

# New Measures of Specificity and Bayesianity of Basic Belief Assignments and of Fusion Rules

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## Abstract.

In this paper we introduce the degree of specificity of a mass, which is the distance between a mass and its most specific associated mass, and we measure the specificity of a fusion rule. Also, we determine the Bayesianity of a mass. We propose certain new distances between masses as well.

**Keywords:** belief function, uncertainty, conflict, auto-conflict, specificity of a mass, specificity of a fusion rule, distance between masses, Bayesianity

## 1. Introduction.

In order for the paper to be self-contained we list the main distances between masses and also the three pignistic transformations.

We list some specificity measures from the known literature and we also propose some new ways of measuring the degree of specificity of a bba.

We also list the known distances and propose some new approaches.

The most specific mass associated to a given mass is defined.

The degree of uncertainty of a set and the degree of Bayesianity/non-Bayesianity is also defined at the end of the paper.

## 2. Specificity.

Yager [1] has defined the **specificity** measure of a mass  $m(\cdot)$  defined on  $2^X$  as):

$$S_m = \sum_{\substack{A \subset X \\ A \neq \Phi}} \frac{m(A)}{|A|} \quad (1)$$

One has  $1/n \leq S_m \leq 1$ , where  $n$  is the cardinality of  $X$ , minimum value occurs for the vacuous belief function  $m_{\text{vbf}}(X) = 1$ , and maximum value occurs for any Bayesian mass.

In our opinion this formula should be adjusted in order to get the minimum specificity value 0 for the vacuous belief function and for uniformly distributed masses (i.e.  $m(A_i) = 1/p$  for each  $A_1, A_2, \dots, A_p$  in the fusion space, while the specificity should be 1 for  $m(A)=1$  where  $A$  has the cardinality 1.

Because, for example, if we have three Bayesian bba's defined on  $\Theta = \{A, B, C\}$ , where all  $A, B, C$  are singletons, and all their intersections are empty:

	A	B	C	
$m_1$	1/3	1/3	1/3	
$m_2$	1/2	1/2	0	(2)
$m_3$	1	0	0	

we get the same specificity for all three of them, i.e.  $S_{m_1} = S_{m_2} = S_{m_3} = 1$ ,

while intuitively there should be  $0 \leq S_{m_1} < S_{m_2} < S_{m_3} = 1$  since  $m_2$  is more specific than  $m_1$ , and  $m_3$  is the most specific than all of them.

Uncertainty results from randomness and non-specificity.

**Non-specificity** is related to vagueness or imprecision (Ristic and Smets, [2]).

## 2. Degree of Specificity.

We define a new **degree of specificity measure of a bba**  $m(\cdot)$  in the following way:

$$S_{SMO}(m) = 1 - d(m, m_s) \quad (3)$$

where  $m_s(\cdot)$  is the most specific mass associated with  $m(\cdot)$ , and  $d(\cdot)$  is a distance function whose values are in the interval  $[0, 1]$  between the masses  $m(\cdot)$  and  $m_s(\cdot)$ .

As distance between masses we prefer to use Jousselme distance which is the most accurate one, but other mass distance can be used as well: Euclidean distance, Bhattacharyya's distance, Tessem's distance, GPT distance, DSMP<sub>ε</sub> distance, etc. The restriction is that each mass distance should have the values in the closed interval  $[0, 1]$ .

We recall some mass distance formulas:

### 3.1) Jousselme Distance:

$$d_j(m_1, m_2) = \sqrt{\frac{1}{2} (\overline{m}_1 - \overline{m}_2)^T D (\overline{m}_1 - \overline{m}_2)} \quad (4)$$

where  $D$  is an  $2^n \times 2^n$  matrix whose elements are  $D(A, B) = \frac{|A \cap B|}{|A \cup B|}$ . (5)

It is easier to take the Jousselme matrix corresponding to the union of all focal elements of bba's  $m_1$  and respectively  $m_2$ , instead of considering the large size matrix defined on the whole fusion space  $2^\Theta$ . The result is the same.

