

A Higher-Order Neural Network Design for Improving Segmentation Performance in Medical Image Series

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Abstract. Segmentation of anatomical structures from medical image series is an ongoing field of research. Although, organs of interest are three-dimensional in nature, slice-by-slice approaches are widely used in clinical applications because of their ease of integration with the current manual segmentation scheme. To be able to use slice-by-slice techniques effectively, adjacent slice information, which represents likelihood of a region to be the structure of interest, plays critical role. Recent studies focus on using distance transform directly as a feature or to increase the feature values at the vicinity of the search area. This study presents a novel approach by constructing a higher order neural network, the input layer of which receives features together with their multiplications with the distance transform. This allows higher-order interactions between features through the non-linearity introduced by the multiplication. The application of the proposed method to 9 CT datasets for segmentation of the liver shows higher performance than well-known higher order classification neural networks.

1. Introduction

Medical imaging devices (i.e. Computed Tomography (CT), Magnetic Resonance Imaging (MRI) etc.) can acquire image slices with very small slice thickness (ST) (i.e. inter-slice distance). Due to the trade-off between efficiency (i.e. computational time) and performance (i.e. accuracy of the segmentation result) extracting a body part of interest (i.e. organ, tissue, tumor etc.) via segmentation from high number of image slices is still an emerging field [1].

Current studies on organ segmentation (i.e. automatic, semi-automatic) area usually are slice-by-slice approaches. Therefore, inter-slice information is very important. The distance transform (DT) can be used to represent inter-slice info as a feature or a multiplier for image prior to extraction of other features [2]. This corresponds to High Order Neural Network (HONN) structures, which are designed to overcome the performance drawbacks of NN architectures at classifying complicated data with high order non-linearity. HONN is suggested by [3] and its learning capabilities are analysed in [3], which shows that the higher order inputs and weights combinations gives higher generalization performance as they need a smaller training set [4].

This study presents a novel approach by constructing an HONN, the input layer of which receives multiplicative pairs of each feature with the DT. The proposed method is applied to



9 Computed Tomography Angiography (CTA) datasets acquired for the measurement of liver volumes of transplantation donors prior to living-donated surgery [2]. The results show higher accuracy, sensitivity and specificity compared to other well known HONN structures such as pi-sigma and productive unit NN.

2. Datasets

CTA datasets, which were obtained by using a Philips Secura CT and a Philips Mx8000 CTA with contrast agent injection at portal phase. The CTA datasets consist of DICOM images, which have 512x512 resolution and 3.2 mm slice thickness. Each data set include 70 to 110 images. The datasets selected for the study are chosen to have challenging difficulties for better illustration of the performance comparison of the different NN designs used in this study. The liver can be adjacent to other organs as seen. According to partial volume effects and their similar texture, the boundary between other organs and liver can become hard to segment. There are numerous variations about the appearances of these organs through different data sets due to countless variations in human anatomy, injection of contrast media, different image characteristics etc.

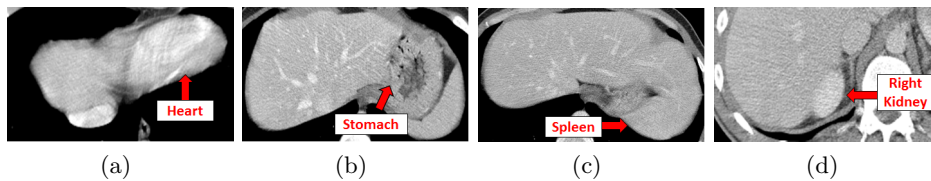


Figure 1: Examples of challenging problems in liver segmentation (a) unclear boundary between liver and heart, (b) unclear liver boundary due to stomach, (c) liver and spleen become adjacent due to atypical shape of the liver that results in visually indistinguishable border between them, (d) the liver is completely connected to right kidney.

3. Methodology

In this paper, the fully automatic three stage (i.e. pre-processing, classification, post-processing) procedure proposed in [2] is used as the main algorithm. The pre-processing part removes the fat tissue, bone structure from images by using a combination of adaptive thresholding and morphological processing. The classification stage takes the output of pre-process as input, and extracts three features that are mean, Standard Deviation (SD), and Distance Transform (DT). The post-processing stage receives classification output and applies non-linear filtering to finish the segmentation process. Since this study deals with the classification stage only, pre-process and post-process operations are the same for all approaches.

In total, 5 different types of input space structures (Table 1) are constructed and tested in this study. The first one uses the algorithm in [2], results of which are known to be clinically acceptable for evaluating living liver transplantation donors. The remaining five systems are constructed by using multiplicative and additive combinations of features at the input of the classifiers. The details of these five NN structures are given below:

If we define mean feature vector with, \mathbf{m} , SD feature vector with, \mathbf{s} , and DT feature vector with, \mathbf{d} , extracted from image, \mathbf{I} , then the input space, \mathbf{x} , is constructed using $\mathbf{x}=[\mathbf{s};\mathbf{m};\mathbf{d}]$. Then the output of the classifier is equal to:

$$o^i = f\left(\sum_{i=1}^n \mathbf{w} * \mathbf{x}^i\right) \quad (1)$$

Table 1: NN input space architectures used in this study

NN type	Information	Source	Feature 1	Feature 2	Feature 3	Feature 4	Feature 5
type 1	0,51	I	M	SD	DT		
type 2	0,51	I*DT	M	SD			
type 3	0,45	I	M*DT	SD*DT			
type 4	0,49	I	M	SD	M*DT	SD*DT	DT
type 5	0,49	I*DT	M	SD	DT		

where, \mathbf{f} is the activation function, \mathbf{w} is the weight vector, and \mathbf{o} is the output of the classifiers.

