A pattern recognition model for automatic classification of ^{1}H MRSI voxels in the prostate

L. Matulewicz[1], K. L. Zakian[1], A. Shukla-Dave[1], J. F. Jansen[1], Y. Mazaheri[1], H. Hricak[1], and J. Koutcher[1]

[1]Department of Medical Physics, Memorial Sloan-Kettering Cancer Center, New York, NY, United States

Introduction

Since visual inspection of large ^{1}H-MRSI (magnetic resonance spectroscopic imaging) datasets of the prostate is time-consuming and requires spectroscopic expertise, introduction of a decision support system based on a pattern recognition (PR) model could help to promote the clinical use of MRSI. A PR approach does not require specific prior knowledge and can extract important spectral patterns from the in vivo training data automatically. It uses the complete information contained in the raw spectral data to address a diagnostic question – malignant vs. benign – directly. In this work, we have applied a Partial Least Squares (PLS) algorithm with Orthogonal Signal Correction (OSC) filtering which encompasses linear regression methods that have been employed successfully for prediction modelling in biological and biochemical applications [1].

Aim of the study

To build a model for automated pattern recognition of ^{1}H MRSI data indicating tumor-suspicious voxels in the prostate to assist clinicians in cancer diagnosis.

Materials and methods

10 men (median age, 63 years; range, 43-68 years) who underwent 1.5-T endorectal MR imaging before radical prostatectomy and who fulfilled all inclusion criteria of no prior hormonal or radiation treatment and at least one tumor lesion at whole–mount pathologic examination were included. MRI and 3D ^{1}H MRSI examinations were performed on a 1.5-T whole-body unit (Signa Horizon; GE Medical Systems) with an endorectal coil (Medrad) and an acquisition package (PROSE; GE Medical Systems). The spectroscopic acquisition parameters were as follows: PRESS voxel excitation, 1000/130 ms [TR/TE]; numbers of averages acquired, one; spectral width, 1250 Hz; number of points, 512; field of view, 11 x 5.5 x 5.5 cm^3; and 16 x 8 x 8 phase encoding steps. Spectral data were processed by using free software 3DiCSI v1.9.11 (http://mrs.cpmc.columbia.edu/3dicsi.html). The MRSI data were spatial zero filled to a 16 x 8 x 16 matrix and zero filled in the spectral dimension to 1024 points. The time-spectral dimension was apodized with a 4-Hz Gaussian function. The spectra were aligned and referenced to the water peak at 4.7 ppm. The range 3.6 - 0.6 ppm (198 points) was chosen. Magnitude spectra were exported to achieve better and reproducible results with the PR method [2, 3] as well as to fully automate and simplify preprocessing. All 2362 voxels within the prostate were labeled as healthy or tumor by an experienced spectroscopist according to established decision rules based on the resonances of total choline (Cho) at 3.2 ppm, creatine/phosphocreatine (Cr) at 3.0 ppm, polyamines (PA) at 3.1 ppm and citrate (Cit) at 2.6 ppm [4]. For all voxels visually marked as tumor, the correct lesion location was confirmed on the basis of histopathology maps with sextant precision. The labels healthy or tumor in the form of "0" or "1" in the Y prediction matrix were used to establish PR models by applying supervised multivariate statistical methods (OSC filtering and PLS analysis) on training sets. Using the "leave-one-patient-out" method, the generated models were applied to predict new data in an unknown test set and to evaluate classification accuracy. Prior to prediction, new samples in the test set were automatically pre-treated in the same way as the training set (scaling, centering, OSC filtering). Multivariate analysis was performed using SIMCA-P software v.11.5 (Umetrics, Sweden). Three different approaches to variable centering and auto scaling were compared (centered and scaled to Unit Variance (UV); centered but not scaled (Ctr); no centering or scaling (None)). The OSC algorithm was used to remove unwanted variation in the spectra that was irrelevant for the classification. Five orthogonal components were extracted removing over 70% of variation that did not contribute to discrimination. The classification accuracy for the model was computed as the ratio of the number of spectra predicted correctly to the total number of spectra in the test set. YPredPS values were provided by the SIMCA-P software. YPredPS is the Y value predicted by the model based upon the X block variables (resonance intensities at given ppm). A YPredPS value close to 1 would indicate that the object is likely to belong to the class. A YPredPS value close to 0 would indicate that the object is unlikely to belong to the class.