### 3.2) Euclidian Distance:

$$d_E(m_1, m_2) = \sqrt{\sum_{A \in 2^\Theta} [m_1(A) - m_2(A)]^2}. \quad (6)$$

### 3.3) Bhattacharya Distance:

$$d_B(m_1, m_2) = \sqrt{\frac{1}{2} \sum_{A \in 2^\Theta} [\sqrt{m_1(A)} - \sqrt{m_2(A)}]^2}. \quad (7)$$

3.4) **Tessem's Distance** between pignistic probabilities  $BetP_1$  and  $BetP_2$  associated to the bba's  $m_1$ , and respectively  $m_2$  (*distance between betting commitments from two pignistic transformations*) of the two bba's is defined as [7, 8]:

$$d_T(m_1, m_2) = \max_{A \in \Theta, A = \text{singleton}} |BetP_1(A) - BetP_2(A)| \quad (8)$$

3.5) This distance extended to DSMT gives the **GPT distance**, between generalized pignistic probabilities:

$$d_{DSMT}(m_1, m_2) = \max_{A \in \Theta, c(A) = 1} |GPT_1(A) - GPT_2(A)| \quad (9)$$

where  $c(A)$  is the DSMT cardinality of  $A$ .

3.6) A **DSMP $_\epsilon$  Distance**, extension of the above two distances should be:

$$d_{DSMT \epsilon}(m_1, m_2) = \max_{A \in \Theta, c(A) = 1} |DSMP_{(\epsilon)1}(A) - DSMP_{(\epsilon)2}(A)|. \quad (10)$$

3.7) Another idea would be to take, instead of "max", the "average" arithmetic operator in the above three formulas of distances between pignistic probabilities, and we get pseudo-distances (the axiom of triangular inequality is in general not verified).

Other way to define the distance between two masses is the following:

3.8-3.10) Use the pignistic transformation ( $BetP$ ), or generalized pignistic transformation ( $GPT$ ), or  $DSMP_\epsilon$  to transform a given bba into a Bayesian mass, and then make a city-block distance between the masses of singletons:

$$d_{PT}(m_1, m_2) = \frac{1}{2} \sum_{\substack{A \in \Theta \\ c(A)=1}} |BetP_1(A) - BetP_2(A)| \quad (11)$$

respectively in DSmT:

$$d_{GPT}(m_1, m_2) = \frac{1}{2} \sum_{\substack{A \in \Theta \\ c(A)=1}} |GPT_1(A) - GPT_2(A)| \quad (12)$$

$$d_{DSmP\epsilon}(m_1, m_2) = \frac{1}{2} \sum_{\substack{A \in \Theta \\ c(A)=1}} |DSmP_{\epsilon_1}(A) - DSmP_{\epsilon_2}(A)|. \quad (13)$$

In a more general way one can construct the above formulas by inserting a lambda parameter

$\lambda \geq 1$ :

$$d_{PT}(m_1, m_2) = \left( \frac{1}{2} \sum_{\substack{A \in \Theta \\ c(A)=1}} |BetP_1(A) - BetP_2(A)|^\lambda \right)^{1/\lambda} \quad (14)$$

$$d_{GPT}(m_1, m_2) = \left( \frac{1}{2} \sum_{\substack{A \in \Theta \\ c(A)=1}} |GPT_1(A) - GPT_2(A)|^\lambda \right)^{1/\lambda} \quad (15)$$

$$d_{DSmP\epsilon}(m_1, m_2) = \left( \frac{1}{2} \sum_{\substack{A \in \Theta \\ c(A)=1}} |DSmP_{\epsilon_1}(A) - DSmP_{\epsilon_2}(A)|^\lambda \right)^{1/\lambda} \quad (16)$$

**Remark** that  $d(m, m_s)$  represents the quantity that misses to  $m(\cdot)$  in order for  $m(\cdot)$  to becoming the most specific mass (closest to it).

