

Fast Nosological Imaging of 2DTSI Brain Data Using Canonical Correlation Analysis

T. Laudadio¹, M. Martinez-Bisbal², B. Celda², and S. Van Huffel³

¹Istituto di Studi sui Sistemi Intelligenti per l'Automazione, Consiglio Nazionale delle Ricerche, Bari, Italy, ²Departamento Química Física, Universitat de Valencia, Valencia, Spain, ³Departement Elektrotechniek (ESAT-SCD), Katholieke Universiteit Leuven, Leuven, Belgium

Introduction Recently, a new fast and accurate tissue typing technique has been successfully applied to prostate MRSI data [1]. This technique is based on Canonical Correlation Analysis (CCA), a statistical method able to simultaneously exploit the spectral and spatial information characterizing the CSI data. Here, the performance of CCA is further investigated by using two-dimensional Turbo Spectroscopic Imaging (2DTSI) brain data measured in patients affected by glioblastoma tumor. The purpose of this study is twofold: to carry out a validation study on CCA when applied to heterogeneous tumors, and to expand the clinical application of 2DTSI, characterized by short acquisition times compared to those of standard CSI, by combining it with the fast and reliable CCA classification method. Furthermore, the performance of CCA is compared to that of ordinary correlation analysis on simulated as well as in vivo data. The results show that CCA outperforms ordinary correlation analysis in terms of robustness and accuracy, especially when data are characterized by a low Signal to Noise Ratio (SNR).

Method CCA represents the multivariate variant of ordinary correlation analysis (OCA), which quantifies the relationship between two random variables x and y by means of correlation coefficients. Given a CSI image, grid of voxels containing time-domain signals, the aim is to detect those voxels whose spectra correlate best with model tissue spectra, which are defined a priori. If OCA is applied, the x variable is the signal spectrum measured in each voxel, while the y variable is the model tissue spectrum. The correlation coefficient between x and y is computed and, afterwards, assigned to the voxel under investigation. Once each voxel has been processed, a new grid of voxels is obtained and called correlation map. Such maps are exploited in order to produce a single nosologic image [1], in which all the detected tissue types are visualized. The difference between OCA and CCA consists in a different choice of the variables x and y . In CCA, the spatial information characterizing the CSI data set is exploited by considering as variable x a multivariate vector with components representing the spectrum characterizing the considered voxel as well as the spectra contained in the neighbor voxels. The variable y also consists of a multivariate vector. Its components represent the basis functions of a signal subspace, that models the specific tissue spectrum we are looking for and its possible variations. Several spatial and subspace models can be adopted and an exhaustive overview is given in [1]. In particular, OCA can be considered as the single voxel model.

Results and conclusions We applied the proposed technique to simulated as well as in vivo brain 2DTSI data. Fig.1 (left) shows the simulated model spectra for necrosis, necrosis+tumor, tumor, tumor+normal (mixed) and normal tissues. They contain different contributions of Choline (3.2 ppm), Creatine (3.0 ppm), NAA (2.0 ppm), lactate (1.3 ppm) and lipids (0.9 and 1.3 ppm). We perturbed the model spectra by adding white Gaussian noise and inserted them in five different regions of a 16x16 grid of voxels. In order to compare the performance of CCA when applying different spatial models, 400 simulation runs were performed for different noise levels. Then, for each simulation run, the correlation coefficients between the original and the detected tissue regions were estimated. Our studies show that the best performance is obtained by CCA while OCA is the least accurate, especially for high noise levels, as it does not exploit any spatial information. Fig.1 (right) shows the detection results obtained for a low SNR. Concerning the in vivo studies, five 2DTSI data sets were measured in patients affected by glioblastoma by a 1.5 T Philips Gyroscan Intera NT (Philips Medical Systems, The Netherlands, TR=5154 ms, TE=13 and 115 ms) using a 90°-180°-180° pulse sequence. The images, grids of 24x24 voxels with FOV=230x230 mm, were processed by applying CCA and OCA after water and lipid removal. Fig. 2 (left) shows the area of interest of one image and the corresponding spectral map. Some spectra are also pointed out as characteristic of some tissue types. Fig. 2 also shows the nosologic images and all the correlation maps corresponding to the different tissue types obtained by applying CCA (middle) and OCA (right). Based on spectroscopy, CCA is able to well describe the different tissue types characterizing the lesion in only 0.63 s. On the contrary, OCA fails in the detection of some tissue types such as edema and normal tissues. In general, our studies show that the proposed technique is accurate, robust and fast and, therefore, might be introduced into routine clinical use in order to help clinicians and radiologists in cancer diagnosis.

