

# Point-wise Diversity Measure and Visualization for Ensemble of Classifiers

## *With Application to Image Segmentation*

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Keywords: Ensemble of Classifiers, Image Segmentation, Diversity.

Abstract: The idea of using ensembles of classifiers is to increase the performance when compared to applying a single classifier. Crucial to the performance improvement is the diversity of the ensemble. A classifier ensemble is considered to be diverse, if the classifiers make no coinciding errors. Several studies discuss the diversity issue and its relation to the ensemble accuracy. Most of them proposed measures that are based on an "Oracle" classification. In this paper, we propose a new probability-based diversity measure for ensembles of unsupervised classifiers, i.e., when no Oracle machine exists. Our measure uses a point-wise definition of diversity, which allows for a distinction of diverse and non-diverse areas. Moreover, we introduce the concept of further categorizing the diverse areas into healthy and unhealthy diversity areas. A diversity area is healthy for the ensemble performance, if there is enough redundancy to compensate for the errors. Then, the performance of the ensemble can be based on two parameters, the non-diversity area, i.e., the size of all regions where the classifiers of the ensemble agree, and the healthy diversity area, i.e., the size of the regions where the diversity is healthy. Furthermore, our point-wise diversity measure allows for an intuitive visualization of the ensemble diversity for visual ensemble performance comparison in the context of image segmentation.

## 1 INTRODUCTION

In pattern recognition and machine learning, several studies confirmed the concept that combining the results of multiple classifiers can yield more reliable and accurate results when compared to the results of a single classifier (Kittler et al., 1998; Sharkey, 1999; Dietterich, 2000; Kuncheva, 2004; Fred and Jain, 2005). This concept is known as committee machine, mixture of experts, or ensemble of classifiers (Mignotte, 2010). An important aspect of establishing ensembles is the diversity such that complementary information of individual classifiers can be combined to improve the final result. An ensemble of classifiers is said to be diverse, if the classifiers make no coinciding errors. Diversity can be achieved through several approaches: Several instances of the same algorithm can be applied on different subsets of the input data or on the same data but initialized using different parameter settings. Diversity can also be achieved either using different representations of the data (e.g., using the same input image represented in different color

spaces), or using different algorithms with sufficiently diverse behaviors on the input data (Fred and Jain, 2005; Mignotte, 2010). Another important issue is the ensemble redundancy (or knowledge redundancy) assuring that the individual classifiers (or experts) share their knowledge in order to make a more accurate decision. In the context of combining the results of classifiers within an ensemble, there have been several combining strategies proposed in the literature. Examples of strategies are majority votes, weighted majority votes, or probability rules such as product, sum, maximum, minimum, median, etc. The majority votes, weighted majority votes, and sum rules, where the individual classifiers contribute to the final ensemble decision, are the most commonly used rules. In general, the concept of ensembles of classifiers was mostly used in machine learning applications for supervised classification. The main focus of the researchers in the field is on the diversity definition and its evaluation (Kuncheva, 2004; Masisi et al., 2008), while the ensemble redundancy is mostly omitted in the discussion. Diversity and redundancy are some-

what conflicting concepts and a desired diversity is a diversity that, at the same time, has sufficiently large redundancy. This explains why most of the proposed diversity measures fail in defining a strong relation between the ensemble diversity and its accuracy. The desired diversity requests that, if a subset of the ensemble classifiers make errors at some point, the remaining classifiers in the ensemble should make correct decisions to allow for a correction. For an ensemble to be robust, the number of correct decisions should be more than the number of erroneous decisions (at each point). Such a diversity is the main motivation behind the concept of ensemble of classifiers methods. Thus, since the diversity is the most important ensemble property, several diversity measures have been proposed for different ensemble design applications. Kuncheva (Kuncheva, 2004) reviewed ten diversity measures and presented several applications of diversity measures in ensemble design, thinning, evaluation, and selection. However, all these measures of diversity require the availability of a ground-truth (or Oracle) classification, which is not always available (especially for unsupervised learning).

