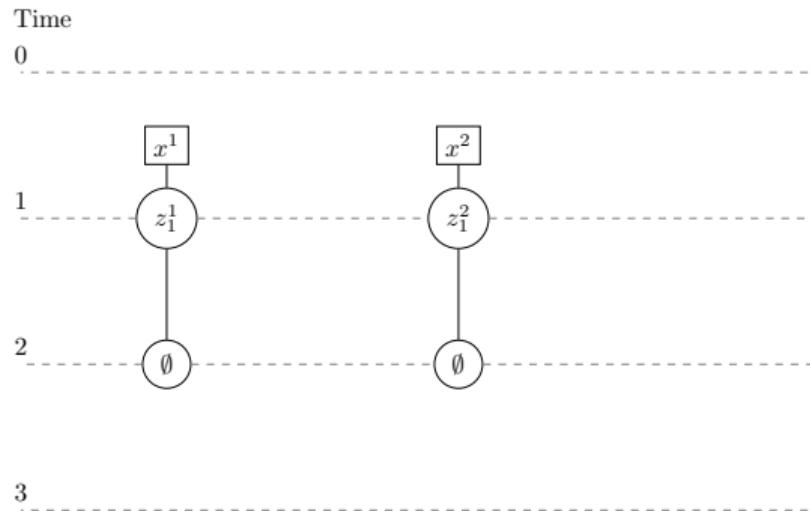
Empty MBM

Illustrative example: local hypotheses



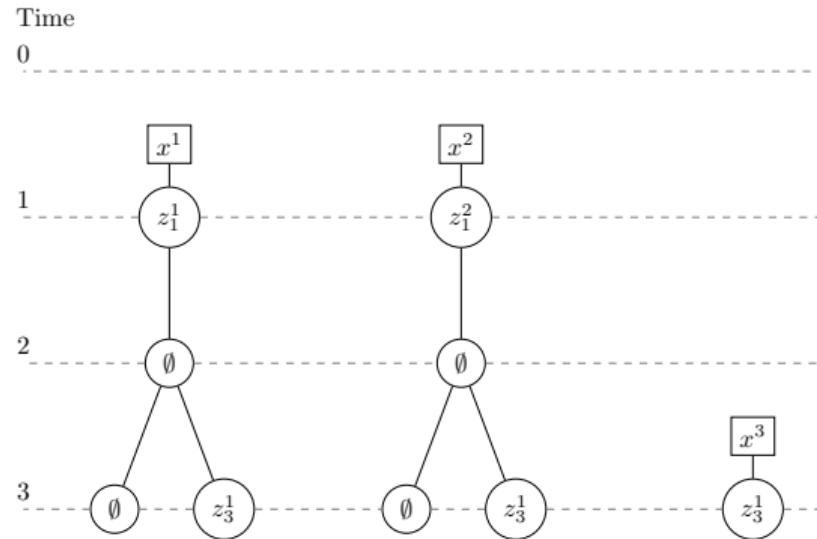
Two new Bernoullis in the MBM
For each leaf node, we have $r_{k'|k}^{i,a^i}$ and $p_{k'|k}^{i,a^i}(\cdot)$

Illustrative example: local hypotheses



Updated local hypotheses in the MBM
For each leaf node, we have $r_{k'|k}^{i,a^i}$ and $p_{k'|k}^{i,a^i}(\cdot)$

Illustrative example: local hypotheses



Updated local hypotheses, one new Bernoulli in the MBM

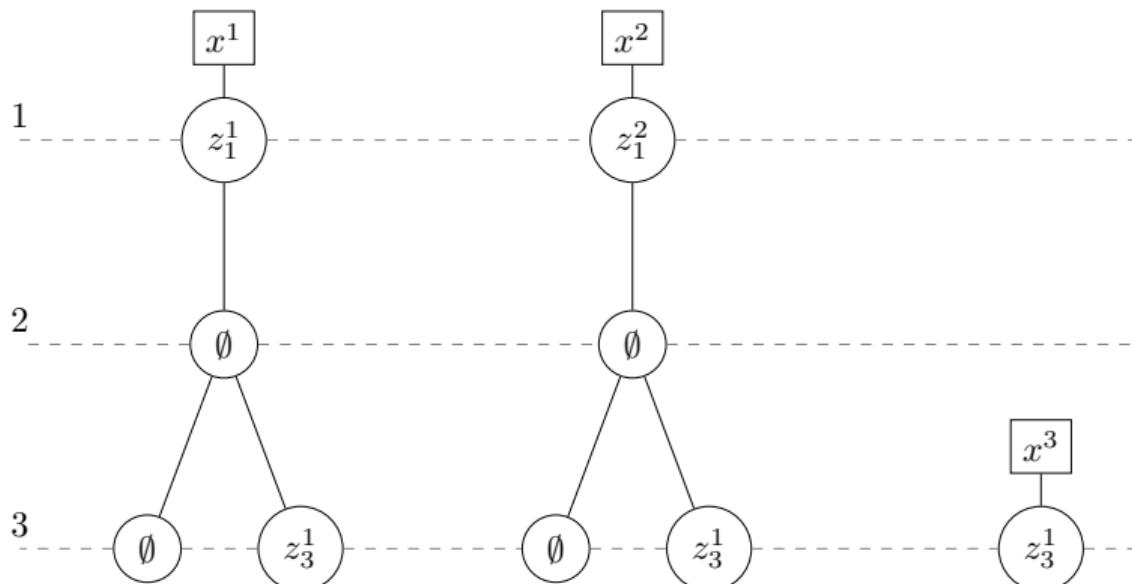
For each leaf node, we have $r_{k'|k}^{i,a^i}$ and $p_{k'|k}^{i,a^i}(\cdot)$

PMBM global hypotheses

Total number of MBs (global hypotheses): 3

Time

0



Look-up table:

$$\begin{bmatrix} 2 & 1 & 0 \\ 1 & 2 & 0 \\ 1 & 1 & 1 \end{bmatrix}$$

For simplicity: local hypotheses indexed from left to right.

Each Bernoulli is not represented in each MB (global hypothesis)

Tutorial: Poisson multi-Bernoulli mixtures for multiple target tracking

End of video

Section 4

PMBM prediction and update

PMBM prediction (I) !!!



- PPP and each Bernoulli is predicted independently.
- PPP prediction (same as in PHD filter) [7, 8, 9]

$$\lambda_{k|k-1}(x) = \overbrace{\lambda_k^B(x)}^{\text{New born}} + \overbrace{\int g(x|y) p^S(y) \lambda_{k-1|k-1}(y) dy}^{\text{Surviving targets}}$$

PMBM prediction (I)

- PPP and each Bernoulli is predicted independently.
- PPP prediction (same as in PHD filter) [7, 8, 9]

$$\lambda_{k|k-1}(x) = \underbrace{\lambda_k^B(x)}_{\text{New born}} + \overbrace{\int g(x|y) p^S(y) \lambda_{k-1|k-1}(y) dy}^{\text{Surviving targets}}$$

- MB prediction.

- No change in the number of Bernoullis or weights.

