

An Evidence Clustering DSMT Approximate Reasoning Method Based on Convex Functions Analysis

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Abstract

With the increasing number of focal elements in frame of discernment, computational complexity of DSMT (Dezert-Smarandache Theory) increases exponentially, which blocks the wide application and development of DSMT. To solve this problem, a new evidence clustering DSMT approximate reasoning method is proposed in this paper based on convex functions analysis. The computational complexity of the method in this paper increases linearly instead of exponentially with the increasing number of focal elements in discernment framework. First, the method clusters the belief masses of focal elements in each evidence. Then, the first step results are obtained by the proposed DSMT approximate convex functions formula. Finally, the method gets the approximate fusion results by normalization method. The results of simulation show that the approximate fusion results of the method in this paper has higher Euclidean similarity with the exact fusion results of DSMT+PCR5, and need less computational complexity than the existing approximate methods. Especially, in the case of large data and complex fusion problems, the method in this paper can get highly accurate results and need low computation complexity.

Keywords: Evidence clustering; Approximate reasoning; Information fusion; Convex functions analysis; Dezert-Smarandache Theory

1. Introduction

As a novel key technology with vigorous development, information fusion can integrate multiple-source incomplete information and reduce uncertainty of information which always has the contradiction and redundancy. Information fusion can improve rapid correct decision capacity of intelligent systems and has been successfully used in the military and economy fields, thus great attention has been paid to its development and application by scholars in recent years¹⁻⁶. As information environment becomes more and more complex, greater demands for efficient fusion of highly conflict evidence are being placed on information fusion. DSMT is a new effective method for the fusion problem of uncertain, imprecise and highly conflict evidence, jointly proposed by French scientist Dr. Jean Dezert and American mathematician Florentin⁶. DSMT can be considered as an extension of the classical Dempster-Shafer.

DSmT is able to solve complex static or dynamic fusion problems beyond the limits of the DST framework, specially when conflicts between sources become large and when the refinement of the frame of the problem under consideration, denoted Θ , becomes inaccessible because of the vague, relative and imprecise nature of elements of Θ ⁶⁻⁸. Recently, DSmT has been applied to many fields, such as, image processing, Robot's Map Reconstruction, Target Type Tracking, Sonar imagery and Radar targets classification and so on^{6,9-12}. The bottleneck problem to block the wide application and development of DSmT is that with the increment of focal element number in frame of discernment, computational complexity increases exponentially.

In order to solve this problem, many scholars presents approximate reasoning method of evidence combination in D-S framework¹³⁻¹⁵. But these methods almost can not satisfy the small amount of computational complexity and less loss of information requirements at the same time. Dr. Li Xinde and other scholars proposed a fast approximate reasoning method in hierarchical DSmT¹⁶⁻¹⁸. However, when processing highly conflict evidence by the method, the belief assignments of correct main focal elements transfer to the other focal elements, which leads to low Euclidean similarity of the results in this case.

Aiming at reducing the computational complexity of DSmT and obtaining accurate results in any case, a new evidence clustering DSmT approximate reasoning method is proposed in this paper. In section 2, information fusion method of DSmT+PCR5 is introduced briefly. In section 3, Mathematical analysis of DSmc+PCR5 formula is conducted, which discovers every conflict mass product satisfies the properties of convex function, obtains the approximate convex function formula of DSmT+PCR5 and analyses approximate convex function formula errors. Then a new approximate reasoning DSmT method is proposed by analysis of approximate convex function formula errors in section 4. In section 5, analysis of computation complexity of DSmT+PCR5 and the method in this paper is carried out. The results of simulation show that the results of the method proposed in this paper have higher Euclidean similarity with the exact fusion results of DSmT+PCR5, and lower computational complexity than existing DSmT approximate method¹⁸ in section 6.

2. Information fusion method of DSmT+PCR5

Instead of applying a direct transfer of partial conflicts onto partial uncertainties as with DSmH, the idea behind the Proportional Conflict Redistribution(PCR) rule¹⁹ is to transfer (total or partial) conflicting masses to non-empty sets involved in the conflicts proportionally with respect to the masses assigned to them by sources as follows⁶:

1. calculation the conjunctive rule of the belief masses of sources;
2. calculation the total or partial conflicting masses;
3. redistribution of the (total or partial) conflicting masses to the non-empty sets involved in the conflicts proportionally with respect to their masses assigned by the sources.

The way the conflicting mass is redistributed yields actually several versions of PCR rules. PCR5 is the most mathematically exact redistribution method of conflicting mass. This rule redistributes the partial conflicting mass to the elements involved in the partial conflict, considering the conjunctive normal form of the partial conflict. It does a better redistribution of the conflicting mass than Dempster's rule since PCR5 goes backwards on the tracks of the conjunctive rule and redistributes the conflicting mass only to the sets involved in the conflict and proportionally to their masses put in the conflict.

The PCR5 formula for the combination of two sources ($s = 2$) is given by⁶:

$$m_{\text{PCR5}}[\emptyset] = 0, \forall X \in G^\ominus \setminus X$$

$$m_{\text{PCR5}}[X] = m_{12}(X) + \sum_{\substack{Y \in G^\ominus \setminus X \\ X \cap Y = \emptyset}} \left[\frac{m_1(X)^2 m_2(Y)}{m_1(X) + m_2(Y)} + \frac{m_2(X)^2 m_1(Y)}{m_2(X) + m_1(Y)} \right] \quad (1)$$

where all sets involved in formulas are in canonical form and where G^\ominus corresponds to classical power set 2^\ominus if Shafer's model is used, or to a constrained hyper-power set D^\ominus if any other hybrid DSm model is used instead, or to the super-power set S^\ominus if the minimal refinement Θ^{ref} of Θ is used; $m_{12}(X) = m_\cap(X)$ corresponds to the conjunctive consensus on X between the $S = 2$ sources and where all denominators are different from zero. If a denominator is zero, that fraction is discarded.

3. Mathematical analysis of DSmc+PCR5 formula

As shown in formula (1), $\sum_{\substack{Y \in G^\ominus \setminus X \\ X \cap Y = \emptyset}} \left[\frac{m_1(X)^2 m_2(Y)}{m_1(X) + m_2(Y)} + \frac{m_2(X)^2 m_1(Y)}{m_2(X) + m_1(Y)} \right]$ has symmetry.

Due to the symmetry, analyse one item $\frac{m_1(X)^2 m_2(Y)}{m_1(X) + m_2(Y)}$.

Let $m_1(X) = a, m_2(Y) = b$,

get $\frac{m_1(X)^2 m_2(Y)}{m_1(X) + m_2(Y)} = \frac{a^2 b}{a + b} = a^2 \left[1 - a \left(\frac{1}{a + b} \right) \right]$, then

$$\sum_{\substack{Y \in G^\ominus \setminus X \\ X \cap Y = \emptyset}} \left[\frac{m_1(X)^2 m_2(Y)}{m_1(X) + m_2(Y)} \right] = a^2 \left[n - a \left(\frac{1}{a + b_1} + \frac{1}{a + b_2} + \dots + \frac{1}{a + b_n} \right) \right], b_1, b_2, \dots, b_n = Y \quad (2)$$

Let $f(x) = \frac{1}{a + x}$,

due to $f(x)$ is continuous function on $[0, 1]$, has second order derivatives on $(0, 1)$, and $f''(x) > 0$ on $(0, 1)$, $f(x)$ is a convex function.