In this paper we distinguish between two types of the ensemble diversity and refer to them as healthy and unhealthy diversity. A diversity area is healthy, iff, in addition to the diversity, enough redundancy exists to compensate for the errors.

For the distinction between healthy and unhealthy diversity areas, we propose a new point-wise diversity measure, which is a non-pairwise measure able to estimate the diversity of the ensemble classifiers (or any subset of classifiers) in the absence of ground truth (i.e., it is suitable for unsupervised classification), see Section 3. Based on a certain threshold, the healthy and unhealthy diversity areas are computed, see Section 4. Our new diversity measure can be used for designing the ensemble classifiers or for estimating the ensemble performance, cf. (Kuncheva, 2004; Masisi et al., 2008). Furthermore, when applied to image segmentation, the point-wise definition of our diversity measure allows for an ensemble diversity visualization, which supports visual ensemble performance comparisons, see Section 5.

The contributions of our paper can be summarized as: (1) Defining a point-wise diversity measure for ensembles, which allows for the definition of healthy and unhealthy diversity regions. (2) Visual representation and analysis of diversity measures. (3) Diversity computation without known ground truth, i.e., it is applicable to unsupervised classification.

Our application domain is medical image segmentation. Thus, we applied the proposed methods on a synthetic image that mimics the properties of

main brain tissues in a T1-weighted MR image corrupted with mixed noise, and on the simulated MR images from Brainweb (MNI, 1997) corrupted with 5% Gaussian noise and 20% Intensity non-uniformity. The synthetic and the simulated data with known ground truth allow for the computation of segmentation accuracy to evaluate our methods, see Section 6 for the experimental set-up and Section 7 for results and discussion.

## 2 RELATED WORK

In recent years, combining ensemble of simple classifiers in order to improve their performance has witnessed a great attention by researchers across diverse fields to solve different classification problems (Kittler et al., 1998; Dietterich, 2000; Mignotte, 2010; Fred and Jain, 2005; Paci et al., 2013; Artaechevarria et al., 2009; Langerak et al., 2010). The ensemble diversity (or error diversity) issue and its relation to the ensemble accuracy attract the most interesting discussion in this concept (Kuncheva, 2004; Kuncheva and Whitaker, 2003). In this paper, we propose a new diversity measure suitable for ensembles of unsupervised classifiers (i.e., in the absence of ground truth). In addition to the importance of diversity for the improvement of ensemble performance, the diversity measure is also useful for several classifier ensemble applications such as ensemble diversity visualization, ensemble overproduce and select, or diversity for building ensembles (for more details see the diversity chapter in (Kuncheva, 2004)). Kuncheva (Kuncheva, 2004) reviewed ten pairwise and non-pairwise diversity measures, but all depend on the availability of ground truth (or Oracle) classification, which is not always provided. Another issue with pairwise measures is their complexity. To get a single value for ensemble diversity, the average across all pairwise diversity values needs to be calculated (i.e.,  $L(L-1)/2$  pairs for an ensemble of size  $L$ ).

The point-wise property for our proposed measure enables us to estimate the local diversity and, consequently, to distinguish among different levels of diversities (i.e., to distinguish between the desired (healthy) and undesired (unhealthy) diversity area for an ensemble of classifiers to be more robust). The diversity measures proposed by Masisi et al. (Masisi et al., 2008) and Sirlantzis et al. (Sirlantzis et al., 2008) are the closest diversity measures to our proposed measure. However, the two measures like the previous measures are global measures (i.e., not point-wise) and, consequently, by computing the average diversity one loses the internal distribution of

the diversity levels in the ensemble. Sirlantzis et al. (Sirlantzis et al., 2008) use  $k$  statistics to produce value 0 for no diversity and 1 for maximum diversity. The measure by Masisi et al. (Masisi et al., 2008) assigns with each individual classifier (for an ensemble of 21 classifiers) the probability that the classifier is selected in the ensemble out of 120 individual classifiers. Based on these probabilities, the entropy is used to measure the diversity of an ensemble. Then, a genetic algorithm that uses the diversity value as fitness function is used to select the best ensemble of size 21 out of 120 classifiers. It is clear that Masisi et al.'s measure is particularly designed for this system and not generally applicable for different ensemble designs and applications as the used probabilities are not related to the error probabilities of the individual classifiers.