#### 4. The most specific mass associated with a given mass.

We define the most specific mass  $m_s(\cdot)$  associated to a given mass  $m(\cdot)$  as follows:

$m_s(A_{\max}) = 1$ , where  $A_{\max} \in G^\Theta$ . The problem is how to find  $A_{\max}$  ?

a) If  $m(\cdot)$  is Bayesian, then we compute

$$A_{\max} = \max \{m(X), X \in \Theta = \{\theta_1, \dots, \theta_1\}\} \quad (17)$$

and therefore  $m_s(\cdot)$  is considered to be  $m_s(A_{\max}) = 1$ ; if there exist many  $A_{\max}$ 's (i.e. having the same maximal mass), we take any of them because the distance between  $m(\cdot)$  and any of these most specific masses  $m_s'(A_{\max}') = 1$  associated with  $m(\cdot)$  will be the same.

b) If  $m(\cdot)$  is non-Bayesian we can compute  $A_{\max}$  in a similar way:

$$A_{\max} = \{ \max \{ m(X)/\text{Card}(X), X \in \Theta = \{ \theta_1, \dots, \theta_1 \} \} \}, \quad (18)$$

but if there exist more maximal masses we take the element with the smallest cardinality.

c) Another method for the case when  $m(\cdot)$  is non-Bayesian is to use the Smets's pignistic transformation, or GPT, or  $\text{DSmP}_\varepsilon$  in order to transform the non-Bayesian mass  $m(\cdot)$  into a Bayesian mass  $m'(\cdot)$  corresponding to  $m(\cdot)$ . And then use case a).

We recall below the three formulas of the pignistic transformations:

4.1. The **pignistic probability**, which transforms a basic belief assignment (bba) to a Bayesian probability, was introduced by Smets [5] and defined as:

$$\text{betP}(X) = \sum_{Y \in 2^\Theta, Y \neq \emptyset} \frac{|X \cap Y|}{|Y|} \frac{m(Y)}{1 - m(\emptyset)}. \quad (19)$$

for all  $X \in \Theta$ .

The following double inequality holds:

$$\text{Bel}(A) \leq \text{BetP}(A) \leq \text{Pl}(A). \quad (20)$$

4.2. An **extension of the pignistic probability** from DST and TBM to  $\text{DSmT}$  is the following (Dezert, Smarandache, Daniel, [9]):

$$\text{GPT}(X) = \sum_{\substack{Y \in D^\wedge \Theta \\ Y \neq \emptyset}} \frac{c_M(X \cap Y)}{c_M(Y)} m(Y) \quad (21)$$

where  $c_M(Y)$  is the  $\text{DSm}$  cardinality of  $Y$  in the given model  $M$ , which means the number of disjoint parts of  $Y$  in the Venn diagram.

4.3. A generalization of the pignistic probability is  **$\text{DSmP}_\varepsilon$**  (Dezert & Smarandache, [6]):

$$\text{DSmP}_\varepsilon(X) = \sum_{Y \in G^\wedge \Theta} \frac{\sum_{\substack{Z \subseteq X \cap Y \\ c(Z)=1}} m(Z) + \varepsilon \cdot c(X \cap Y)}{\sum_{\substack{Z \subseteq Y \\ c(Z)=1}} m(Z) + \varepsilon \cdot c(Y)} m(Y) \quad (22)$$

where  $\varepsilon \geq 0$  is a tuning parameter and  $G^\wedge \Theta$  corresponds to the generic set (power set  $2^\Theta$ , hyper-power set  $D^\Theta$ , or super-power set  $S^\Theta$  -- including eventually all integrity constraints (if any) of the model  $M$ );

$c(Z)$  denote the  $\text{DSm}$  cardinals of the set  $Z$ ;

$\varepsilon$  allows to reach the maximum specificity value of the approximation of  $m(\cdot)$  into a subjective probability measure; the smaller  $\varepsilon$  is the greater the specificity of the mass  $m(\cdot)$  is. DS<sub>m</sub>P provides a better specificity than the pignistic probability and other transformations that map the belief masses to Bayesian probabilities (Sudano's, Cuzzolin's).

Remark: the most specific mass  $m_s(\cdot)$  can also be defined in a different user's need for solving a particular application.

For DS<sub>m</sub>T,  $A_{\max}$  may be, for example, a non-empty intersection, let's say  $A \cap B$  if  $m(A \cap B)$  is maximal and  $\text{Card}(A \cap B) = 1$ .

For UFT (Unification of Fusion Theories) (Smarandache, [3])  $A_{\max}$  may be, for example, a difference of elements, let's say  $A - B$  if  $m(A - B)$  is maximal and  $\text{Card}(A - B) = 1$ .

Examples:

	A	A $\cup$ B	
$m_1$	0.6	0.4	(23)
$m_2$	0.5	0.5	

The most specific mass associated with both of them,  $m_1$  and  $m_2$ , is  $m_s(A) = 1$ .