So $\frac{1}{n} (f(x_1) + f(x_2) + \dots + f(x_n)) \leq f\left(\frac{x_1 + x_2 + \dots + x_n}{n}\right)$, the equality holds iff $x_1 = x_2 = \dots = x_n$.

The approximate convex function formula is given by:

$$\frac{1}{a + x_1} + \frac{1}{a + x_2} + \dots + \frac{1}{a + x_n} = \frac{n}{a + (x_1 + x_2 + \dots + x_n)/n} + \Delta \quad (3)$$

Let $x_1 \leq x_2 \leq \dots \leq x_i \leq \dots \leq x_n$, carry out analysis of convex function formula errors.

$$\begin{aligned} \Delta = & \left[\frac{1}{a + x_1} - \frac{1}{a + (x_1 + x_2 + \dots + x_n)/n} \right] \\ & + \left[\frac{1}{a + x_2} - \frac{1}{a + (x_1 + x_2 + \dots + x_n)/n} \right] + \dots + \left[\frac{1}{a + x_n} - \frac{1}{a + (x_1 + x_2 + \dots + x_n)/n} \right] \end{aligned} \quad (4)$$

analysis of the i item in equality(4).

Let $(x_1 + x_2 + \dots + x_n)/n = x_0$, then $\frac{1}{a + x_i} - \frac{1}{a + (x_1 + x_2 + \dots + x_n)/n} = \frac{1}{a + x_i} - \frac{1}{a + x_0}$.

By Taylor expansion theorem,

$$\frac{1}{a + x_i} - \frac{1}{a + x_0} = f'(x_0)(x_i - x_0) + \frac{f''(x_0)}{2}(x_i - x_0)^2 + \frac{f'''(\delta)}{3!}(x_i - x_0)^3, \delta \in (x_i, x_0) \text{ or } (x_0, x_i).$$

Then equality (4) is transformed to

$$\begin{aligned} \frac{1}{a + x_1} + \frac{1}{a + x_2} + \dots + \frac{1}{a + x_n} - \frac{n}{a + (x_1 + x_2 + \dots + x_n)/n} = & f'(x_0)[(x_1 - x_0) + (x_2 - x_0) + \dots + (x_{n-1} - x_0)] \\ & + \frac{f''(x_0)}{2}[(x_1 - x_0)^2 + (x_2 - x_0)^2 + \dots + (x_{n-1} - x_0)^2] + \sum_{i=1}^{n-1} o(x_i - x_0)^2 \end{aligned}$$

$f'(x_0)[(x_1 - x_0) + (x_2 - x_0) + \dots + (x_{n-1} - x_0)] = 0$, then

$$\frac{1}{a+x_1} + \frac{1}{a+x_2} + \dots + \frac{1}{a+x_n} - \frac{n}{a+(x_1+x_2+\dots+x_n)/n} = \frac{f''(x_0)}{2} \sum_{i=1}^n (x_i - x_0)^2 + \sum_{i=1}^n o(x_i - x_0)^2$$

$$\sum_{i=1}^n o(x_i - x_0)^2 = \frac{f'''(x_0)}{3!} [(x_1 - x_0)^3 + (x_2 - x_0)^3 + \dots + (x_n - x_0)^3] + \frac{f''(\delta_1)}{4!} (x_1 - x_0)^4 + \frac{f''(\delta_2)}{4!} (x_2 - x_0)^4 + \dots + \frac{f''(\delta_n)}{4!} (x_n - x_0)^4$$

Analysis of $|f^m(x)|, m = 2, 3, \dots, \infty$.

$$|f^m(x)| = \left| \left(\frac{1}{a+x} \right)^m \right| = m \left(\frac{1}{a+x} \right)^{m-1}, \text{ then}$$

$$\begin{aligned} \left| \frac{f^{m-1}(x_0)}{(m-1)!} (x-x_0)^{m-1} \right| - \left| \frac{f^m(x_0)}{m!} (x-x_0)^m \right| &= \frac{1}{(m-2)!} \left(\frac{1}{a+x_0} \right)^{m-2} \left| (x-x_0)^{m-1} \right| - \frac{1}{(m-1)!} \left(\frac{1}{a+x_0} \right)^{m-1} \left| (x-x_0)^m \right| \\ &= \frac{1}{(m-2)!} \left(\frac{1}{a+x_0} \right)^{m-2} \left| (x-x_0)^{m-1} \right| \left(1 - \frac{1}{(m-1)} \left(\frac{1}{a+x_0} \right) |x-x_0| \right) \end{aligned}$$

If $x \leq x_0, |x-x_0| = x_0 - x < x_0 + a$,

$$\text{then } \left| \frac{f^{m-1}(x_0)}{(m-1)!} (x-x_0)^{m-1} \right| > \left| \frac{f^m(x_0)}{m!} (x-x_0)^m \right|.$$

$$\text{If } m = 2, x > x_0, x < a + 2x_0, \frac{1}{(m-1)} \left(\frac{1}{a+x_0} \right) |x-x_0| > 0.$$

So if $x_i < a + 2x_0, i = 1, 2, \dots, n$,

$$\left| \frac{f^{m-1}(x_0)}{(m-1)!} (x_i - x_0)^{m-1} \right| > \left| \frac{f^m(x_0)}{m!} (x_i - x_0)^m \right|, m \geq 2.$$

$$\text{Namely, } \left| \frac{f''(x_0)}{2} (x_i - x_0)^2 \right| > \left| \frac{f'''(x_0)}{3!} (x_i - x_0)^3 \right| > \dots > \left| \frac{f^m(x_0)}{m!} (x_i - x_0)^m \right|.$$

Neglect the fourth order item errors and more order item errors.

For the third order item is odd number item, for each $x_i, i = 1, 2, \dots, n$, $\frac{f^3(x_0)}{3!} (x_i - x_0)^3$ can be positive and negative. Then the sum of the third order items is much smaller than the sum of the second order items if $x_i < a + 2x_0, i = 1, 2, \dots, n$. Neglect the third order item and more order item errors if $x_i < a + 2x_0, i = 1, 2, \dots, n$.

$$\text{So, } \frac{1}{a+x_1} + \frac{1}{a+x_2} + \dots + \frac{1}{a+x_n} - \frac{n}{a+(x_1+x_2+\dots+x_n)/n} \approx \frac{M}{2} \sum_{i=1}^n (x_i - x_0)^2 = \frac{\sum_{i=1}^n (x_i - x_0)^2}{2(a+x_0)^3}, x_i < a + 2x_0.$$

$$\text{Then } a^2 \left(\frac{x_1}{a+x_1} + \frac{x_2}{a+x_2} + \dots + \frac{x_n}{a+x_n} \right) - a^2 \left(\frac{x_1+x_2+\dots+x_n}{a+(x_1+x_2+\dots+x_n)/n} \right) \approx a^2 \frac{f''(x_0)}{2} \sum_{i=1}^n (x_i - x_0)^2 = a^2 \frac{\sum_{i=1}^n (x_i - x_0)^2}{2(a+x_0)^3}.$$

From the above analysis, the errors are related to $\sum_{i=1}^n (x_i - x_0)^2$ and $\frac{a^2}{2(a+x_0)^3}$.