The problem of medical image segmentation has been addressed in the framework of ensemble of classifiers methods using several atlas-based segmentations or several human rater segmentations. As pointed out in (Rohlfing and Maurer, 2005), producing multiple atlases is time consuming and tedious. Thus such atlases are not always available. Langerak et al. (Langerak et al., 2010) referred to the shortcoming of atlas-based segmentations as being an equivalent to segmentation by human expert. They also discussed two important drawbacks of using multiple atlases, namely, the large computational costs of the registration process and the shape variance in the atlas ensemble that is not always similar to that of the population from which the input image is drawn. These drawbacks may lead to the ensemble methods that use atlas-based segmentations to be impractical. Although Langerak et al. (Langerak et al., 2010) tried to reduce the effects of these drawbacks by reducing the number of atlases through an atlas selection procedure, the problem is only alleviated and not solved. To avoid such drawbacks, we propose to combine the results of several automatic segmentations of the target image with acceptable accuracies instead of combining the results of registering several atlases to the target image. The diversity is achieved through applying several unsupervised segmentation algorithms that use different approaches under the assumption that the probability that different approaches (with high or acceptable average accuracy, e.g.,  $> 0.80\%$ ) produce the same errors is very low.

### 3 POINT-WISE DIVERSITY

The proposed diversity measure is based on the probability of classes that appear in the ensemble decisions

using the normalized entropy to produce a value between 0 (no diversity) and 1 (maximum diversity). We choose to use the normalized entropy of the classes probabilities, as it is easy to compute, its value reflects both the degree of agreement and the error rate of the individual classifiers (assuming that sufficiently accurate individual classifiers mostly agree on correct decisions), and it allows for both point-wise and global diversity evaluation. The point-wise property for the proposed measure enables us to estimate the local diversity and consequently to distinguish among different levels of diversities. Based on this flexibility, a new diversity view is introduced, which is able to distinguish three diversity areas: (1) the non-diversity area, where all individual classifiers agree on the same decision (which can be assumed to be the correct decision if the individual classifiers have high accuracies); (2) the healthy diversity area, where most of the individual classifiers agree on the same decision; (3) the unhealthy diversity area, where two or more classes have approximately similar probabilities in the ensemble decisions (i.e., when the uncertainty in the ensemble is high). Following this train of thoughts, the *local diversity*  $D(P_v)$ , i.e., the diversity at point  $v$  with the probability vector  $P_v$  (which represents the probability distribution for all classes in the individual classifier's output at that point) is given by the normalized entropy:

$$D(P_v) = H(P_v) / \log_2(c), \quad (1)$$

where  $H(P_v)$  is the entropy of the probability vector  $P_v$  ( $H(P_v) = -\sum_{i=1}^c P_{v_i} \log_2 P_{v_i}$ ),  $c$  the number of classes, and  $\log_2(c)$  the normalization term. Based on the local diversity, the *global diversity*  $D(I_{en})$  for the entire ensemble image (or dataset)  $I_{en}$  can be evaluated by

$$D(I_{en}) = \frac{1}{N} \sum_{v \in I_{en}} D(P_v), \quad (2)$$

where  $N$  is the image cardinality  $|I_{en}|$ .

The *local diversity* is 0 when all classifiers agree on one decision and it is 1 when all classes have equal probability. Otherwise, the measure has values in the interval  $(0, \theta)$  with  $\theta \leq 0.5$  when one class dominates over others and has values in the interval  $[\theta, 1)$  when two or more classes have mostly similar probabilities in the ensemble decisions. The philosophy of the measure is to distinguish between two types of diversity: healthy diversity and unhealthy diversity. The healthy diversity (for a robust ensemble) is located in the interval  $[0, \theta)$  where the probability of errors is low, while the unhealthy diversity is located in the interval  $[\theta, 1]$ , where the probability of errors is high. The selection of threshold  $\theta$  depends on the number of classes and how large the proportion

of the dominating class is in the ensemble decision for a certain point to be considered in the healthy diversity interval. For example, when assuming that a point belongs to the healthy area iff. more than 81% of individual classifiers agree on the same decision, we choose  $\theta = 0.35$  for  $c = 4$ . This follows the observation that the normalized entropy of the vector (0.811,0.199,0,0) is 0.349687, while the normalized entropy of the vector (0.8,0.2,0,0) is 0.360964.