另外这里注意：可以看出，对于PMBM，如果PMBM要是没有最外面一层的那个每个Bernoulli component的hypothesis和对应的weight，换言之，如果把每个MB approximate成PPP，即用 $r^*p(x)$ 来表示Poisson intensity，那么PMBM filter便可以简化成PHD filter了。（因为PHD filter实际就是对一个PMBM RFS把其中每一个MB给approximate成PPP，从而变为了Poisson RFS和Poisson RFS的并集，即还是Poisson RFS，又因为Poisson RFS的intensity等于Poisson RFS的PHD这个first statistics moment，于是可以用propagate intensity的方式利用PHD filter来近似估计这个PMBM的multi-target state）。所以PHD filter实际可以看做是PMBM filter的一种不精确的近似方案。

$$\begin{aligned}n_{k|k-1} &= n_{k-1|k-1} \\h_{k|k-1}^i &= h_{k-1|k-1}^i \\w_{k|k-1}^{i,a^i} &= w_{k-1|k-1}^{i,a^i}\end{aligned}$$

显然对于每一个MB RFS，prediction时候需要根据motion model改变的只是最内一级的每一个Bernoulli component对应的single target state的Gaussian distribution，而外层的所有Bernoulli components的数量n，以及每一个(第i个)Bernoulli component相应的所有Hypotheses的数量 h^i 和该Bernoulli component相应的在任意一个Hypothesis下对应的weight $w^{(i), a^i}$ 都不随motion model的prediction改变。

PMBM prediction (II)

- Define

~~$\langle f, g \rangle = \int f(x) g(x) dx$~~

- Then, each Bernoulli is predicted as

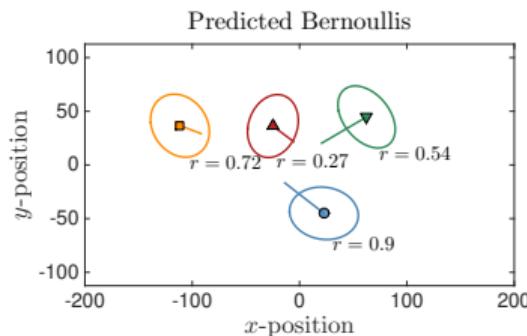
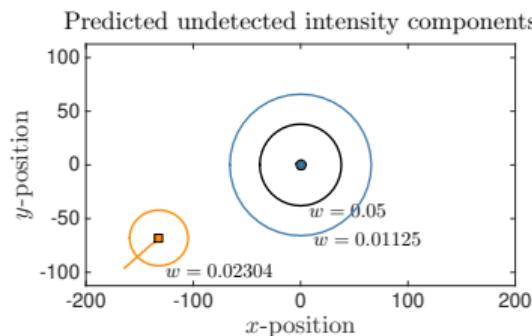
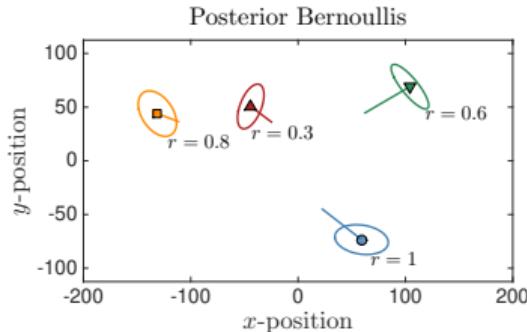
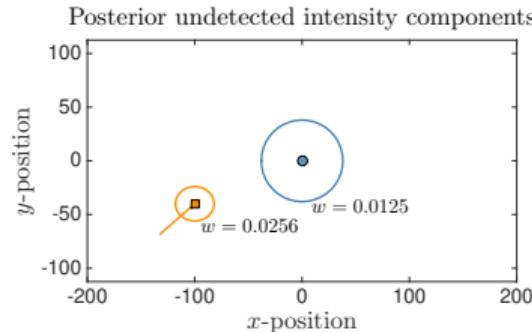
而对于每一个Bernoulli component的exist probability $r^i(i, a^i)$ 和相应Gaussian distribution的pdf $p^i(i, a^i)$ 显然要随 motion model 的prediction改变。

$$r_{k|k-1}^{i,a^i} = r_{k-1|k-1}^{i,a^i} \overbrace{\left\langle p_{k-1|k-1}^{i,a^i}, p^S \right\rangle}^{\text{average } p^S(\cdot)}$$

$$p_{k|k-1}^{i,a^i}(x) = \frac{\int g(x|y) p^S(y) p_{k-1|k-1}^{i,a^i}(y) dy}{\left\langle p_{k-1|k-1}^{i,a^i}, p^S \right\rangle}$$

PMBM prediction: visualisation

- 2D example, linear/Gaussian model.
- Birth intensity with single mixture component, mean position at origin, zero velocity.



PMBM update overview !!!

- There are four steps
 - Update the PPP (misdetection).
 - Update single target hypotheses for previous Bernoulli components.
 - Misdetection
 - Update with each received measurement
 - Create new Bernoulli components.
 - Construct updated global hypotheses table with weights.

PMBM update

!!!

- We receive $Z_k = \{z_k^1, \dots, z_k^{m_k}\}$.
- The PPP is updated as

$$\lambda_{k|k}(x) = (1 - p^D(x)) \lambda_{k|k-1}(x).$$

PMBM update

- We receive $Z_k = \{z_k^1, \dots, z_k^{m_k}\}$.
- The PPP is updated as

$$\lambda_{k|k}(x) = (1 - p^D(x)) \lambda_{k|k-1}(x).$$

potential targets

measurements from single target.

- We have $n_{k|k} = n_{k|k-1} + m_k$ Bernoullis.
- For previous Bernoullis $i = 1, \dots, n_{k|k-1}$
 - Number of local hypotheses $h_{k|k}^i = h_{k|k-1}^i (m_k + 1)$.
 - A new one for each measurement and misdetection.

Previous Bernoullis (misdetection)



- Misdetection hypothesis:

$$w_{k|k}^{i,a^i} = w_{k|k-1}^{i,a^i} \left(1 - r_{k|k-1}^{i,a^i} + r_{k|k-1}^{i,a^i} \overbrace{\left\langle p_{k|k-1}^{i,a^i}, 1 - p^D \right\rangle}^{\text{average } 1 - p^D(\cdot)} \right)$$

$$r_{k|k}^{i,a^i} = \frac{r_{k|k-1}^{i,a^i} \left\langle p_{k|k-1}^{i,a^i}, 1 - p^D \right\rangle}{1 - r_{k|k-1}^{i,a^i} + r_{k|k-1}^{i,a^i} \left\langle p_{k|k-1}^{i,a^i}, 1 - p^D \right\rangle}$$

$$p_{k|k}^{i,a^i}(x) = \frac{(1 - p^D(x)) p_{k|k-1}^{i,a^i}(x)}{\left\langle p_{k|k-1}^{i,a^i}, 1 - p^D \right\rangle}$$

Previous Bernoullis (detection)



- The local hypothesis updated with measurement z_k^j with index a^i and previous index \tilde{a}_i :

$$w_{k|k}^{i,a^i} = w_{k|k-1}^{i,\tilde{a}^i} r_{k|k-1}^{i,\tilde{a}^i} \left\langle p_{k|k-1}^{i,\tilde{a}^i}, p^D I(z_k^j | \cdot) \right\rangle$$

$$r_{k|k}^{i,a^i} = 1$$

$$p_{k|k}^{i,a^i}(x) = \frac{I(z_k^j | x) p^D(x) p_{k|k-1}^{i,\tilde{a}^i}(x)}{\left\langle p_{k|k-1}^{i,\tilde{a}^i}, p^D I(z_k^j | \cdot) \right\rangle}$$

where $I(\cdot | x)$ is the single-measurement density given x .