By the properties of $\frac{a^2}{2(a+x_0)^3}$, if the mean point x_0 increases, $\frac{a^2}{2(a+x_0)^3}$ decreases quickly accordingly.

When the cluster set $\{x_i\}$ is not particularly divergent, $\sum_{i=1}^n (x_i - x_0)^2$ is much smaller than divergent cluster. So get the conclusion that if the distribution of the cluster set $\{x_i\}$ is concentrated and the mean point x_0 is large, the errors can be smaller.

Based on the above analysis, for reducing approximate errors and remaining lower computing complex, an evidence clustering method is proposed as follows:

- 1) Force the mass assignments of focal elements in the evidence to two sets by the standard of $\frac{2}{n}$;
- 2) If $x_i \geq \frac{2}{n}$, x_i is forced to one set, denoted by $\{x_i^L\}$, and the sum of mass assignments for $\{x_i^L\}$ is denoted by S_L , the number of points in $\{x_i^L\}$ is denoted by n_L , otherwise, x_i is forced to the other set, denoted by $\{x_i^S\}$;
- 3) If $x_i \in \{x_i^S\}$, pick the focal element x_i with the maximal value $x_{i\max}$. If $x_{i\max} \geq \frac{2(1-S_L)}{n-n_L}$, x_i is forced to one set $\{x_i^L\}$;
- 4) Go on the step 3), untill $x_{i\max} < \frac{2(1-S_L)}{n-n_L}$, the sum of mass assignments for $\{x_i^S\}$ is denoted by S_S .

After the above cluster steps in the evidence, the mass assignments of focal elements are forced to 2 sets denoted by $\{x_i^L\}$ and $\{x_i^S\}$. Compared to $\{x_i^L\}$, the distribution of $\{x_i^S\}$ may be more concentrated. And compared to $\{x_i^S\}$, the main point of $\{x_i^L\}$ is large. So carry out the above evidence clustering method in front of the approximate convex function formula can make errors of approximate results much smaller.

Let $m_1(X) = a, m_2(Y) = b_1, b_2, \dots, b_n$, the approximate convex function formula of DSmt+PCR5 is given by:

$$\sum_{\substack{Y \in G^{\otimes} / X \\ X \cap Y = \emptyset}} \left[\frac{m_1(X)^2 m_2(Y)}{m_1(X) + m_2(Y)} \right] = a^2 \left[n - a \left(\frac{n}{a + (b_1 + b_2 + \dots + b_n) / n} \right) \right] + \Delta \quad (5)$$

Finally, analysis of relationship between the approximate computation item and its errors item.

$$\begin{aligned} \sum_{\substack{Y \in G^{\otimes} / X \\ X \cap Y = \emptyset}} \left[\frac{m_1(X)^2 m_2(Y)}{m_1(X) + m_2(Y)} \right] &= a^2 \left[n - a \left(\frac{1}{a + b_1} + \frac{1}{a + b_2} + \dots + \frac{1}{a + b_n} \right) \right], b_1, b_2, \dots, b_n = Y \\ &\approx a^2 \left[n - a \left(\frac{n}{a + (b_1 + b_2 + \dots + b_n) / n} \right) \right] + a^2 \frac{\sum_{i=1}^n (x_i - (b_1 + b_2 + \dots + b_n) / n)^2}{2(a + (b_1 + b_2 + \dots + b_n) / n)^3} \\ &= a^2 \left[\frac{b_1 + b_2 + \dots + b_n}{a + (b_1 + b_2 + \dots + b_n) / n} \right] + a^2 \frac{\sum_{i=1}^n (x_i - (b_1 + b_2 + \dots + b_n) / n)^2}{2(a + (b_1 + b_2 + \dots + b_n) / n)^3} \end{aligned}$$

After evidence clustering method, the influence of numerator $b_1 + b_2 + \dots + b_n$ to the approximate computation item and the influence of numerator $\sum_{i=1}^n (x_i - (b_1 + b_2 + \dots + b_n) / n)^2$ to errors item is much smaller than the influence of their denominators. So the approximate computation item $a^2 \left[\frac{b_1 + b_2 + \dots + b_n}{a + (b_1 + b_2 + \dots + b_n) / n} \right]$ is mainly

proportional to the error item $a^2 \frac{\sum_{i=1}^n (x_i - (b_1 + b_2 + \dots + b_n) / n)^2}{2(a + (b_1 + b_2 + \dots + b_n) / n)^3}$. By the properties of convex function, all the error items of focal elements < 0 . Based on the above analysis, normalization method of the first-step approximate

results is applied in this paper for errors redistribution to get the final approximate results.

4. An evidence clustering DSMT approximate reasoning method

Based on the Mathematical analysis of DSMT+PCR5 formula in 3, An evidence clustering DSMT approximate reasoning method is proposed as follows:

Defination1 Assuming the existence of a cluster set $\{c\}$, the definition of the total number of $\{c\}$ is $Num(\{c\}) = number\{c\}$, the sum of each point in $\{c\}$ is $Sum(\{c\}) = \sum\{c\}$ and the mean point of $\{c\}$ is

$$Mean(\{c\}) = \frac{\sum\{c\}}{number\{c\}}.$$

1) Carry out clustering evidence method proposed in 3. Force mass assignments of focal elements in each evidence to two cluster sets. Giving an example of two evidence, denoted by $x = \{x_i\}, y = \{y_i\}, i = 1, 2, \dots, n$. Then force each evidence to two cluster sets, respectively denoted by $x^L = \{x_i^L\}, x^S = \{x_i^S\}, x^L \cup x^S = x$, $y_i^L = \{y_i^L\}, y_i^S = \{y_i^S\}, y_i^L \cup y_i^S = y$.