This philosophy is based on a heuristic assumption that the ensemble consists of a set of individual classifiers with acceptable accuracy (e.g.,  $\geq 0.80\%$ ). If this is the case, then the probability that all (or most of) the classifiers agree on a wrong decision is very low and, consequently, there would be a low error rate on the final ensemble decision. Conversely, in the unhealthy interval, the probability of individual errors increases when two or more classes have similar probabilities. Even though the true class is most likely one of the reported classes, the probability of having an error ensemble decision is still high. Under this interpretation, the majority votes combining strategy where the winner class is the one receiving the largest number of votes in the classifier ensemble (Kittler et al., 1998) is very correlated to our diversity measure.

The proposed diversity measure can be helpful to locally select at each point the suitable combining strategy for each interval of diversity values or to globally evaluate the entire ensemble diversity whether it is healthy or unhealthy in addition to other diversity applications (see (Kuncheva, 2004)).

## 4 DIVERSITY REGIONS

According to our diversity concept, two *global diversity* areas, the non-diversity area  $NDA$  and the diversity area  $DA$ , can be defined to evaluate the ensemble performance as follows:  $DA = \sum_{v \in I_{en}} \delta_v$ , and  $NDA = N - DA$ , where  $\delta_v$  is the binary function

$$\delta_v = \begin{cases} 1 & \text{if } D(P_v) > \theta \\ 0 & \text{otherwise,} \end{cases} \quad (3)$$

and  $N$  is the image cardinality  $|I_{en}|$ .

For further ensemble evaluation, the diversity area can be subdivided into the healthy diversity area  $HDA$  and the unhealthy diversity area  $UDA$  as follows:  $HDA = |\{v \in D_A \wedge D(P_v) < \theta\}|$  and  $UDA = DA - HDA$ , where  $D_A$  is the set of points in the diversity area  $DA$ .

The diversity density  $DD$  can be calculated for the diversity area and its parts the healthy and unhealthy diversity areas densities ( $HDD$  and  $UDD$ ) as

follows:  $DD = \sum_{v \in D_A} \frac{D(P_v)}{DA}$ ,  $HDD = \sum_{v \in HDA} \frac{D(P_v)}{HDA}$ , and  $UDD = \sum_{v \in UDA} \frac{D(P_v)}{UDA}$ , where  $HDA$  and  $UDA$  are the sets of points in the healthy ( $HDA$ ) and unhealthy diversity areas ( $UDA$ ), respectively.

The non-diversity ratio  $NDR$ , diversity ratio  $DR$ , the healthy diversity ratio  $HDR$ , and unhealthy diversity ratio  $UDR$  are given by:  $NDR = NDA/N$ ,  $DR = DA/N$ ,  $HDR = HDA/N$ , and  $UDR = UDA/N$ , respectively.

Then, the ensemble diversity evaluation can be based on two parameters, namely, the non-diversity area  $NDA$  (or  $NDR$ ), as it represents the area of all individual classifiers' agreement (on the correct decision mostly), and the healthy diversity area  $HDA$  (or  $HDR$ ), where the probability for an ensemble in producing the correct decision is very high. Assuming that individual classifiers have a sufficiently high accuracy, the non-diversity and the healthy diversity areas are expected to cover a large amount of points with correct decisions mostly. Consequently, ensembles with larger non-diversity area and larger healthy diversity area perform better.

