Support Vector Machines in DSC-based Glioma Imaging – Suggestions for Optimal Characterization

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Purpose: To assess the diagnostic accuracy of different kernel functions in predictive glioma grading by support vector machines (SVM) using dynamic susceptibility contrast MR imaging (DSC-MRI).

Background: DSC-MRI is a method of choice to differentiate high grade gliomas (HGGs, WHO grade III-IV) from low grade gliomas (LGGs, WHO grade I-II). However, using the conventional "hot-spot" approach , a threshold has to be selected and those reported in literature show large variations[1]. Recently, SVM have been introduced as means to prospectively characterize gliomas [2]. Therefore, the choice of kernel function, a key concept of SVMs, influences prediction outcome and inappropriate kernels might result in poor performance [3]. Furthermore, in contrast to previously published work, the current method is fully-automatic using automatically segmented tumor volumes from DSC-MRI [4].

Materials and Methods

101 previously untreated patients (aged 8-79 yrs, mean age 51; 51 males, 50 females) received a histological diagnosis of primary glioma after MR perfusion imaging and subsequent surgery. DSC-MRI was performed at 1.5 Tesla using a single-shot Gadolinium-based GRE-EPI sequence with TR/TE=1430/46 ms, 12 axial slices, voxel size 1.80x1.80x5 mm^3. For each slice, 50-70 images were recorded at intervals equal to the repetition time. Based on conventional MR images (T2-w, pre/post T1-w and FLAIR), binary glioma region-of-interests (ROIs) where derived from each MR tumor image slice automatic Fuzzy c-means clustering [4]. For each patient, a histogram signature (cf. Fig. 1) was derived from all normalized rCBV values in the glioma ROI [5]. From this, a feature vector was created including the histogram signatures of all patients. In addition, the corresponding patient ages were added to the feature vector, as high age is shown to correlate strongly with lower overall survival in glioma patients [6].

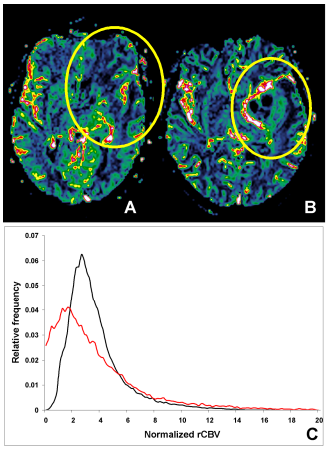

***Fig. 1**: Normalized rCBV maps of the low-grade patient (A) and high-grade patient (B). (C), the histogram signature of the low-grade glioma patient (black line) conveys a more homogenous distribution of normalized rCBV values compared the high-grade glioma patient (red line). Yellow circles depict tumor regions.*

Radial Basis function kernel	$K(x_i, x_y) = e^{-\gamma\|x_i - x_j\|^2}$
Polynomial kernel	$K(x_i, x_y) = \langle x_i, x_j \rangle^d$
Sigmoid kernel	$K(x_i, x_y) = \tanh(\kappa\langle x_i, x_j \rangle + \vartheta)$
Linear kernel	$K(x_i, x_y) = \langle x_i, x_j \rangle$

***Table 1:** Different SVM kernel functions (K) utilized.*

There are currently no techniques available to "learn" the form of the kernel [3]; as a consequence, common known kernel function as in Table 1 are usually applied.
Optimal parameterization of ν,γ, κ, ϑ, and d was performed by grid search calculating maximal area-under-curve (AUC). As the class distribution between high- (63 samples) and low-grade glioma (38 samples) was not equal, the training and test sets were rebalanced by down sampling the larger class. Rebalancing was performed by randomly selecting 38 data sets of 63 HGG samples available to even the class distribution. Of the obtained 76 samples, 70% the formed the training and 30% the test set.

Results

Prediction of glioma grade from the 101 patients employing the 4 kernel functions yielded no good classification accuracy (LGGs <= 60% correct predictions). Rebalancing the training data, however, improved the classification accuracy significantly. Table 2 depicts these classification results. Optimal parameters for the Lin-SVM were ν=0.53, for RBF-SVM ν=0.34, γ = 0.02, for Poly-SVM d=1, ν=0.53, and for Sig-SVM κ=0.01, ϑ=-1.5, υ=0.69. Maximal AUC values obtained for these parameters ranges from 0.83 (Lin-/ Poly-SVM) to 0.87 (RBF-/ Sig-SVM). Best performance is obtained for the RBF-SVM with TPR=83% and TNR=91% (accuracy of 87%). In comparison, a previous study using unbalanced data reported optimal values of TPR=76% and TNR=82% [2].

Model	Accuracy	TPR	TNR
RBF-SVM	87.0%	83%	91%
Poly-SVM	82.6%	83%	82%
Sig-SVM	82.6%	83%	82%
Lin-SVM	82.6%	83%	82%

***Table 2:** Classification results for different combinations of kernel function and SVM on rebalanced data. Results reflect models determined at optimal parameter settings. TPR depicts the percentage of correctly classify low-grade glioma whereas TNR is the rate of correct high-grade glioma classifications.*

Discussion

Glioma grading by SVMs is feasible and the use of balanced subgroups in the training dataset was found to improve the diagnostic accuracy Furthermore, the choice of kernel function seems not to influence the classification results significantly. However, choosing a RBF kernel function yielded best performance. An attractive feature of the current work is that all features used to describe the classes where derived automatically, including tumor segmentation. This, in combination with the presented SVM classifier, a powerful tool is available to characterize glioma patients pre-surgically.

References

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