2) First-step approximate fusion results are calculated by the approximate convex formula as follows

$$m_{CONVEXi} = \begin{cases} x_i \cdot y_i + \frac{x_i^2 Sum(\{y_i^L\}/y_i)}{x_i + Mean(\{y_i^L\}/y_i)} + \frac{x_i^2 Sum(\{y_i^S\})}{x_i + Mean(\{y_i^S\})} + \frac{y_i^2 Sum(\{x_i^L\}/x_i)}{y_i + Mean(\{x_i^L\}/x_i)} + \frac{y_i^2 Sum(\{x_i^S\})}{y_i + Mean(\{x_i^S\})}, y_i \in \{y_i^L\}, x_i \in \{x_i^L\} \\ x_i \cdot y_i + \frac{x_i^2 Sum(\{y_i^L\})}{x_i + Mean(\{y_i^L\})} + \frac{x_i^2 Sum(\{y_i^S\}/y_i)}{x_i + Mean(\{y_i^S\}/y_i)} + \frac{y_i^2 Sum(\{x_i^L\}/x_i)}{y_i + Mean(\{x_i^L\}/x_i)} + \frac{y_i^2 Sum(\{x_i^S\})}{y_i + Mean(\{x_i^S\})}, y_i \in \{y_i^L\}, x_i \in \{x_i^S\} \\ x_i \cdot y_i + \frac{x_i^2 Sum(\{y_i^L\})}{x_i + Mean(\{y_i^L\})} + \frac{x_i^2 Sum(\{y_i^S\}/y_i)}{x_i + Mean(\{y_i^S\}/y_i)} + \frac{y_i^2 Sum(\{x_i^L\})}{y_i + Mean(\{x_i^L\})} + \frac{y_i^2 Sum(\{x_i^S\}/x_i)}{y_i + Mean(\{x_i^S\}/x_i)}, y_i \in \{y_i^S\}, x_i \in \{x_i^S\} \\ x_i \cdot y_i + \frac{x_i^2 Sum(\{y_i^L\}/y_i)}{x_i + Mean(\{y_i^L\}/y_i)} + \frac{x_i^2 Sum(\{y_i^S\})}{x_i + Mean(\{y_i^S\})} + \frac{y_i^2 Sum(\{x_i^L\})}{y_i + Mean(\{x_i^L\})} + \frac{y_i^2 Sum(\{x_i^S\}/x_i)}{y_i + Mean(\{x_i^S\}/x_i)}, y_i \in \{y_i^S\}, x_i \in \{x_i^L\} \end{cases} \quad (6)$$

3) Normalization method of the first-step approximate results is given by

$$m_{GH} = (1 - \sum_{\substack{A=x_i \cap y_j \\ A \in G^\ominus}} m(A)) \frac{m_{CONVEXi}}{\sum_{i=1}^n m_{CONVEXi}} \quad (7)$$

5. Analysis of computation complexity

If there are 2 evidence sources, assume that all singleton focal elements and multiple focal elements have mass assignments in hyper-power sets of 2 evidence, denoted by $G^\ominus = \{\theta_1, \theta_2, \dots, \theta_n, \theta_i \cap \theta_j \dots \theta_k, \dots, \theta_l \cap \theta_g \dots \theta_h\}, \{i, f, k, l, g, h\} \in [1, \dots, n]$, n denote the number of singleton focal elements, c denote the number of multiple focal elements. First, analyse the computation complexity of the processing procedure of 2 evidence sources fusion by DSMT+PCR5. Then, analyse the computation complexity of the same problem by the method in this paper. Computation complexity comparison of two methods can be obtained by the analysis.

Assume that the computation complexity of one time multiplication is denoted by K , the computation complexity of one time addition is denoted by \sum , the computation complexity of one time division is denoted by Ψ and the computation complexity of one time subtraction is denoted by B . The computation complexity

of the processing procedure of 2 evidence sources fusion by DSMT+PCR5 is denoted by $o_{\text{DSMT}}[n]$. Then

$$\begin{aligned} o_{\text{DSMT+PCR5}}[n+c] &= [K + (4K + 2\psi + 4\Sigma)(n+c-1)](n+c) - x(2K + 2\psi + 4\Sigma) + y\Sigma \\ &= (4n+4c-3)(n+c)K + (2n+2c-2)(n+c)\psi + (4n+4c-4)(n+c)\Sigma - x(2K + 2\psi + 4\Sigma) + y\Sigma \end{aligned} \quad (8)$$

x denote the number of multiple focal elements in the results, y denote the number of the same multiple focal elements generated in the procedure of mass assignments combination product. The computation complexity of the same problem by the method in this paper is denoted by $o_{\text{GH}}[n+c]$. Then

$$\begin{aligned} o_{\text{GH}}[n+c] &= 2(n+c)B + (n+c)K + 2(n+c)[2(3K + \Sigma + \Psi) + \Sigma] + \Sigma + n\Psi - x(2K + 2\psi + 4\Sigma) + y\Sigma \\ &= 2(n+c)B + 13(n+c)K + [4(n+c)+1]\Sigma + (5n+4c)\Psi - x(2K + 2\psi + 4\Sigma) + y\Sigma \end{aligned} \quad (9)$$

Computation complexity comparison of two methods obtained from equality (8) and equality (9) shows that the computation complexity comparison of DSMT is almost proportion to $(n+c)^2$ and the computation complexity comparison of the method in this paper is almost proportion to $(n+c)$. Conclusions are drawn that the computation complexity comparison of the method in this paper is much lower than DSMT with increasing number of focal element numbers in hyper-power space.

6. Simulation experiments

For comparison of the approximate method proposed in this paper with the other methods, an Euclidean similarity function²⁰ is introduced in this paper as follows:

$$N_E[m_1, m_2] = 1 - \frac{1}{\sqrt{2}} \sqrt{\sum_{i=1}^{G^\circ} [m_1[X_i] - m_2[X_i]]^2} \quad (10)$$

6.1. Simple cases of cluster sets in each evidence

Example 1. If there are 2 evidence sources, assume that only singleton focal elements have mass assignments in hyper-power sets, denoted by $G_k^\circ = \{\theta_1, \theta_2, \dots, \theta_7\}$, $k=1$ or 2 . The mass assignments in each evidence are $a = \{0.1, 0.1, 0.05, 0.3, 0.2, 0.2, 0.05\}$, $b = \{0.2, 0.05, 0.05, 0.2, 0.15, 0.3, 0.05\}$, the processing of the method is given as follows:

1) Force mass assignments of focal elements in each evidence to two cluster sets, denoted by $a = \{a_1, a_2, a_3, a_5, a_6, a_7\} \cup \{a_4\}$, $b = \{b_1, b_2, b_3, b_4, b_5, b_7\} \cup \{b_6\}$;

2) First-step approximate fusion results are calculated by formula(6)