The SD and the mean features are calculated in a 9 x 9 window size centred for a given pixel. The size of the kernel is determined after extensive experimentation. The mean feature is calculated to represent the regions of low frequency, such as homogeneous areas (i.e. parenchyma), in the slice to segment. The SD feature is used to represent regions of high frequency, such as edges and organ boundaries. These features are calculated as

$$\bar{m}_{ij} = \frac{1}{N} \left(\sum_{i-4}^{i+4} \sum_{j-4}^{j+4} m_{ij} \right), \quad \sigma_{ij} = \frac{1}{N} \left(\sum_{i-4}^{i+4} \sum_{j-4}^{j+4} x_{ij} \right) - \bar{m}$$

where \bar{m}_{ij} is the mean values of the pixel at the point (i,j) and σ_{ij} is the SD of the pixel located at (i,j). N is the total number of the pixels in window and is equal to 81 in this study.

Finally, the DT feature is used to represent the previously segmented image. By creating a distance map from the center of the segmented liver at slice N, the DT shows a probabilistic map of liver position at slice N+1.

In type 2 and type 5, features extracted after multiplying the image by DT. This process reduces the brightness of the pixels according to their locations, where the pixels that are far away from the previously segmented liver become darker and their gray values are reduced. In these approaches, the effect of DT is projected onto mean and SD features. The only difference between them is that the type 5 uses also DT as an input. Therefore, the feature vector of type 2 is $\mathbf{x}=[\mathbf{s}; \mathbf{m}]$ and the feature vector of type 5 is $\mathbf{x}=[\mathbf{s}; \mathbf{m}; \mathbf{d}]$, where \mathbf{s} and \mathbf{m} are extracted from DT*I (i.e. the DT is multiplied by the current image to segment).

In the type 3, the SD and the mean features of the image is multiplied by the DT feature of the previous image. Type 3 is similar to pi-sigma with a single difference. At the input, all combinations of input feature multiplications except one are used. The multiplication of mean with SD feature is not used since the multiplication of these complementary features suppresses the discriminating information coming from both of them. Therefore, the input feature vectors of type 3 is $\mathbf{x}=[\mathbf{s}*\mathbf{d}; \mathbf{m}*\mathbf{d}]$. The output is calculated by using the equation in (1).

In type 4, the SD, the mean and the DT features are used in addition to type 3 features. Thus, this network structure is a mixture of PUNN and pi-sigma network types. The similarity to pi-sigma is due to the reason mentioned in type 3 and the similarity to PUNN is due to the features, which are also used as input besides their multiplications. The input vector of this system becomes $\mathbf{x}=[\mathbf{m}; \mathbf{s}; \mathbf{s}*\mathbf{d}; \mathbf{m}*\mathbf{d}; \mathbf{d}]$ and the output is calculated as in (1).

4. Results

The HONN systems described in the previous section are applied to 9 challenging data sets. The results obtained with different systems are compared image (i.e. algorithm result) by image (i.e. ground truth created by manual delineation of expert physician). The 2D error metrics used to evaluate the results are false positive (FP), false negative (FN), true positive (TP), true negative (TN), accuracy (CC), selectivity (SE), specificity (SP), positive predictive value

(PPV), and negative predictive value (NPV). The results, which show average values of each error metric among all data sets, are presented in Table 2. All HONN structures used in the study (i.e. type 2-5) perform better or equally well when compared to original NN system (i.e. type 1). The results also show that multiplying other features with DT feature gives better results than multiplying image with DT feature before extracting other features. Thus, projecting the DT information onto the other features outperform the projection onto the image with a slight difference. On the other hand, using DT feature itself together with other features extracted from image multiplied with DT is also useful (i.e. type 5) and gives better results than the other systems (i.e. type 2 and type 3). However, according to the results (i.e. type 4), using another feature may not further increase the performance.

Table 2: The results of calculated 2D error metrics

NN type	FP	FN	TP	TN	CC	SE	SP	PPV	NPV
type 1	0,51	31,15	99,49	68,85	84,17	59,10	99,27	99,49	68,85
type 2	0,51	23,04	99,49	76,96	88,23	56,38	99,34	99,49	76,96
type 3	0,45	23,03	99,55	76,97	88,26	56,39	99,41	99,55	76,97
type 4	0,49	23,16	99,51	76,84	88,18	56,43	99,37	99,51	76,84
type 5	0,47	20,44	99,53	79,56	89,55	55,58	99,42	99,53	79,56

5. Conclusions

In this study, the performance of the liver segmentation method in [2] is increased by modifying the classification stage using HONN systems. The simulations show that well-known successful HONN architectures such as pi-sigma and PUNN, which uses multiplicative combinations of inputs, achieve improved performance compared to the direct use of the same features. Moreover, it is shown that even a higher performance can be achieved using 'physically meaningful' combinations of features instead of using all combinations as in pi-sigma and PUNN. Developed HONN designs based on this idea (type 5) qualifies 'physically meaningful' use of multiplicative feature combinations by projecting the most discriminating feature (i.e. DT), which defines a probabilistic map at the vicinity of liver by using adjacent slice information, onto the other features (i.e. mean, SD). By using only the selected combinations in the developed HONN design, the local minima problem of HONN systems is reduced and thus, introduced non-linearity by increasing input space dimension is advantageously used. The results show that proposed HONN system outperforms both well-known HONN systems (i.e. pi-sigma, PUNN) and previously reported system in [2], which is shown to produce results at clinically acceptable levels.

6. Acknowledgments

This study is supported by TUBITAK EEEAG under grant number 112E032.

7. References

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