## 5 DIVERSITY VISUALIZATION

In addition, we propose a point-wise diversity visualization that can be useful for visual diversity comparison in the context of image segmentation. We propose a color mapping of the identified areas in the image domain, potentially overlaid with the original input images. Two color maps are being proposed, a categorical one and a categorical with color transitions within each category. In the first visualization method, the different diversity areas are color-coded using three distinct colors (black: non-diversity area, blue: healthy diversity area, and red: unhealthy diversity area). In the second visualization method, the internal diversity level of the healthy and unhealthy diversity areas are color-coded using a continuous transition between two colors for each area. The healthy diversity area gradually changes from dark blue to light blue, while the unhealthy diversity area gradually changes from red to yellow (the non-diversity area remains black). The proposed discrete and continuous color-coding can be overlaid with the original image by assigning to the non-diversity pixels the original intensities instead of the black color. Examples are given in the subsequent sections.

## 6 EXPERIMENTAL SET-UP

As we mentioned above, to avoid the drawbacks of combining several atlas-based segmentations, we proposed to combine the results of several unsupervised segmentations. In this paper, we use several variants of the fuzzy c-means (FCM) algorithm introduced by Bezdek (Bezdek, 1981). Fuzzy c-means is one of the most commonly used algorithms for image segmentation (Mohamed et al., 1999; Chen S., Zhang D., 2004; Zhang and Chen, 2004; Chuang et al., 2006; Ahmed et al., 2002; Yuan et al., 2005). The FCM variants used in this paper are: (1) the modified fuzzy c-means (mFCM) (Mohamed et al., 1999), (2) the Bias-corrected FCM (BCFCM) (Ahmed et al., 2002) and an improved version thereof, (3) the Bias-corrected FCM with weighted  $\alpha$  (BCFCM\_WA) (Yuan et al., 2005), (4) the spatial fuzzy c-means (sFCM) (Chuang et al., 2006), (5) the spatial kernelized fuzzy c-means (SKFCM) (Chen S., Zhang D., 2004; Zhang and Chen, 2004), (6) the simplified fuzzy c-means method (FCMS1) using mean filter (Chen S., Zhang D., 2004), (7) the CLIC algorithm (Li, C. and Xu, C. and Anderson, A. and Gore, J., 2009), and finally (8) the fuzzy rule based system (FRBS) (Tolias and Panas, 1998).

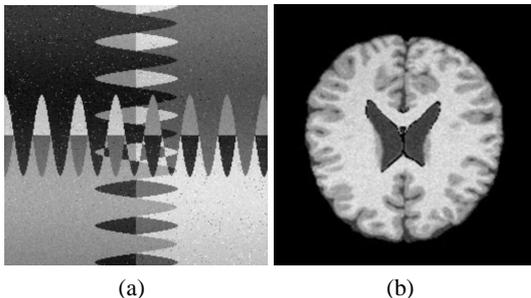


Figure 1: (a) synthetic image corrupted with mixed noise. (b) simulated T1-weighted MRI corrupted with noise.

In the subsequent section, we present and compare the experimental results of applying the proposed methods on the synthetic images in Figure 1(a), and on the simulated T1-weighted MRI in Figure 1(b). For the synthetic image, we tried to mimic the main brain tissues of MR T1- and T2-weighted images in a synthetic image (i.e., the background Bg, the white matter WM, the gray matter GM, and the cerebrospinal fluid CSF). We generate an example of four respective classes with complex structures as shown in Figure 1(a). We corrupted our synthetic image with different types of noise that are common in medical data such as Gaussian, salt-and-pepper, or sinusoidal noise. In first experiment, we use a synthetic image corrupted with a mixture of the three types of noise

Table 1: Segmentation accuracy (SA) in percentage for the synthetic image in Figure 1(a) when applying the modified FCM variants methods that we use as the individual classifiers to assemble the ensemble.