$$\begin{aligned}
m_{\text{CONVEX1}} &= a_1 \cdot b_1 + \frac{b_1^2 \cdot \text{Sum}(\{a_2, a_3, a_5, a_6, a_7\})}{b_1 + \text{Mean}(\{a_2, a_3, a_5, a_6, a_7\})} + \frac{b_1^2 \cdot a_4}{b_1 + a_4} + \frac{a_1^2 \cdot \text{Sum}(\{b_2, b_3, b_4, b_5, b_7\})}{a_1 + \text{Mean}(\{b_2, b_3, b_4, b_5, b_7\})} + \frac{a_1^2 \cdot b_6}{a_1 + b_6} \\
m_{\text{CONVEX2}} &= a_2 \cdot b_2 + \frac{b_2^2 \cdot \text{Sum}(\{a_1, a_3, a_5, a_6, a_7\})}{b_2^2 + \text{Mean}(\{a_1, a_3, a_5, a_6, a_7\})} + \frac{b_2^2 \cdot a_4}{b_2^2 + a_4} + \frac{a_2^2 \cdot \text{Sum}(\{b_1, b_3, b_4, b_5, b_7\})}{a_2^2 + \text{Mean}(\{b_1, b_3, b_4, b_5, b_7\})} + \frac{a_2^2 \cdot b_6}{a_2^2 + b_6} \\
m_{\text{CONVEX3}} &= a_3 \cdot b_3 + \frac{b_3^2 \cdot \text{Sum}(\{a_1, a_2, a_5, a_6, a_7\})}{b_3^2 + \text{Mean}(\{a_1, a_2, a_5, a_6, a_7\})} + \frac{b_3^2 \cdot a_4}{b_3^2 + a_4} + \frac{a_3^2 \cdot \text{Sum}(\{b_1, b_2, b_4, b_5, b_7\})}{a_3^2 + \text{Mean}(\{b_1, b_2, b_4, b_5, b_7\})} + \frac{a_3^2 \cdot b_6}{a_3^2 + b_6} \\
m_{\text{CONVEX4}} &= a_4 \cdot b_4 + \frac{b_4^2 \cdot \text{Sum}(\{a_1, a_2, a_3, a_5, a_6, a_7\})}{b_4^2 + \text{Mean}(\{a_1, a_2, a_3, a_5, a_6, a_7\})} + \frac{a_4^2 \cdot \text{Sum}(\{b_1, b_2, b_3, b_5, b_7\})}{a_4^2 + \text{Mean}(\{b_1, b_2, b_3, b_5, b_7\})} + \frac{a_4^2 \cdot b_6}{a_4^2 + b_6} \\
m_{\text{CONVEX5}} &= a_5 \cdot b_5 + \frac{b_5^2 \cdot \text{Sum}(\{a_1, a_2, a_3, a_6, a_7\})}{b_5^2 + \text{Mean}(\{a_1, a_2, a_3, a_6, a_7\})} + \frac{b_5^2 \cdot a_4}{b_5^2 + a_4} + \frac{a_5^2 \cdot \text{Sum}(\{b_1, b_2, b_3, b_4, b_7\})}{a_5^2 + \text{Mean}(\{b_1, b_2, b_3, b_4, b_7\})} + \frac{a_5^2 \cdot b_6}{a_5^2 + b_6} \\
m_{\text{CONVEX6}} &= a_6 \cdot b_6 + \frac{b_6^2 \cdot \text{Sum}(\{a_1, a_2, a_3, a_5, a_7\})}{b_6^2 + \text{Mean}(\{a_1, a_2, a_3, a_5, a_7\})} + \frac{b_6^2 \cdot a_4}{b_6^2 + a_4} + \frac{a_6^2 \cdot \text{Sum}(\{b_1, b_2, b_3, b_4, b_5, b_7\})}{a_6^2 + \text{Mean}(\{b_1, b_2, b_3, b_4, b_5, b_7\})} \\
m_{\text{CONVEX7}} &= a_7 \cdot b_7 + \frac{b_7^2 \cdot \text{Sum}(\{a_1, a_2, a_3, a_5, a_6\})}{b_7^2 + \text{Mean}(\{a_1, a_2, a_3, a_5, a_6\})} + \frac{b_7^2 \cdot a_4}{b_7^2 + a_4} + \frac{a_7^2 \cdot \text{Sum}(\{b_1, b_2, b_3, b_4, b_5\})}{a_7^2 + \text{Mean}(\{b_1, b_2, b_3, b_4, b_5\})} + \frac{a_7^2 \cdot b_6}{a_7^2 + b_6}
\end{aligned}$$

Get $m_{\text{CONVEX}} = \{0.1588, 0.0558, 0.0273, 0.3108, 0.1926, 0.3108, 0.0273\}$;

3) Get the final approximate results by normalization method of the first-step approximate results

$$m_{\text{GH}} = \{0.1465, 0.0515, 0.0252, 0.2869, 0.1778, 0.2869, 0.0252\} .$$

4) The results of DS_{mc}+PCR5 and the method¹⁸ are also calculated for the parison with the method in this paper.

The results of DS_{mT}+PCR5

$$m_{\text{DSmT+PCR5}} = \{0.1435, 0.0488, 0.0237, 0.2922, 0.1751, 0.2929, 0.0237\}$$

The results of the method¹⁸

$$m_{\text{XDL}} = \{0.1536, 0.0605, 0.0253, 0.2980, 0.1670, 0.2738, 0.0217\} .$$

Calculate the Euclidean similarity between results m_{GH} obtained by the method in this paper and the results $m_{\text{DSmT+PCR5}}$ of DS_{mT}+PCR5. The Euclidean similarity $E_{\text{GH}} = 0.9932$.

In the same way, the Euclidean similarity between the results m_{XDL} of the method¹⁸ and the results $m_{\text{DSmT+PCR5}}$ of DS_{mT}+PCR5 is denoted by $E_{\text{XDL}} = 0.9812$.

From the above results of this example, the results obtained by the method proposed in this paper have higher Euclidean similarity with DS_{mT}+PCR5 than the existing approximate DS_{mT} method¹⁸. The Euclidean Similarity which remains over 99% shows that the method proposed in this paper has high accuracy and has practical meaning .

Example 2. If there are the same 2 evidence sources in example 1, the hyper-power sets are denoted by $G_k^\Theta = \{\theta_1, \theta_2, \dots, \theta_7\}$, $k = 1 \text{ or } 2$. The mass assignments in each evidence are $a = \{0.1, 0.1, 0.05, 0.3, 0.2, 0.2, 0.05\}$, $b = \{0.2, 0.05, 0.05, 0.2, 0.15, 0.3, 0.05\}$. The mass assignments in the second evidence source are unchanged, denoted by $b = \{0.2, 0.05, 0.05, 0.2, 0.15, 0.3, 0.05\}$, and the mass assignments in the first evidence change whose sequence of the mass belief of each focal element moves one position backward at one time to procedure 6 new evidence, such as:

$$a_1 = \{0.1, 0.1, 0.05, 0.3, 0.2, 0.2, 0.05\}, a_2 = \{0.05, 0.1, 0.1, 0.05, 0.3, 0.2, 0.2\}, a_3 = \{0.2, 0.05, 0.1, 0.1, 0.05, 0.3, 0.2\},$$

$$a_4 = \{0.2, 0.2, 0.05, 0.1, 0.1, 0.05, 0.3\}, a_5 = \{0.3, 0.2, 0.2, 0.05, 0.1, 0.1, 0.05\}, a_6 = \{0.05, 0.3, 0.2, 0.2, 0.05, 0.1, 0.1\}.$$

Each new evidence and the evidence b are calculated to obtain the fusion results by DSmt+PCR5 and the approximate fusion results by the method in this paper and the method¹⁸. Then Euclidean similarity of the approximate results of different methods with the results of DSmt+PCR5 is obtained by formula(10) and the average computing time of each method is also taken record as tabel 1. (In this paper, all the simulation experiments are implemented by Matlab simulation in the hardware condition of Pentimu(R) Dual-Core CPU E5300 2.6GHz 2.59GHz, memory 1.99GB.)