New Bernoullis

- For the Bernoulli initiated by z_k^j , whose index is $i = n_{k|k-1} + j$, we have two local hypotheses $(h_{k|k}^i = 2)$.
- The first one for non-existence

$$\mathcal{M}_k^{i,1} = \emptyset, \quad w_{k|k}^{i,1} = 1, \quad r_{k|k}^{i,1} = 0$$

New Bernoullis

- For the Bernoulli initiated by z_k^j , whose index is $i = n_{k|k-1} + j$, we have two local hypotheses ($h_{k|k}^i = 2$).
- The first one for non-existence

$$\mathcal{M}_k^{i,1} = \emptyset, \quad w_{k|k}^{i,1} = 1, \quad r_{k|k}^{i,1} = 0$$

- The second representing that the measurement z_k^j can have been originated by clutter or by a new target

$$\mathcal{M}_k^{i,2} = \{(k, j)\}$$

$$w_{k|k}^{i,2} = \lambda^C(z_k^j) + \langle \lambda_{k|k-1}, p^D I(z_k^j | \cdot) \rangle$$

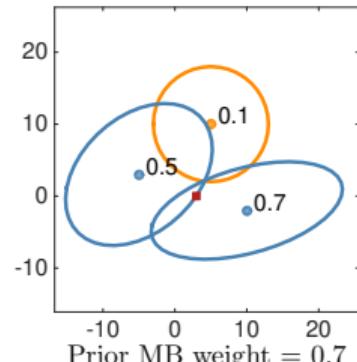
$$r_{k|k}^{i,2} = \frac{\langle \lambda_{k|k-1}, p^D I(z_k^j | \cdot) \rangle}{\lambda^C(z_k^j) + \langle \lambda_{k|k-1}, p^D I(z_k^j | \cdot) \rangle}$$

$$p_{k|k}^{i,a^i}(x) = \frac{p^D(x) I(z_k^j | x) \lambda_{k|k-1}(x)}{\langle \lambda_{k|k-1}, p^D I(z_k^j | \cdot) \rangle}$$

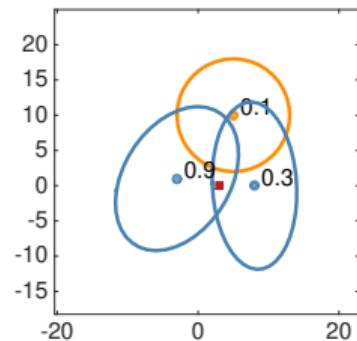
PMBM update: visualisation

Undetected objects PPP (Orange), Detected objects MB (Blue), Measurement (Red)

Prior MB weight = 0.3



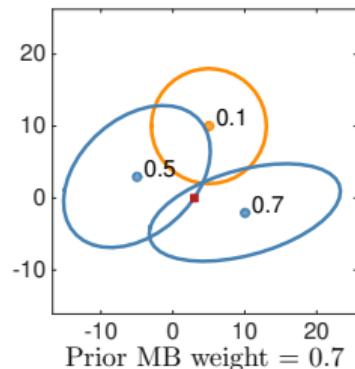
Prior MB weight = 0.7



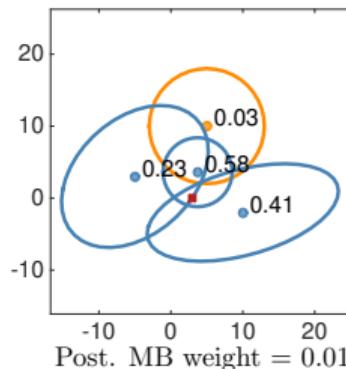
PMBM update: visualisation

Undetected objects PPP (Orange), Detected objects MB (Blue), Measurement (Red)

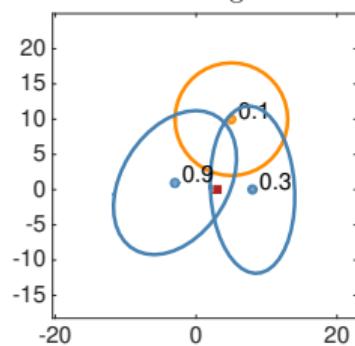
Prior MB weight = 0.3



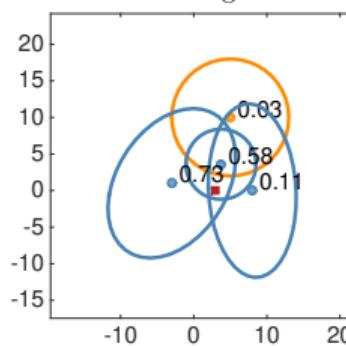
Post. MB weight = 0.01



Prior MB weight = 0.7



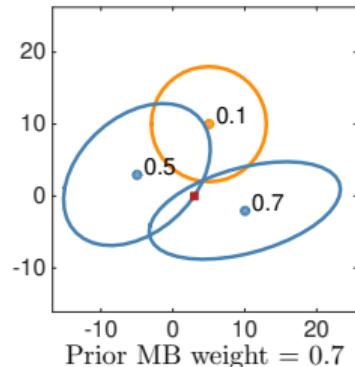
Post. MB weight = 0.01



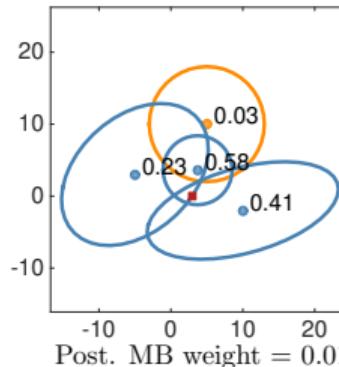
PMBM update: visualisation

Undetected objects PPP (Orange), Detected objects MB (Blue), Measurement (Red)