Results

The best results (highest Q2 value) were obtained using no centered or scaled spectra in comparison to UV and Ctr methods. In the computed models after OSC filtering, the first PLS component explained greater than 82.1% of the variation in the spectra between healthy and tumor voxels (R2Y=0.821). The overall predictive power of the training set calculated by cross-validation was greater than 80.4% (Q2 = 0.804). Using the models generated by the training set, the spectra in the test set were correctly predicted greater than 81% of the time. It must be noted that the results are strongly dependent on the choice of training datasets and peak position variation. Variables (ppm locations) with Variable Importance in the Projection values (VIP) larger than 1 are the most relevant for explaining differences between classes of spectra. Figure 1 contains a plot of the VIP values generated from the training set. The most important variable in differentiating tumor and healthy voxels was Cho. Cr, PA and Cit also had VIP values greater than one and thus were important for differentiating cancer voxels. Figure 2 contains an example of a spectrum from the test set which was classified correctly as tumor by the model.

Discussion and conclusions

The impact of data preprocessing is very important in carrying out this pattern recognition model. MRSI spectra have different ranges of intensities both within a given patient data set and between patients. Therefore, the interpretation can be distorted because these changes are not really responsible for the discrimination between the different classes. Auto-scalling (mean-centering and unit-variance scalling) has the limitation of giving the same weight to all the spectral variables because of their now equal variance. Our study showed that the best results were obtained by not applying scaled or centered spectra. One of the main sources of error in the computed models was applying an alignment method based on water peak referencing. The robustness of the algorithm is strongly dependent on peak alignment; and, since the water peak is partially suppressed, the true center frequency of the peak may not be accurately reflected. Another disadvantage is operating on magnitude spectra which have the advantage of invariance with regard to zero-order phase, but have increased linewidths. Magnitude spectra have been shown previously to yield better performance by pattern recognition methods including PLS [2]. The modelling results presented here are still in development. However, we have shown that the multivariate PLS method with OSC works well with the tested data sets and could help to automatically distinguish the tumor-suspicious voxels. The main advantage of this method is the much shorter time of analysis compared to visual inspection and the possibility of broad implementation in cancer centers not employing experienced spectroscopists. In terms of accuracy, the proposed method is still not comparable to the reference method (a visual inspection by an experienced spectroscopist). Ongoing improvements in preprocessing and refining the model as well as importing more datasets should result in better performance.

References: 1. Trygg and Wold 16 (3): 119. (2002); 2. Kelm et al. 57(1): 150. (2007); 3. Devos et al. 170 (1): 164. (2004); 4. Shukla-Dave et al. 245 (2): 499. (2007)

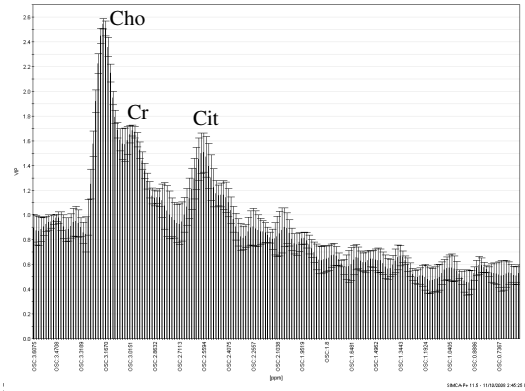

Figure 1. Variable Importance Plot (VIP) values reflect the importance of variables (ppms) in the model differentiating tumor spectra

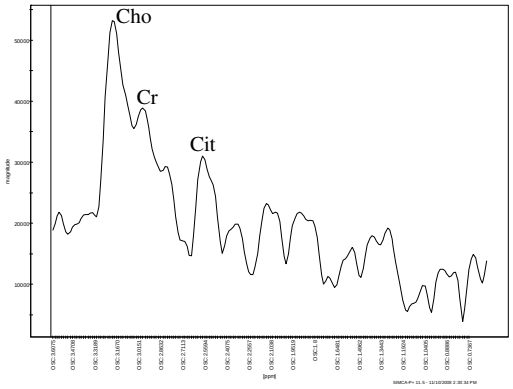

Figure 2. Example of a magnitude spectrum classified by the model as tumorous with high YpredPS value