Table 1 Euclidean similarity and average computing time coparison of the methods

	Euclidean similarity with results of DSmt+PCR5						average computing time
	1	2	3	4	5	6	
The method in this paper	0.9939	0.9911	0.9955	0.9938	0.9965	0.9960	0.0028s
The method ¹⁸	0.9583	0.9791	0.9588	0.9530	0.9443	0.9347	0.0105s

As shown in table 1, under simple cases of cluster sets in each evidence, the accuracy of the method in this paper all remains over 99% and much higher than the method¹⁸. Average computing time of the method in this paper is also lower than the existing approximate method¹⁸. At the same time, the accuracy of the method in this paper in different evidence cases changes little, which proves that the method has higher performance stability.

6.2. Complex cases of cluster sets in each evidence

Example 3. If there are 2 evidence sources, assume that only singleton focal elements have mass assignments in hyper-power sets, denoted by $G_k^\ominus = \{\theta_1, \theta_2, \dots, \theta_{12}\}$, $k = 1 \text{ or } 2$. The mass assignments in each evidence are $a = \{0.3, 0.35, 0.05, 0.05, 0.04, 0.06, 0.02, 0.01, 0.02, 0.01, 0.04, 0.05\}$, $b = \{0.2, 0.05, 0.04, 0.21, 0.15, 0.25, 0.05, 0.01, 0.01, 0.01, 0.01, 0.01\}$, the method processing is given as follows:

1) Force mass assignments of focal elements in each evidence to two cluster sets, denoted by $a = \{a_3, a_4, a_5, a_6, a_7, a_8, a_9, a_{10}, a_{11}, a_{12}\} \cup \{a_1, a_2\}$, $b = \{b_2, b_3, b_7, b_8, b_9, b_{10}, b_{11}, b_{12}\} \cup \{b_1, b_4, b_5, b_6\}$;

2) First-step approximate fusion results are calculated by formula(6)

$$m_{\text{CONVEX}} = \{0.3069, 0.2559, 0.0247, 0.1309, 0.0834, 0.1662, 0.0177, 0.0019, 0.0041, 0.0019, 0.0110, 0.0153\};$$

3) Get the final approximate results by normalization method of the first-step approximate results

$$m_{\text{GH}} = \{0.3009, 0.2509, 0.0242, 0.1283, 0.0818, 0.1630, 0.0174, 0.0019, 0.0041, 0.0019, 0.0108, 0.0150\}.$$

4) The results of DSmt+PCR5 and the method¹⁸ are also calculated for the parison with the method in this paper.

The results of DSmt+PCR5

$$m_{\text{DSmt+PCR5}} = \{0.3019, 0.2524, 0.0235, 0.1282, 0.0811, 0.1635, 0.0169, 0.0018, 0.0039, 0.0018, 0.0104, 0.0146\}.$$

The results of the method¹⁸

$$m_{\text{XDL}} = \{0.3710, 0.1834, 0.0276, 0.1269, 0.0828, 0.1651, 0.0003, 0.0000, 0.0001, 0.0001, 0.0002, 0.0002\}.$$

Calculate the Euclidean similarity between the results m_{GH} and $m_{\text{DSmt+PCR5}}$. The Euclidean Similarity $E_{\text{GH}} = 0.9984$ and computing time is 0.0035s.

In the same way, the Euclidean similarity between the results m_{XDL} and $m_{\text{DSmt+PCR5}}$ is denoted by

$E_{\text{XDL}} = 0.9287$ and computing time is 0.0185s.

As shown in the above experiment results in this example, the results obtained by the method proposed in this paper have higher Euclidean Similarity and lower computation complexity than the existing DSMT approximate method¹⁸. The Euclidean Similarity which remains over 99% shows that the method proposed in this paper has higher accuracy and has practical meaning .

Example 4. If there are the same 2 evidence sources in example 3 , the hyper-power sets are denoted by $G_k^\ominus = \{\theta_1, \theta_2, \dots, \theta_{12}\}$, $k = 1 \text{ or } 2$. The mass assignments in the second evidence source are unchanged, denoted by $b = \{0.2, 0.05, 0.04, 0.21, 0.15, 0.25, 0.05, 0.01, 0.01, 0.01, 0.01, 0.01\}$, and the mass assignments in the first source change whose sequence of the mass belief of each focal element moves one position backward at one time to procedure 11 new evidence.

Each new evidence and the second evidence b are calculated to get the fusion results of DSMT+PCR5 and the approximate results by the method in this paper and the method¹⁸. Then Euclidean similarity of the approximate results of different methods with the results of DSMT+PCR5 and the average computing time of each method are taken record as tabel 2.

Table 2 Euclidean similarity and average computing time coparison of the methods

	Euclidean similarity with results of DSMT+PCR5											Average computing time
	1	2	3	4	5	6	7	8	9	10	11	
The method in this paper	0.9987	0.9983	0.9982	0.9979	0.9981	0.9985	0.9985	0.9983	0.9984	0.9983	0.9983	0.0038
The method ¹⁸	0.8795	0.9330	0.9514	0.9484	0.8112	0.8636	0.8253	0.8342	0.8331	0.8189	0.8483	0.0186

As shown in table 2, under complex cases of cluster sets in each evidence, the accuracy of the method in this paper also remains over 99% and much higher than the method¹⁸. Average computing time of the method in this paper is lower than the method¹⁸. At the same time, the accuracy of the method in this paper in different evidence cases changes little, which proves that the method has higher performance stability.

6.3. cases of highly conflict evidence sources

Example 5. In order to verify information fusion of highly conflict evidence sources can be effective solved by the method in this paper. Assume there are two highly conflict evidence sources with the hyper-power set denoted by $D^\ominus = \{a, b, c, d\}$. The mass assignments of two evidenece sources are shown in tabel 3.

Table 3 The mass assignments of highly conflict evidenece sources

Conflict evidenece sources	a	b	c	d
S_1	$x - \varepsilon$	ε	$1 - x - \varepsilon$	ε
S_2	ε	$y - \varepsilon$	ε	$1 - y - \varepsilon$

Let $\varepsilon = 0.01, x, y \in [0.02, 0.98]$. The fusion results are obtained by different methods when x, y is increasing from 0.02 to 0.98 by 0.01 step at the same time. Euclidean similarity of the method¹⁸ with DSMT+PCR5 is shown in figure1. Euclidean similarity of the method in this paper with DSMT+PCR5 is shown in figure2.