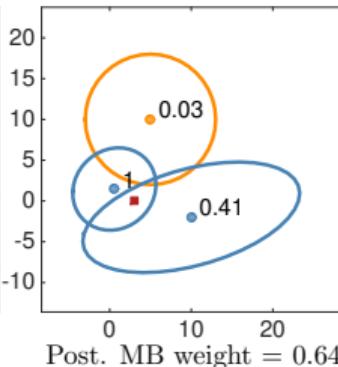
Prior MB weight = 0.3



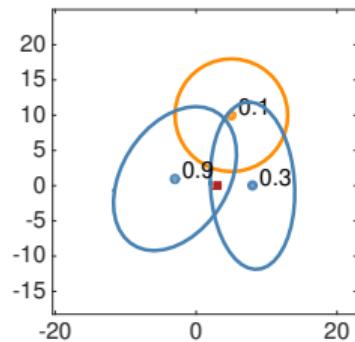
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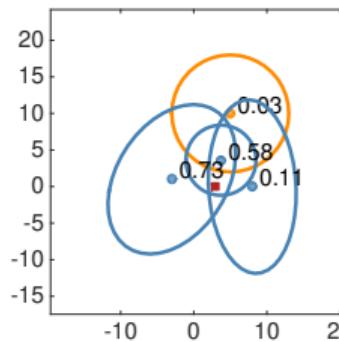
Post. MB weight = 0.05



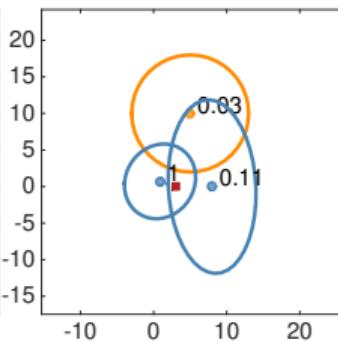
Prior MB weight = 0.7



Post. MB weight = 0.01



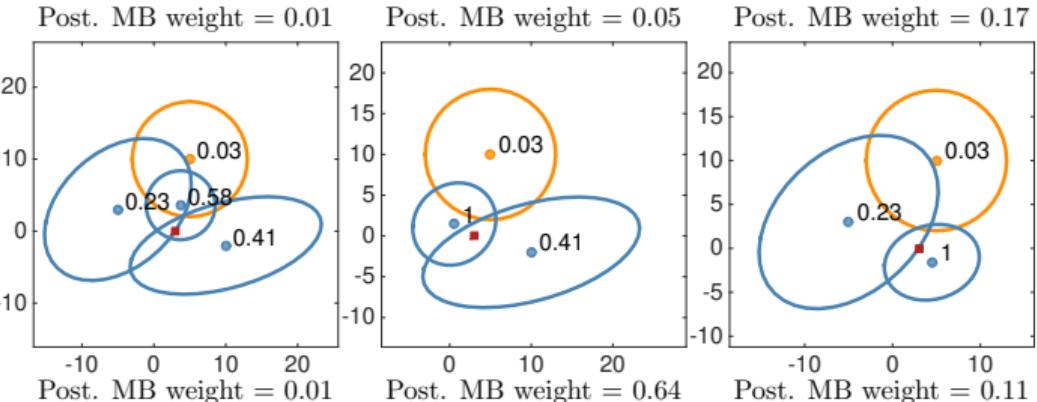
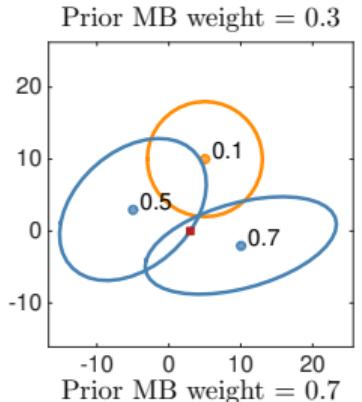
Post. MB weight = 0.64



PMBM update: visualisation

非常好的例子，展示了在上一帧的两个不同的hypotheses的MB条件下。新的某一个measurement如何与不同的Bernoulli RFS进行association而产生了6个hypotheses（因为有一个描述undetected objects的PPP和2个描述detected objects的Bernoulli components，所以针对每种上一帧的hypotheses生成了3种新的hypotheses，分别是measurement update object1的Bernoulli component, measurement update object2的Bernoulli component, measurement update undetected objects PPP，共计3种）

Undetected objects PPP (Orange), Detected objects MB (Blue), Measurement (Red)



Tutorial: Poisson multi-Bernoulli mixtures for multiple target tracking

End of video

Section 5

Practical aspects - pruning

Practical aspects

- The previous recursion can be implemented in closed-form using Gaussian single-target densities [6].
 - Linear/Gaussian models
 - Constant probabilities of detection and survival.
 - PPP birth intensity is Gaussian or Gaussian mixture.
- It uses Kalman filters.

Practical aspects

- The previous recursion can be implemented in closed-form using Gaussian single-target densities [6].
 - Linear/Gaussian models
 - Constant probabilities of detection and survival.
 - PPP birth intensity is Gaussian or Gaussian mixture.
- It uses Kalman filters.
- Problem: unbounded increase in the number of
 - Local hypotheses.
 - Global hypotheses.
 - Bernoullis.
 - PPP components (Gaussian mixture implementation).

Pruning

- Discard (Gaussian) components in $\lambda_{k|k}(\cdot)$ whose weight is below a threshold Γ_p .

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- Keep the global hypotheses
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- Remove the local hypotheses of the Bernoullis that do not take part in the considered global hypotheses.
- Remove the Bernoulli components whose existence is less than a threshold Γ_b .
 - It is also possible to recycle these components in the PPP [10].

Pruning while updating

- Even if we perform the previous pruning, the update step generates too many local and global hypotheses with negligible weight.
 - It is better to remove these hypotheses before they are calculated.
 - Pruning while updating.

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 - It is better to remove these hypotheses before they are calculated.
 - Pruning while updating. 
-  Gating: we only consider associations Bernoulli-to-measurement, such that measurements fall within a gate [11].
- Find global hypotheses with high weight
 -  Murty's algorithm [12] to obtain the k -best newly generated global hypotheses from a hypothesis.
 -  Sampling techniques: Markov chain Monte Carlo [13, 14], Gibbs sampling [15].
- Details of these operations for the PMBM filter can be found in [6].

Pruning in mathematical sense (I)

- Full PMBM posterior has an MBM component

$$f_{k|k}^{mbm}(X_k) = \sum_{a \in \mathcal{A}_{k|k}} w_{k|k}^a \underbrace{\sum_{\biguplus_{l=1}^{n_{k|k}} X^l = X_k} \prod_{i=1}^{n_{k|k}} f_{k|k}^{i,a^i}(X^i)}_{\text{Multi-Bernoulli}}$$

- Consider $w_{k|k}^a \approx 0$ for $a \in \mathcal{A}_{k|k} \setminus \tilde{\mathcal{A}}_{k|k}$, pruning sets $w_{k|k}^a = 0$, $f_{k|k}^{mbm}(X_k) \approx \tilde{f}_{k|k}^{mbm}(X_k)$

$$\tilde{f}_{k|k}^{mbm}(X_k) = \sum_{a \in \tilde{\mathcal{A}}_{k|k}} \tilde{w}_{k|k}^a \underbrace{\sum_{\biguplus_{l=1}^{n_{k|k}} X^l = X_k} \prod_{i=1}^{n_{k|k}} f_{k|k}^{i,a^i}(X^i)}_{\text{Multi-Bernoulli}}$$