$d_J(m_1, m_s) = 0.2828$  where  $d_J(\cdot, \cdot)$  is Jousselme distance, whence the specificity of  $m_1$  is  $\mathcal{S}(m_1) = 1 - 0.2828 = 0.7172$ .

$d_J(m_2, m_s) = 0.3535$ , whence  $\mathcal{S}(m_2) = 1 - 0.3535 = 0.6465$ .

So,  $m_1$  is more specific than  $m_2$ .

If we take  $m_3(A) = 0.5$ ,  $m_3(B) = 0.5$ , with  $A \cap B = \phi$ , the specificity of  $m_3$  is smaller than  $m_2$ 's specificity although the masses are the same.

The above  $m_s(A) = 1$  can serve as the most specific mass associated with  $m_3$ , then  $d_J(m_3, m_s) = 0.50$ , whence  $\mathcal{S}(m_3) = 1 - 0.50 = 0.50 < 0.6465$ .

More Bayesian examples in order to observe the convergence of specificity:

	A	B	C	$d_J(m_i, m_0)$	$S(m_i)$
$m_0$	1	0	0	0	1
$m_4$	0.4	0.4	0.2	0.529	0.471
$m_5$	0.45	0.45	0.10	0.507	0.493
$m_6$	0.45	0.40	0.15	0.492	0.508
$m_7$	0.45	0.30	0.25	0.477	0.523
$m_8$	0.45	0.275	0.275	0.476	0.524
$m_9$	1/3	1/3	1/3	0.577	0.423
$m_{10}$	0.6	0.3	0.1	0.361	0.639

The smallest specificity of a Bayesian mass is when the bba has a uniform distribution (in these examples  $m_9$ ), and the largest specificity is of course when the mass of a singleton is 1 ( $m_0$ ).

The specificity increases when the differences between the mass of the largest singleton and the masses of other singletons are getting bigger:  $S(m_5) < S(m_6) < S(m_7) < S(m_8)$ .

In the case when one has three disjoint singletons and the largest mass of one of them is 0.45, we have the minimum specificity when the masses of B and C are getting further from the mass of A ( $m_8$ ).

The problem becomes more complex for non-Bayesian masses about how to find the most specific mass.

Let's consider these examples where we apply method b):

	A	B	C	$A \cup B$	$A \cup C$	$B \cup C$	$A \cup B \cup C$	$m_{si}$	$d_J(m_i, m_0)$	$S(m_i)$
$m_{11}$				0.7	0.3			$m_{s11}(A \cup B)=1$ {if one decides on ignorances} or	0.245 or	0.755 or

								$m_{s11}(A)=1$	0.889	0.111
								{ if one decides on singletons }		
$m_{12}$		0.4			0.6			$m_{s12}(B)=1$	0.6	0.4
$m_{13}$	0.1						0.9	$m_{s13}(A)=1$	0.735	0.265

Table 1

For  $m_{11}$  (second case),  $m_{12}$  and  $m_{13}$  we applied method c).

### 5. Contradiction of an element with respect to a mass.

The contradiction of an element  $A$  with respect to a mass  $m_i(\cdot)$  is the distance between the masses  $m_i(\cdot)$  and  $m_A(\cdot)$ , where  $m_A(A)=1$ :

$$c(A) = d(m_i, m_A) \quad (24)$$

We define the **weighted contradiction  $c_i$  of a mass  $m_i(\cdot)$**  as:

$$c_i = \sum_{A \in G^{\wedge \Theta}} m_i(A) d(m_i, m_A) \quad (25)$$

and the **contradiction between two masses  $m_1(\cdot)$  and  $m_2(\cdot)$**  as:

$$c(m_1, m_2) = c_1 + c_2 - d(m_1, m_2) \quad (26)$$

### 6. Measure of specificity of a fusion rule.

Let's consider two masses  $m_1$  and  $m_2$ . One applies the rules  $R_1, R_2, \dots, R_p$

$m_1(R_1)m_2, m_1(R_2)m_2, \dots, m_1(R_p)m_2,$

and then one computes the specificity measure of each result and compare the results: what specificity (corresponding to what fusion rule) is bigger.