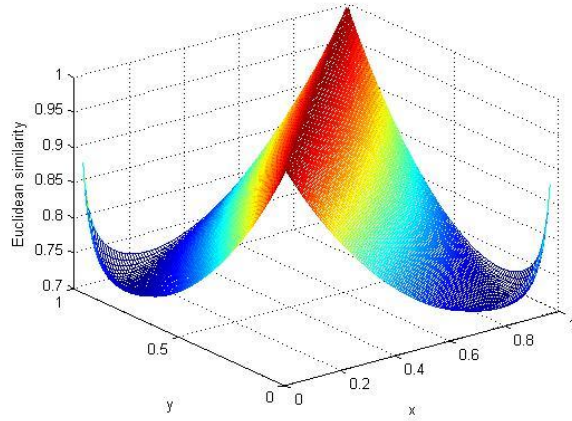


Fig. 1. Euclidean similarity of the method¹⁸ with DSMT+PCR5

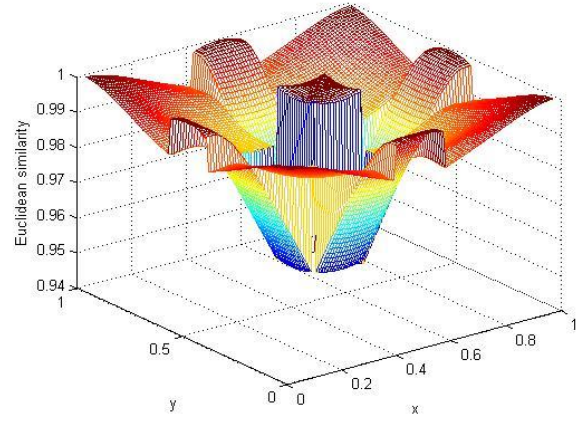


Fig. 2. Euclidean similarity of the method in this paper with DSMT+PCR5

The average Euclidean Similarity of the method in this paper is 0.9873 and the average Euclidean Similarity of the method¹⁸ is 0.8513. It's shown that the method in this paper can effectively solve information fusion problem of highly conflict evidence sources.

6.4. convergence analysis

Example 6. If there are 2 evidence sources, assume that only singleton focal elements have mass assignments in hyper-power sets, denoted by $G_k^\Theta = \{\theta_1, \theta_2, \dots, \theta_{12}\}$, $k = 1 \text{ or } 2$. The mass assignments in each evidence are $a = \{0.1, 0.01, 0.02, 0.25, 0.15, 0.05, 0.1, 0.1, 0.1, 0.05, 0.05, 0.02\}$ and $b = \{0.5, 0.35, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.04\}$. First, fusion results of two evidence a and b are obtained by different fusion methods. Then, fuse the prior fusion results with b repeatedly. Through the experiment results each time, analyze different method's convergence.

Table 3 The mass assignments of highly conflict evidence sources

		Fusion results
1	DSMT+PCR5	0.4287,0.2600,0.0058,0.1163,0.0539,0.0109,0.0297,0.0297,0.0109,0.0109,0.0136
	The method ¹⁸	0.4067,0.0994,0.0212,0.1888,0.0798,0.0385,0.0027,0.0027,0.0027,0.0010,0.0010,0.0019
	The method in this paper	0.4285,0.2610,0.0060,0.1151,0.0535,0.0110,0.0296,0.0296,0.0296,0.0110,0.0110,0.0141
2	DSMT+PCR5	0.5829,0.3324,0.0031,0.0388,0.0120,0.0017,0.0053,0.0053,0.0053,0.0017,0.0017,0.0099
	The method ¹⁸	0.5687,0.1686,0.0036,0.0642,0.0202,0.0127,0.0000,0.0000,0.0000,0.0000,0.0000
	The method in this paper	0.5705,0.3459,0.0031,0.0371,0.0116,0.0018,0.0052,0.0052,0.0052,0.0018,0.0018,0.0109
3	DSMT+PCR5	0.6439,0.3342,0.0018,0.0084,0.0016,0.0006,0.0008,0.0008,0.0008,0.0006,0.0006,0.0060
	The method ¹⁸	0.6171,0.1968,0.0009,0.0109,0.0027,0.0021,0.0000,0.0000,0.0000,0.0000,0.0000
	The method in this paper	0.6118,0.3655,0.0021,0.0078,0.0015,0.0006,0.0008,0.0008,0.0008,0.0006,0.0006,0.0069
4	DSMT+PCR5	0.6726,0.3181,0.0012,0.0017,0.0004,0.0004,0.0004,0.0004,0.0004,0.0004,0.0040
	The method ¹⁸	0.6152,0.2047,0.0008,0.0018,0.0004,0.0003,0.0000,0.0000,0.0000,0.0000,0.0000
	The method in this paper	0.6264,0.3626,0.0015,0.0017,0.0004,0.0004,0.0004,0.0004,0.0004,0.0004,0.0048

As shown in tabel 3, the convergence of three methods is similar. The results of each method can converge to the main focal elements afer 3 times of evidence fusion. However, the results of the method in this paper have higher Euclidean similarity with DSMT+PCR5, and lose less information than the method¹⁸ each time.

6.5. monte carlo simulations in the case of non-empty multiple focal elements

If there are 2 evidence sources, assume that singleton focal elements and multiple focal elements have mass

assignments in hyper-power sets, denoted by $P^\ominus = \{\theta_1, \theta_2, \dots, \theta_{20}, \theta_1 \cap \theta_3 \cap \theta_{10} \cap \theta_{20}\}$. Carry out 1000 times monte carlo simulation experiments. First, assign random mass value to every focal elements of hyper-power sets in each evidence each time. Then, the fusion results of 2 evidence are obtained by DSMT+PCR5 and the method in this paper seperately. Thirdly, calculate the Euclidean similarity of the method in this paper with DSMT+PCR5 and computing time in each monte carlo experiment. The monto carlo simulation results are shown in figure 3, figure 4 and table 4.

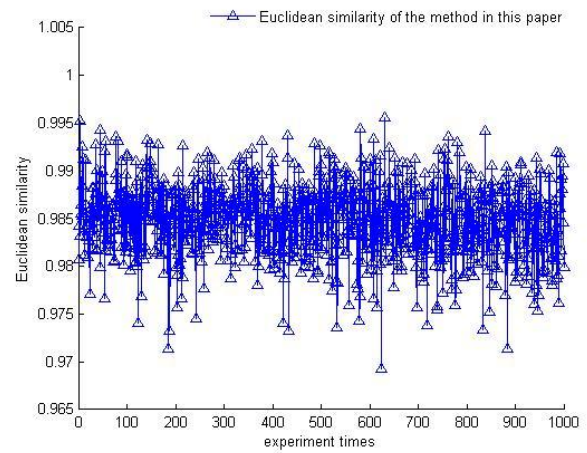
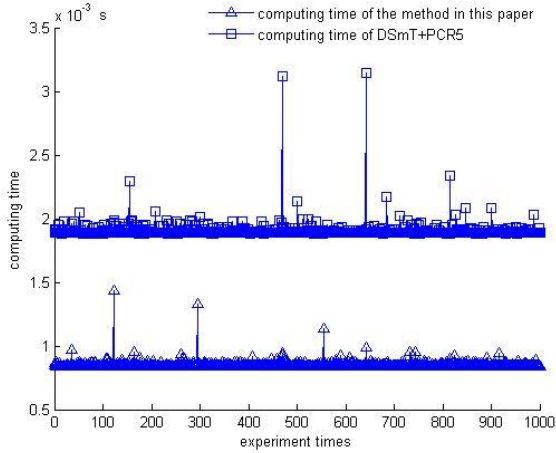


Fig. 3. Computing time comparison of the method in this paper with DSMT+PCR5 Fig. 4. Euclidean similarity of the method in this paper with DSMT+PCR5

Table 4 fusion results comparison in the case of increasing focal elements number

	Average Euclidean Similarity	Max Euclidean Similarity	Min Euclidean Similarity	Average computing time(ms)	Max computing time(ms)	Min computing time(ms)
DSMT+PCR5				1.9	3.1	1.9
The method in this paper	0.9849	0.9956	0.9693	0.84911	1.4	0.83593

As shown in figure3, figure4 and tabel 4, in the case of non-empty multiple focal elements, the average Euclidean similarity of the method in this paper can reach 98.49% and Euclidean similarity changes little with different evidence. Computing time of the method in this paper almost reduce halfly than DSMT+PCR5.