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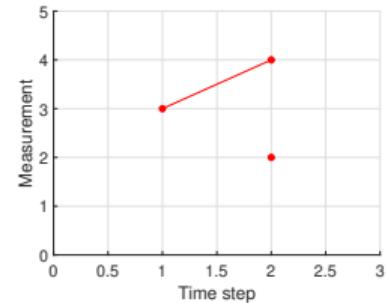
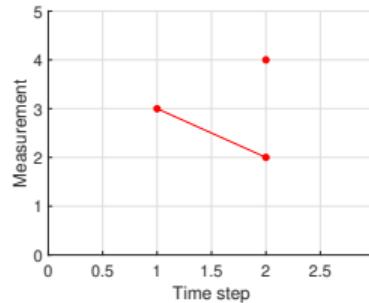
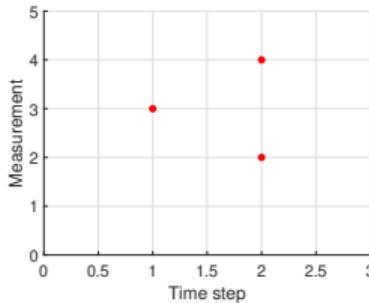
$$\tilde{w}_{k|k}^a = \frac{w_{k|k}^a}{\sum_{a \in \tilde{\mathcal{A}}_{k|k}} w_{k|k}^a}$$

Pruning in mathematical sense (II)

- Pruning global hypotheses in PMBM does not affect symmetry of posterior.
- Pruning Bernoullis simply sets $r_{k|k}^{i,a^i} = 0$ for $r_{k|k}^{i,a^i} \approx 0$.
- Pruning global hypotheses with the smallest weights minimises an upper bound of the L_1 error [16, Eq. (28)].

$$\left\| f_{k|k} - \tilde{f}_{k|k} \right\|_1 = \int \left| f_{k|k}(X) - \tilde{f}_{k|k}(X) \right| \delta X$$

Pruning - Example (I)



- Bernoulli $i = 1$: $a^i \in \{1, 2, 3\}$
- Bernoulli $i = 2$: $a^i \in \{1, 2\}$, $a^i = 1$ implies $r_{k|k}^{2,a^i} = 0$.
- Bernoulli $i = 3$: $a^i \in \{1, 2\}$, $a^i = 1$ implies $r_{k|k}^{3,a^i} = 0$.
- 3 Global hypotheses
 - (1, 2, 2) (potential target 1 misdetected at time step 2, potential targets 2 and 3 may exist).
 - (2, 1, 2) (potential target 1 detected at time step 2, potential target 2 does not exist and 3 may exist).
 - (3, 2, 1) (potential target 1 detected at time step 2, potential target 2 may exist and 3 does not exist).

Pruning - Example (II)

- Full MBM component in the PMBM posterior

$$f_{k|k}^{mbm}(X_k) = \sum_{a \in \mathcal{A}_{k|k}} w_{k|k}^a \underbrace{\sum_{\bigcup_{l=1}^{n_{k'|k}} X^l = X_k} \prod_{i=1}^{n_{k'|k}} f_{k|k}^{i,a^i}(X^i)}_{\text{Multi-Bernoulli}}$$

with $\mathcal{A}_{k|k} = \{(1, 2, 2), (2, 1, 2), (3, 2, 1)\}$.

- Let $w_{k|k}^{(3,2,1)} = 10^{-5}$ and prune this hypothesis such that $w_{k|k}^{(3,2,1)} \approx 0$ and

$$\tilde{f}_{k|k}^{mbm}(X_k) = \sum_{a \in \tilde{\mathcal{A}}_{k|k}} \tilde{w}_{k|k}^a \underbrace{\sum_{\bigcup_{l=1}^{n_{k|k}} X^l = X_k} \prod_{i=1}^{n_{k|k}} f_{k|k}^{i,a^i}(X^i)}_{\text{Multi-Bernoulli}}$$

where $\tilde{\mathcal{A}}_{k|k} = \{(1, 2, 2), (2, 1, 2)\}$.

Tutorial: Poisson multi-Bernoulli mixtures for multiple target tracking

End of video

Section 6

Relation to other filters: MHT, δ -GLMB, PMB, JIPDA

Multi-Bernoulli mixture (MBM) filter

- PMBM is a state-of-the-art multiple hypothesis tracking (MHT) algorithm [17, 18, 19, 20, 21].
 - Data-to-data hypotheses.
 - Information on undetected targets.
 - Probabilistic target existence per local hypothesis.

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- A PMBM becomes MBM if intensity of Poisson is zero.
- If the birth process is multi-Bernoulli (or MBM), the posterior is MBM [6].

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- If the birth process is multi-Bernoulli (or MBM), the posterior is MBM [6].
- MBM filter:
 - Same update as PMBM (with $\lambda_{k'|k}(x) = 0$).
 - In prediction, we add the new Bernoullis.

Benefits PPP birth over MB birth

- PPP birth does not set a maximum on the number of new born targets (MB does).
 - MB can miss new born targets if there is model mismatch.
- Resulting PMBM has a more efficient representation of the hypotheses than MBM filter.
 - Measurement-driven Bernoulli initiation [22].
- PPP birth is suitable for continuous time multi-target modelling.

Multi-Bernoulli mixture 01 (MBM₀₁) filter

- A Bernoulli can be written as a mixture of Bernoulli densities with existence probabilities that are either zero or one as

$$f_{k'|k}^{i,a^i}(X) = (1 - r_{k'|k}^{i,a^i}) f_{k'|k}^{i,a^i,0}(X) + r_{k'|k}^{i,a^i} f_{k'|k}^{i,a^i,1}(X)$$

where

$$f_{k'|k}^{i,a^i,\theta_i}(X) = \begin{cases} 1 - \theta_i & X = \emptyset \\ \theta_i p_{k|k-1}^{i,a^i}(x) & X = \{x\} \end{cases}$$

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- MB can be expanded into MBM₀₁.
- Exponential increase in number of global hypotheses.
- MBM₀₁ filter corresponds to the same recursion as MBM filter but performing the 01 expansion after prediction.
 - Inefficient hypothesis representation compared to PMBM and MBM.

Labelling MBM and MBM_{01} filters

- Unlabelled MB birth

$$f_k^b(X_k) = \sum_{X^1 \uplus \dots \uplus X^{n_k^b} = X_k} \prod_{l=1}^{n_k^b} f_k^{b,l}(X^l)$$

where l -th Bernoulli component is

$$f_k^{b,l}(X_k) = \begin{cases} 1 - r_k^{b,l} & X_k = \emptyset \\ r_k^{b,l} p_k^{b,l}(x) & X_k = \{x\} \\ 0 & \text{otherwise.} \end{cases}$$

- Both MBM and MBM_{01} filters can handle labelled Bernoullis [6, Sec. IV] [22].
 - Single-target state becomes $x = (x', \ell)$.
 - The density $p_k^{b,l}(\cdot)$ becomes $p_k^{b,l}((x', \ell)) = p_k^{b,l}(x') \delta[\ell - (k, l)]$.
 - Each Bernoulli is uniquely labelled upon birth.
 - The single target transition density $g(\cdot | \cdot)$ is $g((x', \ell_x) | (y', \ell_y)) = \delta[\ell_x - \ell_y] g(x' | y')$.
 - Each Bernoulli does not change its (unique) label.