This can be generalized to  $s$  bba's in the following way:

If we combine more bba's,  $m_1, m_2, \dots, m_s$ , in the same way we compute the specificity of each mass  $m_i$ , and then the arithmetic average of these specificity. Afterwards, we fusion all these  $s$  masses simultaneously with a fusion rule, and then compute the specificity of the resulted mass.

Let's take the masses  $m_4$  and  $m_{10}$  that have the same most specific mass  $m_0(A)=1$ . {It is true that the most specific mass of  $m_4$  could equally be  $m_B(B)=1$  too.}



### 6.1. Bayesian Example.

	A	B	C	$A \cup B$	$A \cup C$	$B \cup C$	$A \cup B \cup C$	$\phi$	$m_S$ of $m_i$	$d_J(m_i, m_S)$	$S(m_i)$
<b>m<sub>4</sub></b>	0.4	0.4	0.2						$m_S(A)=1$	0.529	0.471
<b>m<sub>10</sub></b>	0.6	0.3	0.1						$m_S(A)=1$	0.361	0.639
<b>m<sub>conj</sub></b>	0.2 4	0.12	0.02					0.62	$m_S(A)=1$	0.712 9	0.287 1
<b>m<sub>DS</sub></b>	0.6 31	0.31 6	0.05 3						$m_S(A)=1$	0.346	0.654
<b>m<sub>Smets</sub></b>	0.2 4	0.12	0.02					0.62	$m_S(A)=1$	0.712 9	0.287 1
<b>m<sub>Yager</sub></b>	0.2 4	0.12	0.02				0.62		$m_S(A)=1$	0.562 1	0.437 9
<b>m<sub>DP</sub></b>	0.2 4	0.12	0.02	0.36	0.16	0.10			$m_S(A)=1$ or $m_S(A \cup B)=1$	0.720 5 or 0.867 0	0.279 5 or 0.133 0
<b>m<sub>PCR5</sub></b> or 6	0.5 74 57	0.33 543	0.09						$m_S(A)=1$	0.420 8	0.589 2.
<b>m<sub>Florea</sub></b>	0.3 13 97	0.15 699	0.02 6164	0.29 199	0.129 77	0.081 109			$m_S(A)=1$	0.462 3	0.537 7
<b>m<sub>dis</sub></b>	0.2 4	0.12	0.02	0.36	0.16	0.1			$m_S(A)=1$ or $m_S(A \cup B)=1$	0.497 9 or 0.348 2	0.502 1 or 0.651 8
<b>m<sub>mean</sub></b>	0.5 0	0.35	0.15						$m_S(A)=1$	0.444 4	0.555 6
<b>m<sub>DP-mixt</sub></b>	0.2 4	0.12	0.02	0.36	0.16	0.1			$m_S(A)=1$ or $m_S(A \cup B)=1$	0.497 9 or 0.348 2	0.502 1 or 0.651 8
<b>m<sub>Martin</sub></b>	0.2	0.12	0.02	0.36	0.16	0.1			$m_S(A)=1$	0.497	0.502

Osswald-mixt	4								or $m_S(A \cup B)=1$	9 or 0.348 2	1 or 0.651 8
$m_{DPCR}$	0.2 4	0.12	0.02	0.36	0.16	0.1			$m_S(A)=1$ or $m_S(A \cup B)=1$	0.497 9 or 0.348 2	0.502 1 or 0.651 8
$m_{MDPCR}$	0.2 4	0.12	0.02	0.36	0.16	0.1			$m_S(A)=1$ or $m_S(A \cup B)=1$	0.497 9 or 0.348 2	0.502 1 or 0.651 8
$m_{Zhang}$	0.6 31 58	0.31 579	0.05 2632						$m_S(A)=1$	0.345 1	0.654 9

Table 2.

