Non-negative matrix factorization for differentiation of brain metastasis and glioblastoma multiforme, and visualization of tumor infiltration

J. Luts¹, T. Laudadio^{1,2}, M. Martinez-Bisbal^{3,4}, S. Van Cauter¹, E. Molla⁵, J. Piquer⁵, J. Suykens¹, U. Himmelreich¹, B. Celda^{3,4}, and S. Van Huffel¹

¹Katholieke Universiteit Leuven, Leuven, Belgium, ²Istituto Applicazioni Calcolo, CNR, Bari, Italy, ³University of Valencia, Valencia, Spain, ⁴Networking Research Center on Bioengineering, Biomaterials and Nanomedicine (CIBER-BBN), Valencia, Spain, ⁵Hospital de La Ribera, Valencia, Spain

Introduction – This study focuses on the differentiation between solitary brain metastasis and glioblastoma multiforme based on conventional magnetic resonance imaging (MRI) and two-dimensional turbo spectroscopic imaging (2D-TSI) data. The infiltrative nature of glioblastoma multiforme has been further investigated by using non-negative matrix factorization (NNMF) [1,2].

Materials and methods – Fifteen patients with a brain tumor, nine affected by glioblastoma multiforme and six by metastasis, were considered in this study. The data were acquired with 1.5 T Philips magnets (Philips Medical Systems, The Netherlands) at the Radiology Service of Clínica Quirón, and the Hospital La Ribera, Alzira, Valencia (Spain), as a part of the routine clinical preoperative MRI and spectroscopy protocol for the brain and using eTUMOUR FP6 project protocols [3]. High-resolution MRI (T1-weighted (preand post-gadolinium injection) and T2-weighted images) data were acquired prior to the 2D-TSI study (24x24, TE = 272 ms, TR = 2000 ms, FOV = 230x230 mm, slice thickness = 20 mm, 256 points). Each volume unit dimension was 9.6x9.6x20 mm (1.8 ml). Data processing included zero filling to 512 points, water removal by using HLSVD-PRO, Fourier transformation, peak integration of NAA, Cr and Cho. For each patient 2D-TSI voxels were assigned to three groups by radiologists: non-T2 hyperintense/non-enhancing, perienhancing and enhancing tumor. Furthermore, two constituent vectors of length 3 were extracted from each patient's 2D-TSI data using NNMF. These constituents correspond to a normal component and a tumor component, respectively.

Results and conclusion – Figure 1 shows a scatter plot (Cho/Cr versus Cho/NAA) of the difference of the patients' averaged ratio in the enhancing tumor and the non-T2 hyperintense/non-enhancing area. Glioblastomas and metastases form two separated clusters, the latter having smaller ratio values. Figure 2 provides a scatter plot of the result of automated processing with NNMF. The horizontal axis corresponds to the difference between the ratio element3/element2 of the tumor component and the normal component. Similarly, the vertical axis depicts this difference measure for element3/element1. The NNMF approach results in a clear separation of glioblastomas

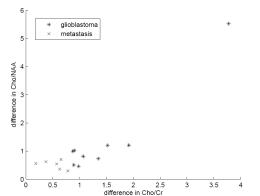


Figure 1. Scatter plot of the difference between the averaged Cho/Cr and Cho/NAA ratio from the enhancing tumor and the non-enhancing/non-T2 hyperintense area for each patient. Metastases and glioblastomas form two separated clusters.

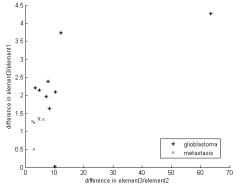


Figure 2. Scatter plot of the difference between the ratios element3/element2 and element3/element1 from the first constituent vector and the second constituent vector for each patient. Metastases and glioblastomas are separated.

and metastases. Figures 3 and 4 visualize the abundances of the normal component that is obtained with NNMF for two cases with glioblastoma multiforme. These abundances indicate tumor infiltration. In conclusion, the use of enables 2D-TSI to visualize metabolic differences between glioblastomas and metastases. Automated processing with NNMF allows differentiation of these tumors and enables to visualize tumor infiltration.

References – [1] M. Law et al., Neuroradiology 222 (2002), pp. 715-721; [2] Y. Su et al., NMR Biomed 21 (2000), pp.1030-1042; [3] FP6-2002-LSCH-503094 www.etumour.net.

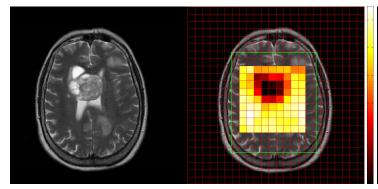


Figure 3. Left: T2-weighted MR image of a patient with glioblastoma multiforme. Right: NNMF abundances for the normal constituent vector [0.651 0.194 0.156]. White reflects high abundances and black corresponds to low abundances. The abundances visualize tumor infiltration.

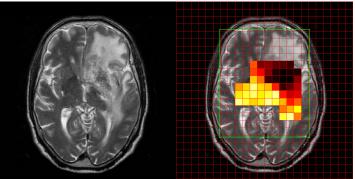


Figure 4. Left: T2-weighted MR image of a patient with glioblastoma multiforme. Right: NNMF abundances for the normal constituent vector [0.789 0.082 0.129]. White reflects high abundances and black corresponds to low abundances. The abundances visualize tumor infiltration in adjacent tissue in the contralateral hemisphere.