Labelling MBM and MBM_{01} filters

- Labelling does not change the filtering recursion.
 - Same prediction and update as unlabelled MBM and MBM_{01} filters.
- The posterior now represents a labelled RFS [23].
 - Labels can be used for sequential track formation.
 - It works well in many cases but it does not in some cases, e.g., IID births [24].

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 - Same prediction and update as unlabelled MBM and MBM_{01} filters.
- The posterior now represents a labelled RFS [23].
 - Labels can be used for sequential track formation.
 - It works well in many cases but it does not in some cases, e.g., IID births [24].
- The δ generalised labelled multi-Bernoulli (δ -GLMB) [23] is equivalent to the labelled MBM_{01} filter
 - Less efficient representation of hypotheses compared to PMBM and MBM.

Number of global hypotheses after first update (I)

- We analyse the number of global hypotheses after the initial prediction/update for the different filters.
 - Closed-form expressions for all filters.
 - Insights into how filters deal with hypotheses.
- For Poisson birth model at time step 0, the updated posterior by the PMBM filter has one global hypothesis.
 - Posterior is in PMB form, regardless of the number of measurements.
 - Fast to calculate.
- For multi-Bernoulli birth with n components and m measurements, the MBM posterior has $N_A^{\text{MBM}}(m, n)$ global hypotheses

$$N_A^{\text{MBM}}(m, n) = \sum_{p=0}^{\min(m, n)} p! \binom{m}{p} \binom{n}{p}$$

Number of global hypotheses after first update (II)

- For multi-Bernoulli birth with n components, the number of MBM_{01} predicted global hypotheses with n_a alive targets is $\binom{n}{n_a}$.
- The number of updated global hypothesis in $\text{MBM}_{01}(\delta\text{-GLMB})$ form for m measurements is

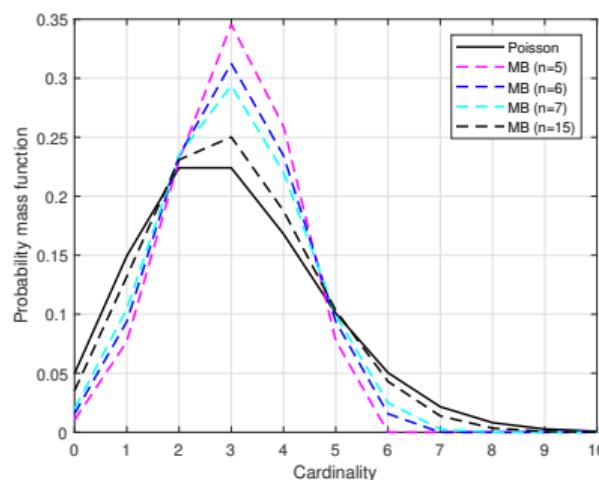
$$N_A^{\text{MBM}_{01}}(m, n) = \sum_{n_a=0}^n \binom{n}{n_a} N_A^{\text{MBM}}(m, n_a)$$

Example on number of global hypotheses

- Poisson birth model with intensity at time step 0

$$\lambda^0(x) = 3\mathcal{N}(x; \bar{x}, P)$$

that covers the whole surveillance area. The mean number of expected targets is 3.



- We can approximate the PPP, with n Bernoullis with existence $3/n$, $n \geq 3$, and same spatial distribution.
- We need at least 5 Bernoullis components to roughly cover the main cardinalities of relevance.

Example on number of global hypotheses (II)

- For $m = 14$, the number of global hypotheses is

n	MB birth		PPP birth
	MBM	MBM_{01}/δ -GLMB	PMBM
4	33.909	46.328	
5	384.091	583.552	
6	4.010.455	6.882.352	1
7	38.398.641	75.826.144	

- PMBM only requires one global hypothesis.
- MBM and MBM_{01}/δ -GLMB show remarkable increase in the number of global hypotheses.

PMB approximations

- A PMBM can also be approximated by a PMB, collapsing all global hypotheses into a single one.
- There are several possible algorithms.
- The track-oriented PMB filter is an RFS version of joint integrated probabilistic data association (JIPDA) filter [5].
- Variational PMB filter aims to obtain the best fitting PMB [25].
 - Quite beneficial for targets moving in close proximity.

Tutorial: Poisson multi-Bernoulli mixtures for multiple target tracking

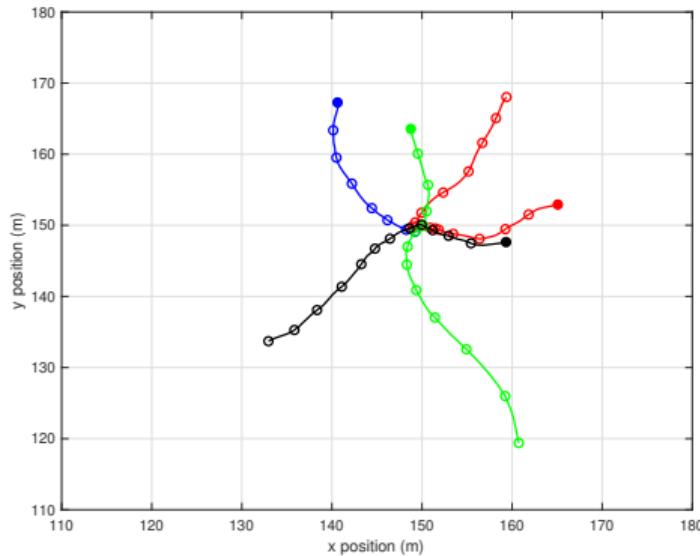
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Section 7

Simulation example
Extension to sets of trajectories

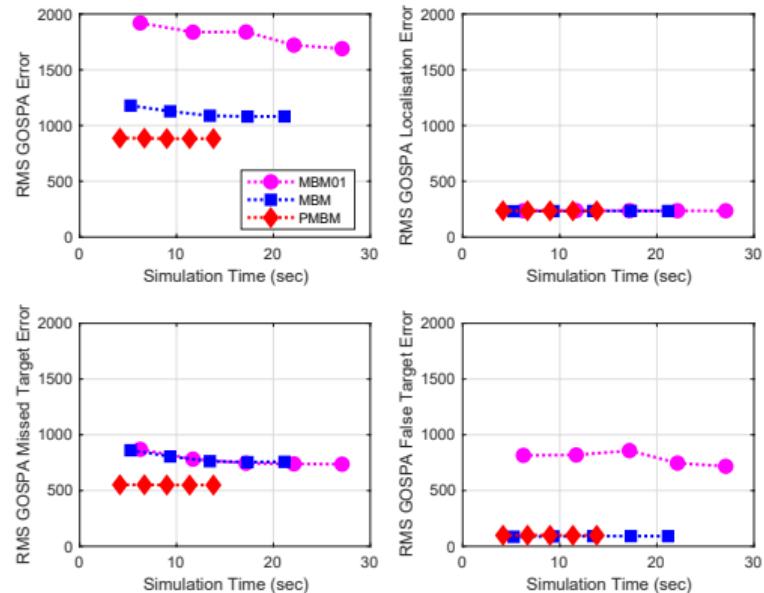
Simulation scenario

- Targets move in proximity and one target dies around the midpoint.
- Two targets born at time step 1, and two targets born at time step 21.
- We evaluate the multi-target filtering performance of PMBM [6], MBM [22] and MBM_{01} (δ -GLMB) [15].
- Poisson birth and MB birth have the same PHD.



