Analysis of 2D Phase Contrast MRI in Renal Arteries by Self Organizing Maps
Initial Experiences

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Abstract. We present an approach based on self organizing maps to segment renal arteries from 2D PC Cine MR images to measure blood velocity and flow. Such information are important in grading renal artery stenosis and support the decision on surgical interventions like percutan transluminal angioplasty. Results show that the renal arteries could be extracted automatically. The corresponding velocity profiles show high correlation (r=0.99) compared those from manual delineated vessels. Furthermore, the method could detect possible blood flow patterns within the vessel.

1 Introduction

Renal artery stenosis (RAS) is the leading cause of secondary hypertension caused by the reduced flow triggering the auto-regulation (renin-angiotesin) of the systemic circulation including the contralateral kidney. By time this may lead to loss of renal parenchyma in the stenosed kidney and microangiopathy in the glomeruli of the non-stenosed contralateral kidney. To be successful, a percutan transluminal angioplasty (PTA) should be performed before these changes have developed past certain limits in flow-reduction, flow velocity, kidney-size and the overall- and split-renal function. Ignoring these measures may lead to a wrong selection of patients treated with PTA and might be a reason why improvement after PTA has shown to be rather low [1]. Thereby, MRI provides a good tool for measuring these processes [2]. Cine Phase-Contrast MR (PC-MRI) blood flow measurements can be used for non-invasive quantification of renal artery blood flow. During acquisition two images are generated, a magnitude image and a phase image, encoding blood velocity and direction. From these images the blood flow within the vessel can be quantified and abnormalities in the flow or velocity profiles over the cardiac cycle can be assessed and RAS can be graded.

Blood flow quantification from PC-MRI acquisition is usually performed by manual delineations of the vessel area [3]. This is time consuming and subject to operator dependent variability. Kozerke et al. [4] proposed an active contour approach for vessel segmentation from PC-MRI. A segmentation approach taking

the waveform of the velocities into account and applying correlation and thresholding has been proposed in [5] and segmentation by k-means clustering has been presented in [6]. However, all these approaches still involve manual interaction during the initialization and thus, operator dependent variability. In the present approach we utilize self organizing maps (SOM)[7] for the segmentation task. This technique provides a model free and unsupervised approach to the segmentation task. Similar to [6] it further allows for a functional segmentation, i.e. to take the velocity profiles into account.

2 Materials and methods

2.1 Data acquisition

Ten subjects (3 healthy volunteers, 7 patients) underwent renal blood flow measurements on a 1.5 T scanner as described in [8]. We used a ECG gated 2D cine PC-MR sequence with TR=37ms, TE=4ms, FA=30°, VENC=100 cm/s. Within the cardiac cycle between 20 and 25 images with matrix 256x192 and spatial resolution 0.9x0.9x6 mm^3 were acquired.

2.2 Self organizing maps for PC-MRI analysis

Self organizing maps generate nodes on a two-dimensional grid. The distribution of these nodes on the grid corresponds to the distribution of the associated node patterns in feature space. Thereby, a mapping of a high dimensional feature space onto a 2D grid is reached maintaining the underlying topology of the feature space. Briefly, each node n on a $N \times N$ regular grid a prototype vector $u^{(k)}$, $k = 1, \ldots, N^2$ is assigned and initialized randomly. Then, a data sample $x^{(i)}$is presented and the best matching or winning node $n^{(\kappa)}$ (BMU) on the grid is searched:

$$\kappa = \arg\min_k \{|u^{(k)} - x^{(i)}|^2\} \tag{1}$$

The $u^{(\kappa)}$'s prototype vector is then updated according to its distance to the training sample. In addition, the neighbors' prototype vectors on the grid are updated, too. This update process is controlled by a iteratively decreasing learning rate $\epsilon(t)$ and is described by the Kohonen's learning rule [7]

$$u^{(k)}(t+1) = u^{(k)}(t) + \epsilon(t) \exp(-\frac{d_{ij}}{\sigma^2})(x^{(i)}(t) - u^{(k)}(t)) \tag{2}$$

where d_{ij} is the distance between nodes i and j determined by the neighborhood relation. σ^2 is an operating parameter, $\epsilon(t) \exp(-\frac{d_{ij}}{\sigma^2})$ is one for $i = j$, namely the BMU, and decreases when the distance becomes large. For flow analysis, the sequence of phase images were transformed into a 2D matrix of size # pixels $\times$ time points and then processed using the SOM toolbox [9]. Critical parameters of the SOM are the number of node $N \times N$, the initial and final neighborhood size (σ_i, σ_f) and the number of iterations ν. Following [10] we set $\nu = 10^3 * N^2$, a linear decrease of $\sigma_i = N$ to $\sigma_f = 0.2 * N$, and a linear decrease of $\epsilon(t)$. The size of the grid was varied from N=2 to N=8.

2.3 Evaluation

To evaluate the influence of the grid size on the segmentation of the vessel within the phase images the quantization error and the topology error derived from the trained maps was calculated. The quantization error depicts the average distance between each data vector and its BMU. The topology error describes the proportion of all data vectors for which first and second BMUs are not adjacent units. Furthermore, to evaluate the clustering, our approach has been compared to the k-means segmentation presented in [6] and to available manual delineated vessel lumen. Here, the correlation between the velocity profiles derived by the different methods was investigated.

3 Results

Twenty data sets (10 subjects) were analyzed by the SOM. Fig. 1 shows the results of varying the number of nodes, i.e. grid size. Whereas the quantization error steadily decreases, the topology error mainly keeps constant for different values of N.