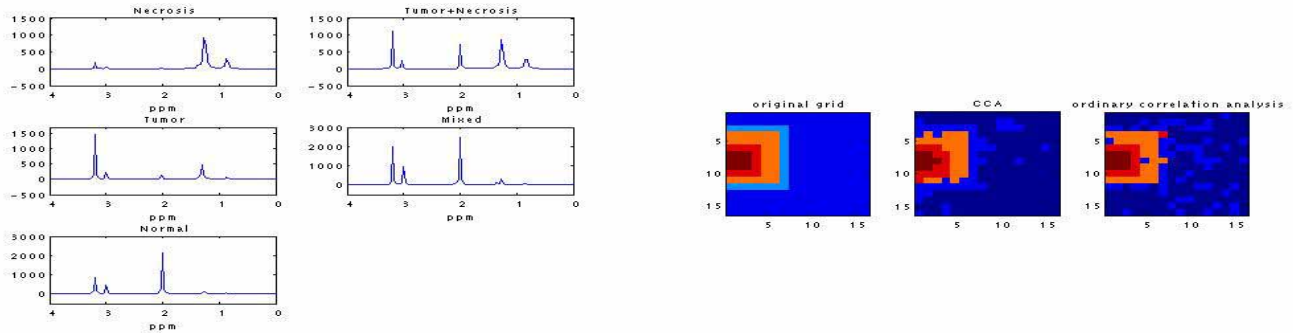


Fig. 1 Left: noiseless simulated model spectra. Right: detection results obtained by CCA and OCA (noise standard deviation=200). Brown: necrosis tissue; red: necrosis+tumor tissue; orange: tumor tissue; light blue: mixed tissue; dark blue: normal tissue.

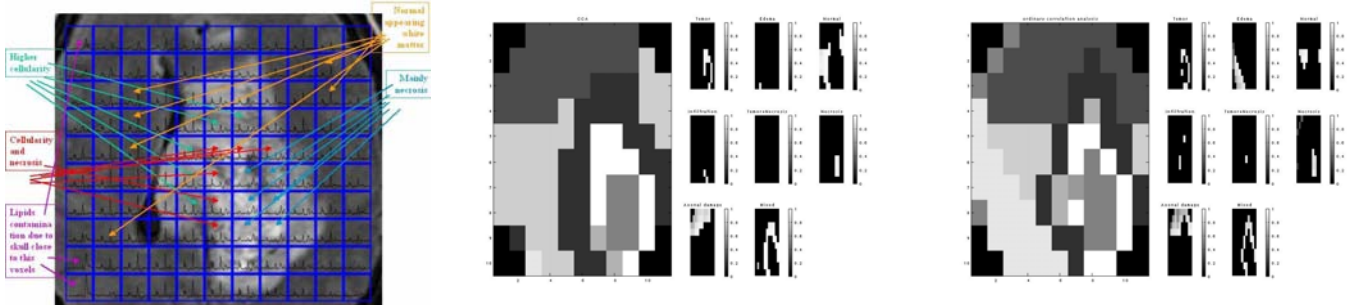


Fig 2 Area of interest and corresponding spectral map (left). Nosologic images and correlation maps obtained by CCA (middle) and OCA (right).
References [1] Laudadio T, Pels P, De Lathauwer L, Van Hecke P, Van Huffel S. Tissue segmentation and classification of MRSI data using Canonical Correlation Analysis, Magn. Reson. Med. Vol. 54, 1519-1529, 2005.