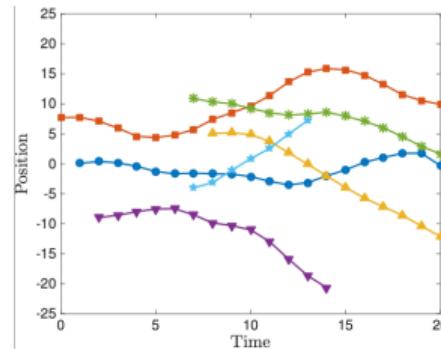
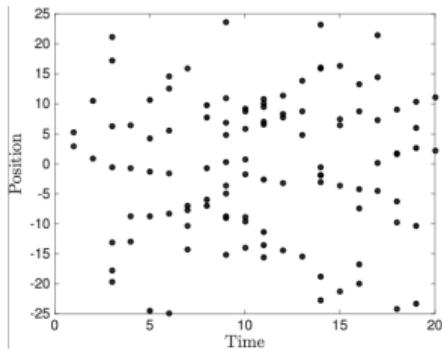
Simulation results

- GOSPA [2] error and its decomposition: localisation error, missed detection error, false detection error.
- We analysed multi-target filtering performance for different global hypotheses capping threshold $N_h \in \{100, 200, 300, 400, 500\}$.
- MBM outperforms $\text{MBM}_{01}/\delta\text{-GLMB}$ mainly due to fewer false targets.
- PMBM outperforms MBM mainly due to fewer missed targets.



Sets of trajectories: motivation

- We have so far focused on multi-target **filtering** whose objective is to estimate the **target states**.
- The goal of multi-target **tracking** is to estimate **target trajectories**
 - Input: cluttered and noisy sequences of measurements.
 - Output: state sequences from time of birth to time of death (or current time, if still alive).

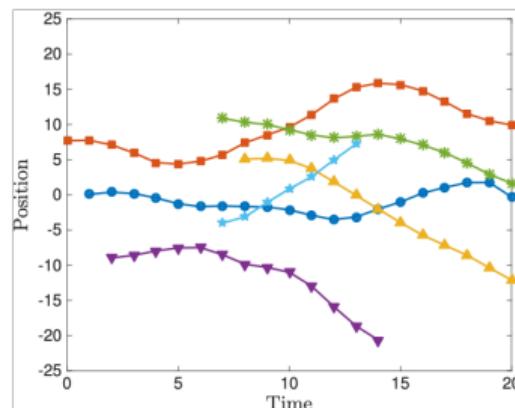


- Computing only the multi-target filtering densities creates difficulties when forming trajectories.
- Sequential track formation using labelling information may not work well, e.g., when birth is IID.
- An optimal way to estimate trajectories is to consider **posterior densities on sets of trajectories** [24].

Sets of trajectories: possible problem formulations

The set of all trajectories

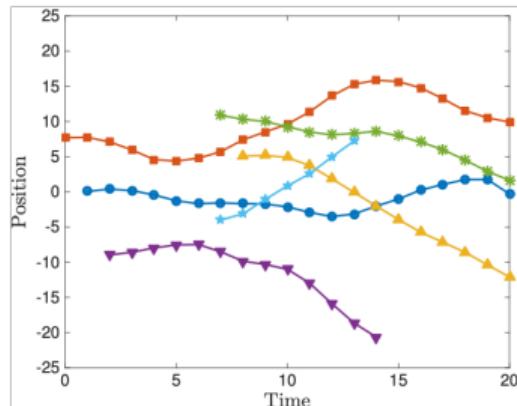
- Estimate trajectories of all targets present at some point in time ($\leq k$).
- Example: to collect ground truth data for self-driving vehicles. To track human cells, sport athletes, etc.



Sets of trajectories: possible problem formulations

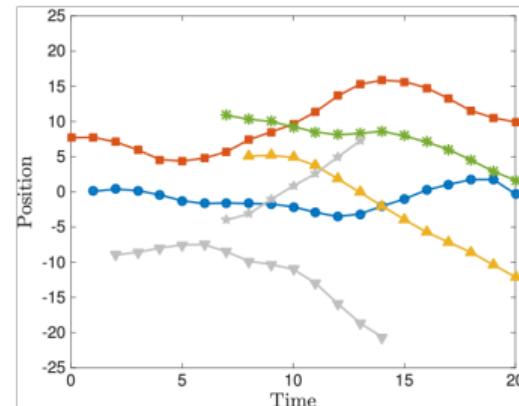
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- Estimate trajectories of all targets present at some point in time ($\leq k$).
- Example: to collect ground truth data for self-driving vehicles. To track human cells, sport athletes, etc.



The set of current trajectories

- Estimate trajectories of all currently present targets.
- Example: for surveillance systems. For instance, of ships at sea, people at airports, etc.



Sets of trajectories: parameterisation

Single trajectory parameterisation

We write single trajectories as

$$(t, x^{1:i})$$

where t is the time of birth, i is the length of trajectory and $x^{1:i}$ is the sequence of states.

Sets of trajectories: parameterisation

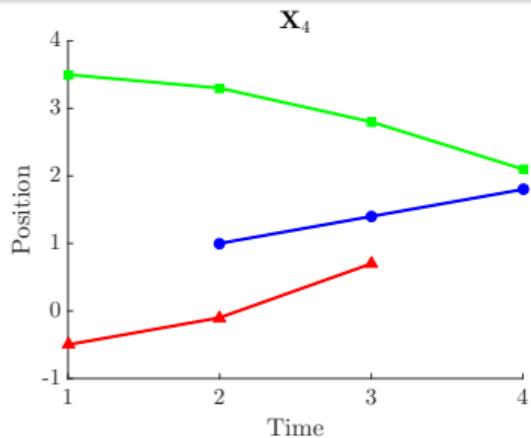
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$$(t, x^{1:i})$$

where t is the time of birth, i is the length of trajectory and $x^{1:i}$ is the sequence of states.

- $t + i - 1 = k$ means trajectory is ongoing.
- $t + i - 1 < k$ means trajectory ended at time $t + i - 1$.
- We use \mathbf{X}_k to denote the set of trajectories at time k .
- The number of trajectories may be larger than the number of targets at time k .
- The set \mathbf{X}_k is a random finite set.