## 6.2. Non-Bayesian Example.

	<b>A</b>	<b>B</b>	<b><math>A \cup B</math></b>	$\phi$	<b><math>m_S</math> of <math>m_i</math></b>	<b><math>d_J(m_i, m_S)</math></b>	<b><math>S(m_i)</math></b>
<b><math>m_1</math></b>	0.7	0.2	0.1		$m_S(A)=1$	0.2550	0.7450
<b><math>m_2</math></b>	0.4	0.5	0.1		$m_S(B)=1$	0.4528	0.5472
<b><math>m_{conj}</math></b>	0.39	0.17	0.01	0.43	$m_S(A)=1$	0.5393	0.4607
<b><math>m_{DS}</math></b>	0.68421	0.29825	0.017544		$m_S(A)=1$	0.3071	0.6929
<b><math>m_{Smets}</math></b>	0.39	0.17	0.01	0.43	$m_S(A)=1$	0.5393	0.4607
<b><math>m_{Yager}</math></b>	0.39	0.17	0.44		$m_S(A)=1$	0.4478	0.5522
<b><math>m_{disjunctive}</math></b>	0.28	0.1	0.62		$m_S(A)=1$	0.5140	0.4860
<b><math>m_{Floreau}</math></b>	0.45397	0.18532	0.36071		$m_S(A)=1$	0.4077	0.5953
<b><math>m_{PCR5}/m_{PCR6}</math></b>	0.6475	0.3425	0.01		$m_S(A)=1$	0.3475	0.6525
<b><math>m_{mean}</math></b>	0.55	0.35	0.10		$m_S(A)=1$	0.4031	0.5969
<b><math>m_{DuboisPrade}</math></b>	0.28	0.10	0.62		$m_S(A)=1$	0.5140	0.4860
<b><math>m_{DPmixt}</math></b>	0.39	0.17	0.44		$m_S(A)=1$	0.4478	0.5522
<b><math>m_{MartinOsswald-mixt}</math></b>	0.335	0.135	0.53		$m_S(A)=1$	0.4798	0.5202
<b><math>m_{DPCR}</math></b>	0.39	0.17	0.44		$m_S(A)=1$	0.4478	0.4798
<b><math>m_{MDPCR}</math></b>	0.335	0.135	0.53		$m_S(A)=1$	0.4798	0.5202
<b><math>m_{Zhang}</math></b>	0.70526	0.28421	0.010526		$m_S(A)=1$	0.2895	0.7105

Table 3.

In [4], Osswald and Martin computed the distance between fusion operator results using a class of random belief functions.

Roussilhe [10] compared the fusion rules from a statistical point of view. Randomly generating masses and fusing them 1000 times using various fusion rules, then with the classical pignistic transformation each non-Bayesian result was converted into a Bayesian result, which was interpreted as a random variable. Then one calculated the correlation coefficients (similarities) as in statistics between the decision vectors.

### 6.3. Continuous Frame Example.

	[1, 2]	[3, 5]	$[1, 2] \cup [3, 5]$	$\phi$	$m_S$ of $m_i$	$d_j(m_i, m_S)$	$S(m_i)$
<b>m<sub>1</sub></b>	0.2	0.8			$m_S([3,5])=1$	0.2	0.8
<b>m<sub>2</sub></b>	0.4	0.6			$m_S([3,5])=1$	0.4	0.6
<b>m<sub>conj</sub></b>	0.08	0.48	0.44		$m_S([3, 5])=1$	0.743	0.257
<b>m<sub>1</sub></b>	0.2	0.8			$m_S([3,5])=1$	0.2	0.8
<b>m<sub>2</sub></b>	0.4	0.6			$m_S([3,5])=1$	0.4	0.6
<b>m<sub>conj</sub></b>	0.08	0.48		0.44	$m_S([3, 5])=1$	0.743	0.257
<b>m<sub>D</sub>S</b>	0.14286	0.85714			$m_S([3, 5])=1$	0.1429	0.8571
<b>m<sub>S</sub>smets</b>	0.08	0.48		0.44	$m_S([3, 5])=1$	0.743	0.257
<b>m<sub>Yager</sub></b>	0.08	0.48	0.44		$m_S([3, 5])=1$	0.3720	0.6280
<b>m<sub>disjunctive</sub></b>	0.08	0.48	0.44		$m_S([3, 5])=1$	0.3720	0.6280
<b>m<sub>Florea</sub></b>	0.10616	0.63694	0.2569		$m_S([3, 5])=1$	0.2675	0.7325
<b>m<sub>PCR5/mPCR6</sub></b>	0.21667	0.78333			$m_S([3, 5])=1$	0.2167	0.7833
<b>m<sub>mean</sub></b>	0.3	0.7			$m_S([3, 5])=1$	0.3	0.7
<b>m<sub>DuboisPrade</sub></b>	0.08	0.48	0.44		$m_S([3, 5])=1$	0.3720	0.6280
<b>m<sub>DPmixt</sub></b>	0.08	0.48	0.44		$m_S([3, 5])=1$	0.3720	0.6280
<b>m<sub>MartinOsswald-mixt</sub></b>	0.08	0.48	0.44		$m_S([3, 5])=1$	0.3720	0.6280
<b>m<sub>DPCR</sub></b>	0.08	0.48	0.44		$m_S([3, 5])=1$	0.3720	0.6280

