Gaussian mixture model based analysis of apparent diffusion coefficient maps for differentiation between malignant and benign brain tumours – preliminary results.

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Abstract

Introduction: Diffusion weighted imaging (DWI) is a nuclear magnetic resonance method that allows to observe effective movement of water molecules in inter- and extracellular space. In pure water molecular movement depends on temperature only while in human organism it is affected by biochemical properties of tissue, such as the cell shape, size, composition and density as well as on the properties of cell membranes and macromolecules content. DWIs collected for at least two different values of diffusion coefficient allow for quantitative measurement of the degree of mobility of water molecules. In clinical practice it is determined by the apparent diffusion coefficient (ADC) and is used in the cancer diagnosis at several stages: for the detection and diagnosis of neoplastic infiltration, determination of cancer stage, assessment of treatment response and its efficiency and to detect tumor recurrence.

Aim: The aim of the paper is to develop the novel Gaussian mixture model (GMM) based methodology for the analysis of apparent diffusion coefficient's distribution in tumor and healthy tissue.

Material and methods: Normalized DWIs obtained for 14 patient diagnosed with malignant glioblastoma multiforme (GBM) and 14 patients with benign low grade astrocytoma (AWHO) were used in pilot study. For all DWI images, apparent diffusion coefficient was calculated and its distributions in tumor tissue and healthy brain tissue for every patient were modeled as an individual GMMs. Expectation Maximization (EM) algorithm put together with Bayesian Information Criterion (BIC) allowed for the estimation of the component number and their parameters: mean values, standard deviations and weighting coefficients. The next step involved standard clusterization techniques, such as k-means or hierarchical clustering with correlation distance measure, to group obtained set of Gaussian components. The criterion proposed by Ray et al. was used to estimate the number of clusters in k-means algorithm.

Results: Exemplary GMM decompositions with corresponding transition to ADC map are presented on Figure 1. Normalized parameters of GMM components were then clusterized with the use of unsupervised techniques. Results, by means of number of obtained clusters and their members, were comparable. The distribution of clusters obtained with the use of k-means algorithm in the domain of normalized component parameters presents Fig. 2. The detailed information on classification results are presented in Table 1.

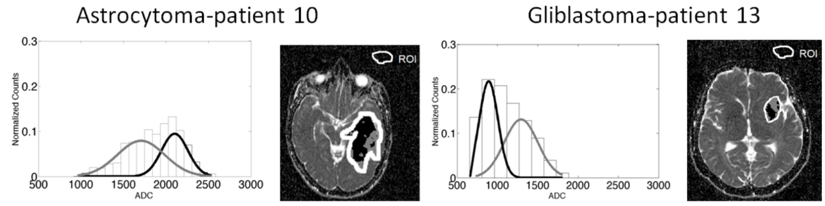

Fig. 1. Exemplary GMM modeled histograms, obtained for GBM and AWHO (left hand side) and corresponding their color-coded ADC maps (right hand side).

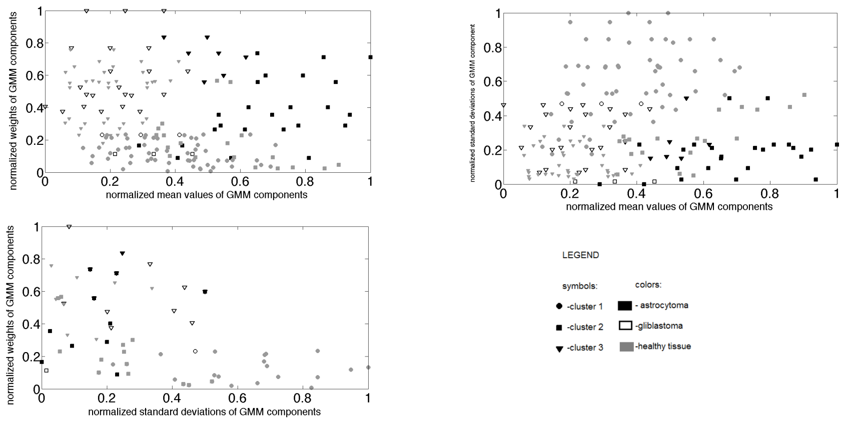

Fig. 2. Result of clusterization with the use of k-means method.

Tissue/ Cluster	Astrocytoma (observed counts)	Astrocytoma [%]	GBM (observed counts)	GBM [%]	Healthy (observed counts)	Healthy [%]
1	0	0	3	5	56	95
2	24	52	3	6,5	19	41,5
3	7	10,6	22	33	37	56,4

Table 1. Results of GMM components' clusterization.

Discussion: Observed changes in water diffusion mainly result from changes in the extracellular volume. In malignant tumors, as a result of increased density of the cellular structure, disorganization of the tissue, and increasing irregularity of the extracellular space, there are limitations of the water molecules mobility. That leads to diffusion limitations, and thus the tissue is characterized by high signal intensity in DWI images and low ADC values. Lack of diffusion limitation is taken as a feature of benign and most often benign DWI images are isointensive in comparison to the proper organ, and ADC maps are of high value.

Conclusion: The proposed data-driven technique of estimating, based on Gaussian mixture modeling, the ADC threshold levels for distinguishing among healthy tissue and AWHO tumors gives promising results. It was noticed that for distinguishing GBM it is required to operate in different space of features that would be specified in future research.

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