Sets of trajectories: Bayesian filtering

- There is a one-to-one mapping between \mathbf{X}_k and the physical reality:
 \mathbf{X}_k is a minimal representation of the quantity of interest!
- We now obtain the multi-trajectory posterior density of \mathbf{X}_k using Bayesian filtering:
 - Chapman-Kolmogorov prediction

$$f_{k|k-1}(\mathbf{X}_k) = \int f_{k|k-1}(\mathbf{X}_k|\mathbf{X}_{k-1}) f_{k-1|k-1}(\mathbf{X}_{k-1}) \delta \mathbf{X}_{k-1}$$

- Bayes update

$$f_{k|k}(\mathbf{X}_k) = \frac{f(Z_k|\mathbf{X}_k) f_{k|k-1}(\mathbf{X}_k)}{\int f(Z_k|\mathbf{Y}) f_{k|k-1}(\mathbf{Y}) \delta \mathbf{Y}}$$

- Concepts and models on RFSs of targets, e.g., set functions/densities, set integrals, can be generalized to sets of trajectories in straightforward and theoretically rigorous manners.
- Measure theoretic aspects of sets of trajectories are covered in [26].
- Sets of trajectories can be used to develop performance metrics [27].

PMBM for sets of trajectories

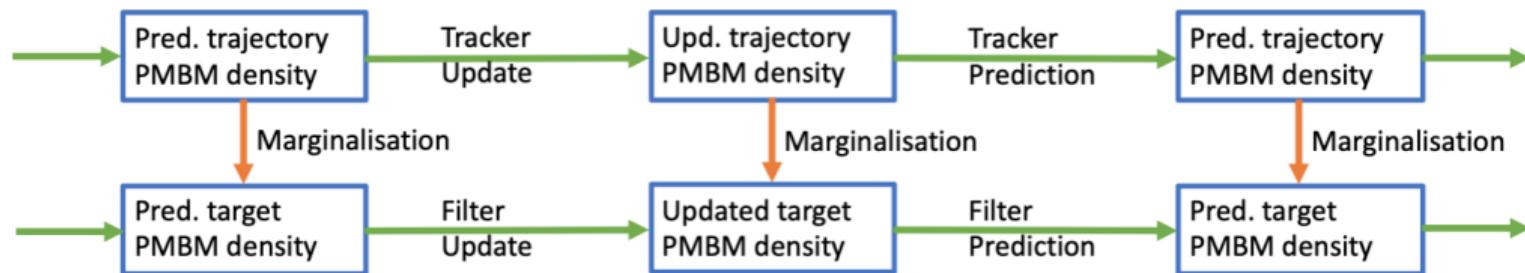
- The PMBM multi-trajectory density is a conjugate prior to the standard models (Poisson birth).
- We call the resulting multi-trajectory filter the PMBM tracker or trajectory PMBM filter [28, 26].
- Conjugacy also holds for MB (mixture) birth [24, 26].
- Global hypotheses and weights are similar as those in the PMBM filter for sets of targets.

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- Conjugacy also holds for MB (mixture) birth [24, 26].
- Global hypotheses and weights are similar as those in the PMBM filter for sets of targets.
- Interpretation:
 - Poisson RFS:
 - Models the set of undetected targets.
 - Its intensity describes a single trajectory distribution over $(t, x^{1:i})$.
 - Bernoulli RFS:
 - Models a single potential trajectory given a sequence of associations.
 - Its density describes a single trajectory distribution over $(t, x^{1:i})$.
 - MB RFS models set of detected trajectories for a global hypothesis.
 - MBM RFS models trajectories of targets that have been detected (information conveyed through multiple global hypotheses).

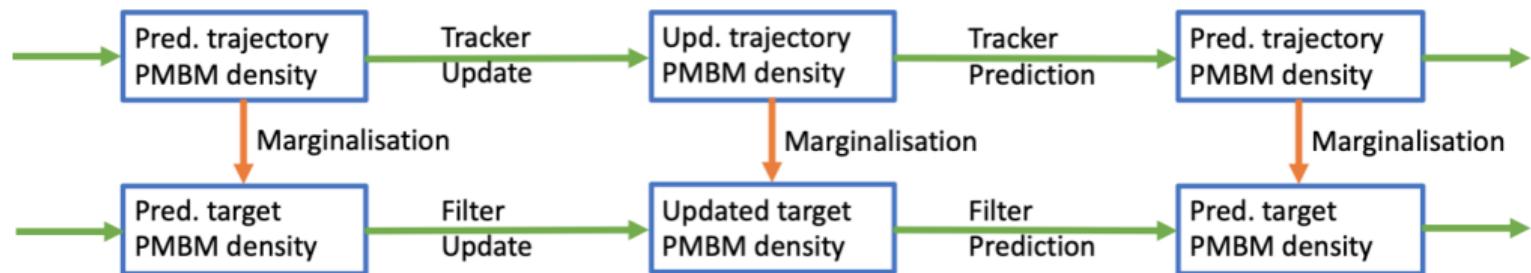
PMBM trackers vs. PMBM filters

- A trajectory Bernoulli density can be marginalised to the current time to obtain a target Bernoulli density.
- \Rightarrow Marginalising PMBM set of trajectories density gives a PMBM set of targets density (set of targets' current states).



PMBM trackers vs. PMBM filters

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- Key insights:
 - In PMBM filtering we marginalize out the history in every prediction step.
 - In PMBM trackers, we maintain knowledge about the past which enables us to estimate trajectories directly from posterior.

Simulation example

- Three targets first move close to each other and then separate.
- After time 50, ambiguous which target goes where.
- Example results: PMBM tracker (top) and δ -GLMB filter (bottom).
- PMBM tracker:
 - estimates the set of trajectories directly from posterior density,
 - can use smoothing to further improve trajectory estimates, though not necessary.
 - does not report trajectories with unrealistic switches.

Sets of trajectories: conclusions

- Sets of trajectories can leverage on the many advantages with PMBM filters, e.g., few hypotheses and initiate tracks based on measurements.
- We obtain trajectory estimates directly from the posterior, without necessarily increasing the computational complexity.
- The challenges (track fragmentation and switches) that we observed with labels are resolved: every trajectory estimate in \mathbf{X}_k originates from a single local hypothesis.
- Using smoothing, we can improve performance further.

Summary

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- We have introduced random finite sets and its properties.
- The PMBM filter is the closed-form solution to multi-target filtering problems for Poisson birth.
- The structure of the PMBM filter enjoys very efficient representation of global hypotheses compared to MBM, MBM_{01} filters.
- PMBM can be extended to include information on sets of trajectories.

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- PMBM can be extended to include information on sets of trajectories.
- Complementary materials:
 - EdX course “Multi-Object Tracking for Automotive Systems”:
<https://www.edx.org/course/multi-object-tracking-for-automotive-systems>.
 - Multiple Object Tracking YouTube channel:
<https://www.youtube.com/channel/UCa2-fpj6AV8T6JK1uTRuFpw/about>.
 - GitHub repositories for variants of PMBM implementations:
 - <https://github.com/Agarciafernandez>.
 - <https://github.com/yuhsuansia>.

Tutorial: Poisson multi-Bernoulli mixtures for multiple target tracking

End of video

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