Method	SA%	Method	SA%
BCFCM	85.33	FCMS1	98.5565
CLIC	88.8062	FRBS	98.5657
SKFCM	94.0079	mFCM	98.7747
BCFCM_WA	94.30	sFCM	99.388

as shown in Figure 1(a). Before describing the experiments, we show in Table 1 the segmentation accuracy for each of the above FCM variants (individual classifiers). The segmentation accuracy that is used throughout this paper is given by

$$SA = \frac{|\text{correctly classified pixels}|}{\text{Total number of pixels}} \times 100\%. \quad (4)$$

As our experimental results showed that the majority votes rule almost always achieved the best performance in terms of segmentation accuracy and due to its relation to the proposed diversity measure, we use it as the combining strategy in our experiments in the results and discussion section. The majority votes rule selects the class that has been reported the most by the individual classifiers as the combined classification result.

## 7 RESULTS AND DISCUSSION

In our experiments, we apply the proposed diversity measures, the diversity areas ratios, and the diversity densities on five ensembles with different sizes (4,5,6,7,7). The experiments confirm our discussion on the proposed diversity measure and the healthy and unhealthy diversity areas. Figure 2(a) shows the majority rule (MajR) segmentation accuracy(SA), and the different diversity areas ratios (NDR, DR, HDR, and UDR). Figure 2(b) shows the misclassified ratios (NDA MR, DA MR, HDA MR, and UDA MR) of the different diversity areas regarding the corresponding diversity areas. Figure 2(c) shows the diversity density of the different diversity areas (DD, HDD, and UDD). The sizes of ensembles from Ens\_1 to Ens\_5 are 4,5,6,7, and 7, respectively. We start with an ensemble of size 4 (BCFCM, BCFCM\_WA, SKFCM, and FCMS1). Then, we add a fifth classifier FRBS for Ens\_2, add a sixth classifier sFCM for Ens\_3, and add a seventh classifier mFCM for Ens\_4. Finally, for Ens\_5, we take Ens\_4 and replace sFCM with CLIC. The first four experiments show that the NDR for the ensembles are approximately equal and that the performance of the ensembles with larger healthy diversity area (HDA) is better. While the non-diversity

ratios are approximately similar for ensembles Ens\_1 and Ens\_2, the healthy diversity area is zero for Ens\_1 and the accuracy (SA) increases as the size of ensembles increases (from Ens\_2 to Ens\_1). This is indicated by the increase of the performance of UDA (reduced UDA MR for Ens\_2), although UDA was similar for both ensembles. The same behavior or trend can be seen when adding even more classifiers in Ens\_3 and Ens\_4. The misclassified ratio UDA MR is steadily decreasing.

In general, we judge the performance of an ensemble by first inspecting the non-diversity area where the ensemble with the larger non-diversity area (all classifiers agree in those areas) typically leads to better segmentation accuracy. If the non-diversity area is comparable, then the ensemble with larger healthy diversity area (HDA) shall be preferred, as there is a higher chance of compensating for the error and making the right decision. If the healthy diversity area for two ensembles is also comparable (as in Ens\_1 and Ens\_2 or in Ens\_3 and Ens\_4), then we inspect the diversity density of the diversity areas: The ensemble with lower density (especially in the UDA) has better accuracy.

Comparing the results of Ens\_4 and Ens\_5, where we exchanged the individual classifier with best accuracy (99.3%) with a low-accuracy classifier (88%), we can observe that the accuracy was not affected very much, even though the NDR is decreased by 8%. This can be explained by observing that the healthy area increased, i.e., the lower accuracy estimates could be compensated.

In Figure 2(b), we can observe that most of the misclassified ratios are in the unhealthy diversity area, while the non-diversity and healthy diversity areas have very small error ratios. This finding confirms that our diversity measures are indeed suitable and appropriate.

