# Semi-Automated Lymph Node Staging Using LN-MRI

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Abstract

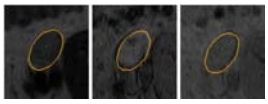
MR nodal staging with lymphotropic magnetic nanoparticles (LN-MRI) has the potential to provide highly accurate non-invasive cancer staging [2]. Images are currently assessed "visually" or by manually outlining node borders, which is a laborious and impractical approach given the multitude of lymph nodes. We have therefore developed automated image analysis tools including 1) identification, 2) segmentation, 3) calculation of tissue parameters (T2*, variance) and 3D display of results (color-coded tissue parameters superimposed on angiographic MIP).

Introduction

The automated analysis of the lymph node staging described here follows through 2 steps. First the segmentation takes place, which identifies the voxels which belong to the region covered by the lymph node; in this phase several features are extracted related to the lymph nodes which describe its magnetic, spatial and geometric properties. These data are subsequently used for an automated classification, based on a probabilistic model. The result is a probability assigned to each lymph node for being malignant. Figure 1 depicts the properties of the lymph nodes in a prostate MR scan 24 hours after the supermagnetic nano-particles have been administered to the patient.

Theory and Methods

Segmentation: We developed an algorithm that couples the information from given MR sequences. This is done through a simultaneous evolution of a contour as well as parameters of registrations onto multiple image domains using differential equations. The shape model we choose to represent lymph nodes is a simple parametric form, which is an ellipse. The algorithm extends 2D segmentations to 3D in an automatic fashion by carrying a converged contour onto next slice and using appearance and geometry constraints. Thus, a 3D representation of a lymph node is obtained by reconstructing a surface from the final set of 2D ellipses. Both region-based and edge-based descriptions from the input image volumes are utilized in the evolution of the contours, and the segmentation masks of the lymph nodes on all input volumes are provided as the output of the segmentation algorithm, as depicted in Figure 2.


(2.a)

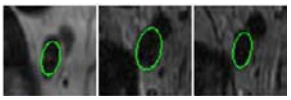

(2.b)

Figure 2: MR Sequence of a Lymph Node region in a prostate. Left: T2, Middle: T2* Gradient Echo1, Right: T2* Gradient Echo2; The shape of the lymph node is estimated by ellipses. (a) Malignancy shows up by the lightened intensity (b) Benign-ness shows up by the darkened intensity inside the node.

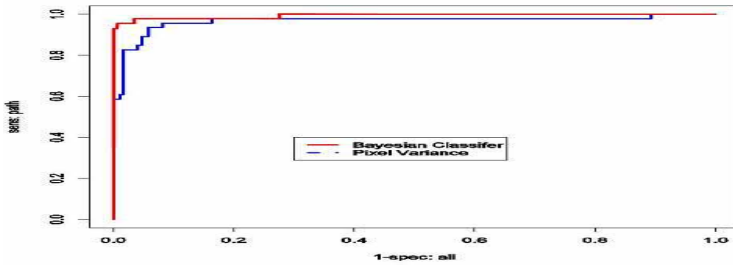
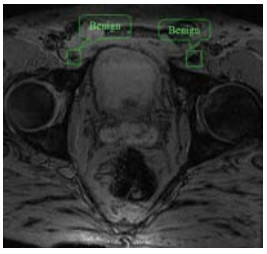



Figure 3: Receiver operating characteristic of the Bayesian Classifier using all features compared to a linear classifier using only one feature (pixel variance). The combination of several features results in a significantly more robust decision model.


Figure 4: Graph of a Bayesian Network Model; arrows symbolize a dependency (the decision is based on 4 features, SNR, ΔSNR, pixel variance and ΔT2*, [2])


(a)

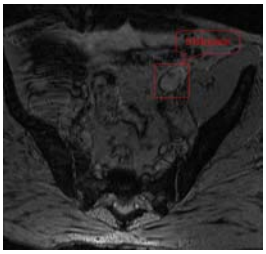

(b)

Figure 1: MR T2* Gradient Echo of Lymph Nodes in a prostate study: (a) Benign-ness shows up by a decreased and homogeneous signal intensity, (b) Malignancy shows up by an increased signal intensity.

Classification: The extracted features in the segmentation are subsequently used to classify the lymph node as malignant versus benign. This process utilizes features like ΔT2*, ΔSNR, SNR, and the pixel variance. Each feature is then preprocessed with an entropy-based discretizer[4] and binned in either two or three segments, depending on the distribution of each feature. We combine these features by using an advanced Bayesian network classifier[3], which generates a graph model describing dependencies between the features on the one hand and the pathological status of the lymph node on the other. As a criterion for constructing the network, we evaluate the conditional mutual information among the features and the pathological class. The network also reveals underlying patterns not visible to a human reader visualized as a graph (Figure 4). Based on this probabilistic model we can support a reader's decision by classifying each lymph node and also assigning a probability to the decision.

Results and Discussion

The classification algorithms were evaluated on data extracted in studies related to Ref. [1]. On a data set of 216 nodes we found the classification method to achieve a sensitivity of 95.7% at a specificity of 99.4%, the ROC curve is given in Fig. 3. We are aiming to increase the performance of the method by introducing additional information of the patient into the decision model and to apply it also to related classification problems in the area of MR imaging.

References

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