<b>mMPCR</b>	0.08	0.48	0.44		$m_S([3, 5])=1$	0.3720	0.6280
<b>mZhang</b>	0.14286	0.85714			$m_S([3, 5])=1$	0.1429	0.8571

Table 4.

In order to define the Bayesianity (non-Bayesianity) we present the measures of uncertainty of a set and of a mass.

### 7. Measure of Uncertainty of a Set.

In *DST* (Dempster-Shafer's Theory), Hartley defined the measure of uncertainty of a set  $A$  by:

$$I(A) = \log_2 |A|, \text{ for } A \in 2^\theta \setminus \{\Phi\}, \quad (27)$$

where  $|A|$  is the cardinality of the set  $A$ .

We can extend it to *DSmT* in the same way:

$$I(A) = \log_2 |A|, \text{ for } A \in G^\theta \setminus \{\Phi\} \quad (28)$$

where  $G^\theta$  is the super-power set, and  $|A|$  means the *DSm* cardinality of the set  $A$ ; in the case of Shafer's model (i.e. all intersections of the sets in the frame of discernment are empty), *DSm* cardinality coincides with classical cardinality in *DST*.

We even improve it to a **degree of uncertainty of a set**:

$$\cup_d^s : G^\theta \setminus \{\Phi\} \rightarrow [0, 1], \quad \cup_d^s(A) = \log_2(A) / \log_2 |I_t| \quad (29)$$

If  $A$  is a singleton, i.e.  $|A|=1$ , then  $\cup_d^s(A) = 0$  (minimum degree of uncertainty of a set),

For the total ignorance  $I_t$ , since  $|I_t|$  is the maximum cardinality, we get  $\cup_d^s(I_t) = 1$  (maximum degree of uncertainty of a set).

For all other sets  $X$  from  $G^\theta \setminus \{\Phi\}$ , whose cardinality is in between 1 and  $|I_t|$ , we have  $0 < \cup_d^s(X) < 1$ .

We consider our degree of uncertainty of a set works better than Hartley Measure since it is referred to the frame of discernment.

Let's see an **Example 1**.

If  $\theta = \{A, B\}$  and  $A \cap B \neq \Phi$ , we have the model

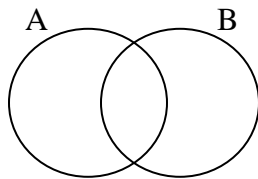


Fig. 1

$$I(A) = \log_2 |A| = \log_2 2 = 1$$

$$\text{While } \cup_d^s(A) = \frac{\log_2 |A|}{\log_2 |A \cup B|} = \frac{\log_2 2}{\log_2 3} = 0.63093$$

**Example 2.**

If  $\theta = \{A, B, C\}$ , and  $A \cap B \neq \Phi$ , but  $A \cap C = \Phi$ ,  $B \cap C = \Phi$ , we have the model

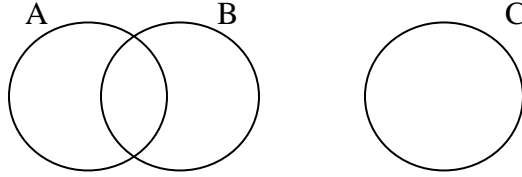


Fig. 2

$$I(A) = \log_2 |A| = 1 \text{ as in Example 1.}$$

$$\text{While } \cup_d^s(A) = \frac{\log_2 |A|}{\log_2 |A \cup B \cup C|} = \frac{\log_2 2}{\log_2 4} = \frac{1}{2} = 0.5 < 0.63093$$

It is normal to have a smaller degree of uncertainty of set  $A$  when the frame of discernment is larger, since herein the total ignorance has a bigger cardinality.