Figure 3 shows examples of the proposed visual encoding of the ensemble diversity areas. The examples relate to the experiments shown in Figure 2. The first column shows the purely categorical color mapping while the second column shows the color mapping with continuous two-color transitions per category. The images show the following ensembles: (a and b) the second ensemble (Ens\_2), (c and d) the third ensemble (Ens\_3), (e and f) the fourth ensemble (Ens\_4), (g and h) fifth ensemble (Ens\_5), and (i and j) fourth ensemble (Ens\_4) again but overlaid with the original image in non-diversity areas. Figure 3(k) shows the legends of the discrete color mapping (DCM) and the continuous color mapping (CCM) that were used to visualize the healthy (HD) and unhealthy (UD) diversity areas. We can observe that in the en-

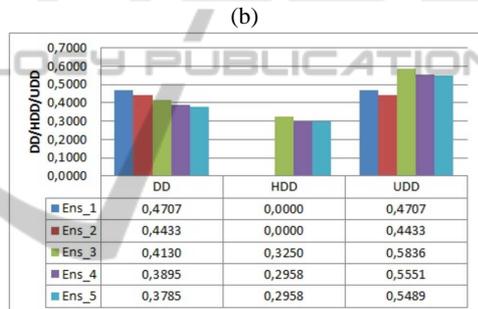
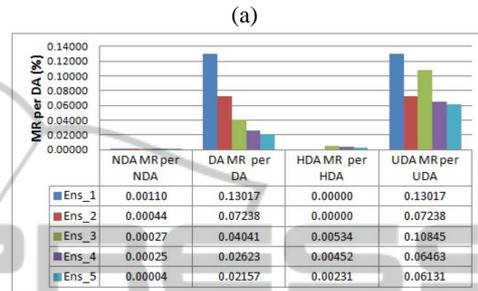
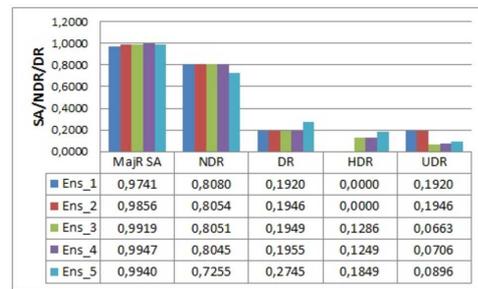


Figure 2: (a) The segmentation accuracy (SA) with the (non-diversity(ND), diversity(D), healthy diversity(HD), and unhealthy diversity(UD)) ratios; (b) their misclassified ratios (MR), and (c) their diversity densities (DD) comparison for ensembles of different sizes on the synthetic image.

semble of Figure 3(a) only unhealthy diversity areas exist, while for the ensemble in Figure 3(c) parts of the unhealthy diversity area converted to healthy diversity areas (the blue area). Some scattered healthy points in Figure 3(c) (Ens\_3) become unhealthy in Figure 3(e), which explains the increment of UDA in the fourth ensemble (Ens\_4), cf. Figure 2. In general, the visualizations allow for a quick overview comparison of the quality of the chosen ensembles and for a more detailed visual analysis on which areas cause problems.

To further validate the proposed methods, we applied them to simulated MR brain images (MNI, 1997). In Figure 4, we show the results for T1-weighted images corrupted with 5% Gaussian noise and 20% intensity non-uniformity shown in Figure 1(b). In this experiment, we compare the results of five ensembles (T1\_Ens\_1-T1\_Ens\_5) with