Fig. 2, as an example, depicts the results of the SOM algorithm for one data set. Each node on the grid subsumes a certain amount of pixels with similar velocity time profiles (VTP). The prototypes are given in Fig. 2c. Similar colors represent close nodes, i.e. possible super cluster structures (Fig. 2 a, b). Here, the yellow color node represents the vessel lumen (white round region in Fig. 2 d). From the analysis, four clusters could be identified (yellow, red, blue, and green). Figure 3 depicts the comparison of the derived VTP from the segmentations of the same data set depicted in Fig. 2. The k-means has been initialized by four classes. The manual delineation however could only provide two classes. The correlation between the VTP of the clusters representing the vessel lumen by each method is high (r=0.99).

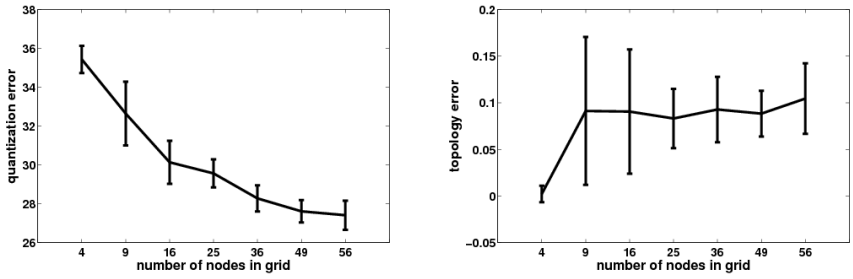


Fig. 1. Quantization and topology error for all subjects for the given range of grid sizes. Error bars depict the standard deviations within the 20 data sets.

4 Discussion

In this contribution an approach to segment and analyze 2D PC-MRI examinations using SOMs was presented. The SOM method could automatically segment the vessel from the images. From Fig. 1 a grid size of $N = 2-5$ seems reasonable. For a lower N the topology of the underlying feature space is more preserved, however, the quantization error is higher since also feature vectors that are more far away from the BMU are subsumed. For larger N the topology error increases because data samples with lower similarity are assigned to different (probably nearby) nodes. Thus, the quantization error is reduced while the topology error increases. However, for higher N, the beneficial property of the SOM to form super clusters could be exploited. By visualizing the similarities within nodes on the grid (here via color coding) the relation between sub and super cluster could be assessed (Fig. 2). Such merging could also be automatized, e.g. by applying hierarchical clustering of the SOM. In contrast to other proposed techniques like k-means [6] or to Alperin's work [5], no operator given initialization is needed. Comparing the velocity profiles derived from SOM, k-means, and manual delineation a high correlation is yielded suggesting a valid segmentation. In summary, by using SOM as a tool to analyze PC-MRI flow and velocity data a flexible and automated approach is available.

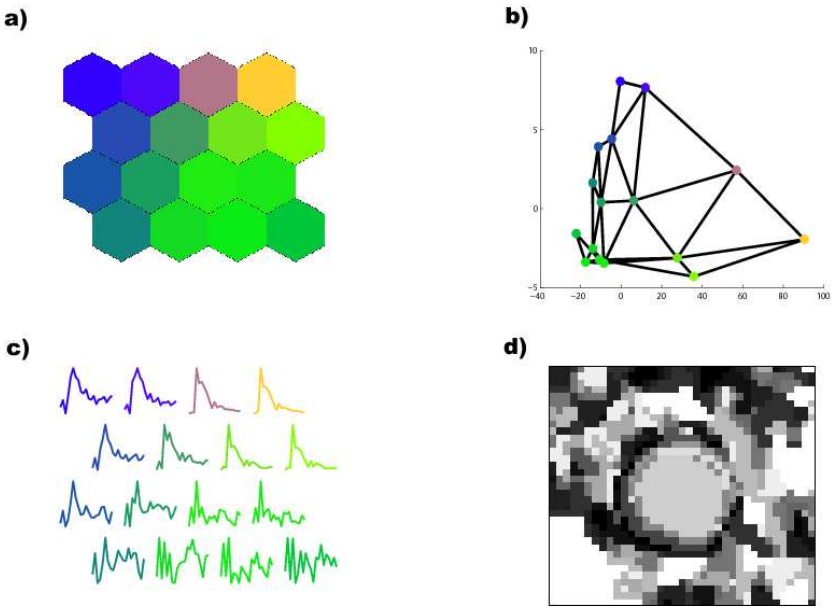
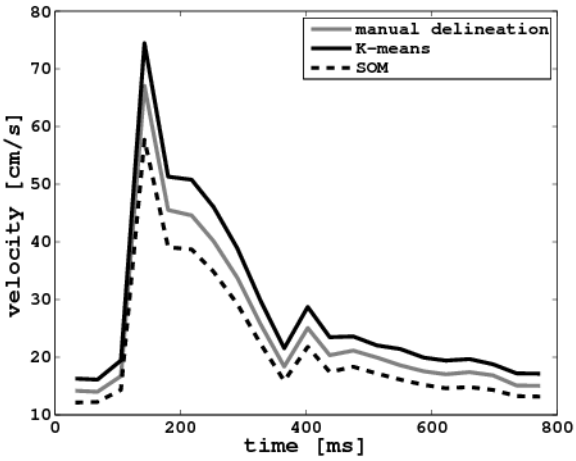


Fig. 2. Results of SOM analysis. Here a 4×4 hexagonal lattice has been used. a) depicts the similarity between neighboring nodes, b) shows a 2D projection of the prototypes onto the grid, c) prototypes associated by the nodes, and d) labeled image according to the best matching node. In a)- c) colors are corresponding.

Fig. 3. Comparison of velocity profiles by different methods for one data set. Solid black curve: derived by k-means clustering, gray curve: derived by manual delineation of vessel lumen, dashed curve: results by SOM algorithm.



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