There are two types of uncertainty: nonspecificity and discord.

8. **Generalized Hartley Measure of uncertainty for masses** is defined as:

$$GH(m) = \sum_{A \in 2^\theta \setminus \{\Phi\}} m(A) \log_2 |A| \quad (30)$$

This is also called **non-specificity**.

From *DST* we simply extend the  $GM(\cdot)$  to *DST* as follows:

$$GH(m) = \sum_{A \in G^\theta \setminus \{\Phi\}} m(A) \log_2 |A| \quad (31)$$

**Degree of Uncertainty (or Degree of non-Bayesianity) of a mass.**

We go further and define a degree of uncertainty of a mass  $m$  as

$$\cup_d^M(m) = \sum_{A \in G^\theta \setminus \{\Phi\}} m(A) \cdot \frac{\log_2 |A|}{\log_2 |I_t|} = \sum_{A \in G^\theta \setminus \{\Phi\}} m(A) \log_{|I_t|} |A| \quad (32)$$

where  $I_t$  is the total ignorance.

If  $m(\cdot)$  is a mass whose focal elements are only singletons then  $\cup_d^M(m) = 0$  (minimum uncertainty degree of a mass).

If  $m(I_t) = 1$ , then  $\cup_d^M(m) = 1$  (maximum uncertainty degree of a mass).

For all other masses  $m(\cdot)$  we have  $0 < \bigcup_d^M(m) < 1$ .

Whence we can define a **Degree of Bayesianity** of a mass, which means how close is a bba to a Bayesian (probability) measure:

$$B(m) = 1 - \sum_{A \in \mathcal{G}^{\theta} \setminus \{\Phi\}} m(A) \cdot \frac{\log_2 |A|}{\log_2 |I_t|}. \quad (33)$$

If  $m(\cdot)$  is Bayesian, then  $\mathcal{B}(m) = 1$ .

For the vacuous belief assignment  $m_{VBA}(I_t) = 1$  we have  $\mathcal{B}(m_{VBS}) = 0$

If  $m(\cdot)$  is non-Bayesian, with  $m(\cdot) \neq m_{VBA}(\cdot)$ , then  $0 < \mathcal{B}(m) < 1$ .

Examples:

	A	B	C	$A \cup B$	$A \cup C$	$B \cup C$	$A \cup B \cup C$		$N\mathcal{B}(m_i)$	$\mathcal{B}(m_i)$
$m_{10}$	1	0	0	0	0	0	0		0	1
$m_{11}$	0.5	0.3	0.2	0	0	0	0		0	1
$m_{12}$	0.4	0.1	0.1	0.3	0.1	0	0		0.25	0.75
$m_{13}$	0.3	0.1	0.1	0.3	0.2	0	0		0.32	0.68
$m_{14}$	0.3	0.1	0.1	0.5	0	0	0		0.32	0.68
$m_{15}$	0.3	0.1	0.1	0	0	0	0.5		0.50	0.50
$m_{16}$	0	0	0	0.6	0.4	0	0		0.63	0.37
$m_{17}$	0	0	0	0.6	0	0	0.4		0.77	0.23
$m_{18}$	0	0	0	0.4	0	0	0.6		0.85	0.15
$m_{19}$	0	0	0	0.2	0	0	0.8		0.92	0.08
$m_{20}$	0	0	0	0	0	0	1		1	0

Table 5

Remark.

The degree of uncertainty (or non-Bayesianity) and respectively the degree of Bayesianity depend on the cardinality of the frame of discernment.

For example  $B(m_{12}) = 0.75$  in the frame  $\Theta_1 = \{A, B, C\}$  where the cardinality of the total ignorance  $I_t = A \cup B \cup C$  is 3, but if we consider  $m_{12}$  in the frame  $\Theta_2 = \{A, B, C, D\}$  where the cardinality of the total ignorance is 4, its Bayesianity increases:  $B(m_{12}') = 0.80$ . The larger is the frame, the larger becomes the Bayesianity.

## 9. Conclusion.

In this paper we introduced a new degree of specificity measure of a belief function, a degree of specificity measure of a set, and a degree of Bayesianity/non-Bayesianity of a belief function. We also introduced new distances between masses based on GPT and DS<sub>m</sub>P pignistic transformations from DS<sub>m</sub>P.

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