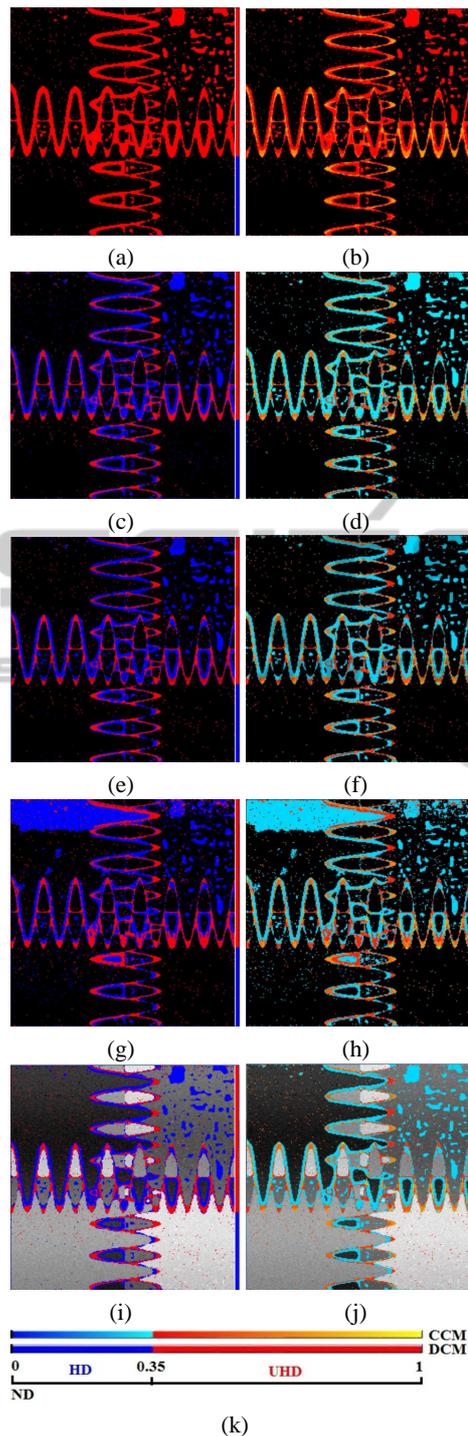
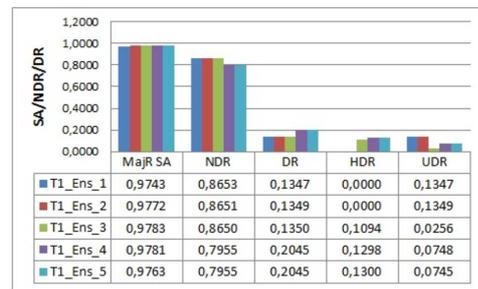
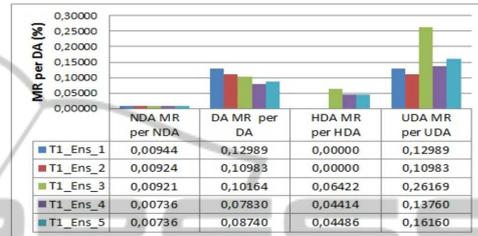


Figure 3: The proposed diversity visualizations for the experiments in Figure 2. Ens\_2 (a) and (b), Ens\_3 (c) and (d), Ens\_4 (e) and (f), Ens\_5 (g) and (h), Ens\_4 (i) and (j), (k) the legend.

sizes (4,5,6,7, and 6), respectively. The first ensemble T1\_Ens\_1 consists of 4 classifiers (CLIC, BCFCM\_WA, FCMS1, and FRBS). Then, we add a



(a)



(b)



(c)

Figure 4: (a) The segmentation accuracy (SA) with the (non-diversity(ND), diversity(D), healthy diversity(HD), and unhealthy diversity(UD)) ratios; (b) their misclassified ratios (MR), and (c) their diversity densities (DD) comparison for ensembles of different sizes on the simulated MRI of Figure 1(b).

fifth classifier mFCM for T1\_Ens\_2, a sixth classifier sFCM for T1\_Ens\_3, and a seventh classifier SKFCM for T1\_Ens\_4. Finally, for T1\_Ens\_5 we remove sFCM from T1\_Ens\_4. Figure 4 shows the diversity areas for these ensembles, their misclassified ratios, diversity densities, and segmentation accuracies. We can observe a similar behavior in the performance of the ensembles to the one we observed when investigating the synthetic image. Hence, similar conclusions can be drawn.

## 8 CONCLUSIONS

In recent years, the concept of combining several classifiers in order to produce classification accuracy that outperforms the accuracy of the individual classifiers attracted the attention of researchers in different fields to improve the segmentation accuracy or to evaluate

the performance level of the individual segmentation. We proposed a novel probability-based diversity measure with a new concept that is suitable for unsupervised classifiers. In this concept, we distinguish between healthy and unhealthy diversity areas for an ensemble design. The experimental results show the appropriateness of our approach and how it can be used to evaluate the performance of ensembles. We also proposed a color-coded diversity visualization to visually encode the healthy and unhealthy diversity areas and their diversity level. This means that the diversity visualization can be used in comparing the performance of different ensembles.

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