6.6. monte carlo simulations in the case of increasing focal elements number

Example 7. If there are 2 evidence sources, assume that only singleton focal elements have mass assignments in hyper-power sets, denoted by $G_k^\ominus = \{\theta_1, \theta_2, \dots, \theta_{10}\}$, $k = 1$ or 2 . Increase 10 focal elements each time until 500 to the hyper-power sets and assign random mass value to every focal elements of hyper-power sets in each evidence each time. Carry out 1000 times monto carlo simulation in each hyper-power set, calculate the average Euclidean similarity of the method in this paper with DSMT+PCR5 as shown in figure 5. Compare the average computing time of the method in this paper with DSMT+PCR5 in each hyper-power sets is shown in figure 6.

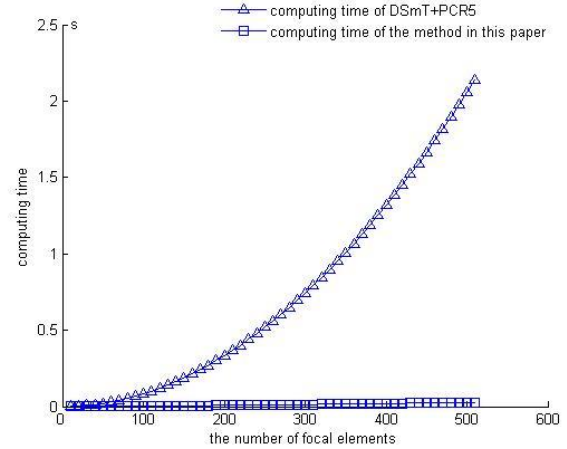
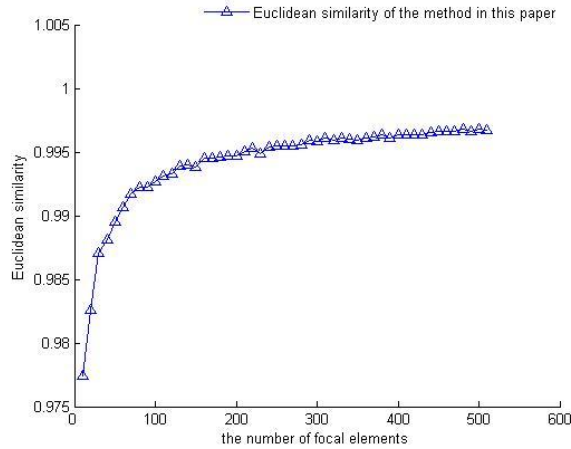


Fig. 5. Euclidean similarity of the method in this paper with DSMT+PCR5 Fig. 6. computing time comparison of the method in this paper with DSMT+PCR5

The fusion results comparison in the case of increasing focal elements number is shown in table 4. (As the increasing number of focal elements, the mass assignment of average cluster center is decreasing sharply. For reducing computation complexity, neglect the influence of the different classification of clusters and apply the standard of $\frac{2}{n}$ as one step cluster method, n denote the focal elements number of hyper-power sets.)

Table 5 Fusion results comparison in the case of increasing focal elements number

	The focal elements number of hyper-power sets is increasing from 10 to 510											
Average computing time of DSMT+PCR5 (s)	0.0008	0.0032	0.0073	0.0132	0.0208	0.0297	0.0406	0.0530	0.0670	0.0829	0.1017	0.1219
	0.1405	0.1636	0.1867	0.2133	0.2431	0.2685	0.3009	0.3319	0.3698	0.4013	0.4427	0.4816
	0.5212	0.5588	0.6011	0.6462	0.6959	0.7413	0.7909	0.8425	0.8962	0.9505	1.0082	1.0659
	1.1263	1.1882	1.2516	1.3166	1.3828	1.4509	1.5225	1.5926	1.6660	1.7409	1.8174	1.8946
Average computing time of the method in this paper (s)	0.0003	0.0006	0.0010	0.0013	0.0017	0.0020	0.0024	0.0028	0.0032	0.0036	0.0040	0.0044
	0.0048	0.0053	0.0057	0.0062	0.0067	0.0071	0.0076	0.0081	0.0087	0.0092	0.0098	0.0103
	0.0108	0.0114	0.0118	0.0124	0.0130	0.0136	0.0142	0.0148	0.0154	0.0160	0.0167	0.0173
	0.0180	0.0186	0.0193	0.0200	0.0207	0.0214	0.0222	0.0229	0.0236	0.0244	0.0251	0.0259
Average Euclidean similarity with results of DSMT+PCR5	0.9774	0.9826	0.9871	0.9881	0.9895	0.9907	0.9917	0.9922	0.9922	0.9927	0.9931	0.9933
	0.9939	0.9940	0.9938	0.9945	0.9945	0.9946	0.9947	0.9947	0.9950	0.9953	0.9949	0.9954
	0.9955	0.9955	0.9955	0.9956	0.9959	0.9958	0.9961	0.9959	0.9961	0.9960	0.9959	0.9961
	0.9962	0.9964	0.9961	0.9964	0.9964	0.9964	0.9964	0.9965	0.9966	0.9966	0.9966	0.9968

As shown in figure 5, figure 6 and table 5:

- 1) In the case of increasing focal elements number, computing time of the method in this paper decreases significantly, and the computation complexity of the method almost appears linear growth instead of exponential growth, which proves that the method in this paper has a high application in the case of complex fusion problems;
- 2) The accuracy of the method in this paper is increasing with the growth of focal elements number of hyper-power sets as the errors item becomes much smaller. The minimum average Euclidean Similarity is 0.9974 in the case of the minimum number of hyper-power sets. When number of hyper-power sets increases over 50, the average Euclidean similarity exceeds 99%, which proves that the method in this paper can effectively support correct and quick decision in the case of large data.

4. Conclusions

A new evidence clustering DSMT approximate reasoning method is proposed by analysis of convex function errors in this paper. The method reduces computation complexity of DSMT+PCR5 significantly which blocks the wide application and development of DSMT and remains high accuracy. Simulation results show that in different cases the method in this paper can process evidence fusion problems effectively and efficiently, especially, in the case of large data and complex fusion problems, the method can get highly accurate results and need low computation complexity.

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