1-D MATHEMATICAL MORPHOLOGY FOR WATER REMOVAL IN ^{1}H MR SPECTROSCOPY TOOL

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Abstract: This work shows the basics and performance of a new morphological signal method for 1-D water signal removal included in a simple and interactive multivoxel spectroscopy tool to help surgeons detect brain cancer. It consists of mathematical morphology usually applied in 2D images to filter 1D spectroscopic signals. 1D water signal reconstruction from the original data is performed in frequency domain through the use of an elementary operation: geodesic dilation. Then, the water signal is subtracted from the original signals due to the large amount of water which exists in the brain compared to the rest of molecules, making possible quantitation procces. The goal of this paper is to present this new morphological method commonly used in 2D domain for 1D water removal, spreading its use to several processing methods as quantitation.

1 INTRODUCTION

Many spectroscopic algorithms have been developed to solve the problem of quantifying signals in ^{1}H MRS data in the last 20 years, being them included in the most popular software tools, such as the jMRUI software package (Stefan, Di Cesare, Andrasescu, Popa, Lazariev, Vescovo, Strbak, Williams, Starcuk, Cabanas, Van Ormondt and Graveron-Demilly, 2009) and the AQSES software (Simonetti, Poullet, Sima, De Neuter, Vanhamme, Lemmerling and Van Huffel, 2006). One of the most important algorithms in ^{1}H MRS is the water suppression from original signals, in order to eliminate the large amount of water which exists in the brain compared to the rest of molecules. The so-called blackbox methods based on singular value decomposition (SVD) such as HSVD (De Beer and Van Ormondt, 1992), HLSVD (Pijnappel, Van den Boogaart, De Beer and Van Ormondt, 1992) and HTLS (Van Huffel, Chen, Decanniere and Van Hecke, 1994), have been successful in reconstructing the signal as a sum of Lorentzians, but the influence that the users have when the estimated parameters are chosen could reduce the quality of the signal fitting. Another important method is the maximum-phase Finite Impulse Response (MP-FIR) which has been shown to be one of the most accurate and efficient technique for quantifying MRS spectra (Sundin, Vanhamme, Van Hecke, Dologlou, and Van Huffel, 1999). In addition, MP-FIR allows the inclusion of prior knowledge that may be taken into account during quantitation; however the drawback of these filters is that they are linear phase filters which generate distortion due to the fact that the signals are composed of exponentially damped sinusoids and not pure sinusoids, and this distortion cannot be totally neglected. Other techniques as Wavelets (Günther, Ludwig, and Rüterjans, 2002) or Gabor transforms (Coron, Vanhamme, Antoine, Hecke, and Van Huffel, 2001) have also used for water removal but with lower accuracy than the other ones. These methods are compared in a filtering review to solve suppression in MRS (Coron et al., 2001): the MP-FIR method was the most accurate and efficient technique. The water suppression method presented in this paper belongs to a general process where the main steps included in most of spectroscopy software tools are illustrated in Figure 1:

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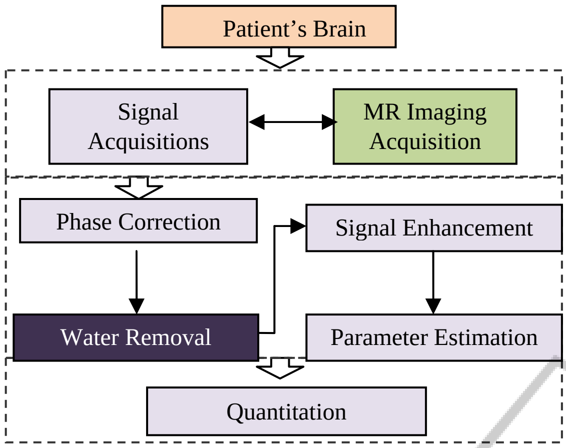

Figure 1: Block diagram for [1]H MR spectroscopy analysis.

In this work we are focusing on the dominant signals removal, specifically in the water suppression algorithm. This method is included in a software tool (See Figure 2) which also incorporates the main algorithms to process data, performs the registration between spectroscopic data and MR images, and generates the metabolite maps. In short, the aim of this paper is to provide researchers with a new morphological method for water suppression, introducing it for a future use in quantitation metabolite signals.

This paper is set up as follows: section 2 reminds some basics of morphology and the main characteristics of mathematical algorithms: dilation, erosion, opening and closing. In section 3, the water removal algorithm based on mathematical operations is shown. Section 4 explains the experiments and finally, a brief conclusion is given in section 5 together with the future work.

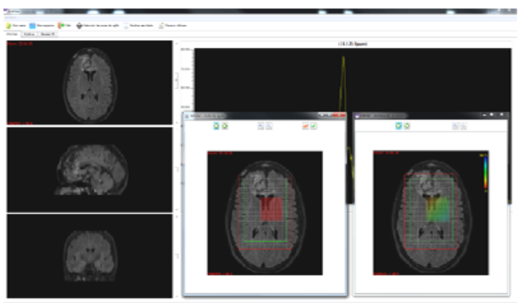

Figure 2: Main window of the [1]H MR Spectroscopy tool.

2 MATHEMATICAL MORPHOLOGY

Mathematical morphology is a non-linear image/signal processing methodology based on minimum and maximum operations (Serra, 1982), in order to extract relevant components of an image/signal respectively. In the last years, this technique has been commonly used in 2D images, but its use for 1D signal processing is also possible.

Let f be a signal which is defined as:

$$f(\boldsymbol{t_n}): E \rightarrow T \tag{1}$$

where $\boldsymbol{t_n} \in B$ is the time sample. In the case of discrete valued signals, $T = \{t_{min}, t_{min}+1, \ldots t_{max}\}$ is an ordered set of amplitude-levels.

Furthermore, let $B(t_n)$ be a sub-set of $\mathbb{Z}$ called structuring element (shape probe) centred at point t_n. The size of the structuring element (SE) is usually chosen according to some a priori knowledge about the geometry of the relevant and irrelevant signal components. The two basic morphological operators are:

- Dilation: $[\delta_B(f)](\boldsymbol{t_n}) = max_{b\in B(\boldsymbol{t_n})} f(\boldsymbol{t_n} + \boldsymbol{b})$
- Erosion: $[\varepsilon_B(f)](\boldsymbol{t_n}) = min_{b\in B(\boldsymbol{t_n})} f(\boldsymbol{t_n} + \boldsymbol{b})$

Those elementary operations can be combined to obtain a new set of operators or basic filters given by:

- Opening: $\gamma_B(f) = \delta_B(\varepsilon_B(f))$
- Closing: $\varphi_B(f) = \varepsilon_B(\delta_B(f))$

There are other complex filters derived from the basic operator based on geodesic transformations of a signal f (marker) and a second signal g (reference):

- Geodesic reconstruction: $\delta_g^{(n)}(f) = \delta_g^{(1)}\delta_g^{(n-1)}(f)$ with $\delta_g^{(1)}(f) = \delta_B(f) \wedge g$
- Opening by reconstruction: $R_g(f) = \delta_g^{(i)}(f)$ with $\delta_g^{(i)}(f) = \delta_g^{(i+1)}(f)$.

A combination of these operators can be used if we want to reconstruct the water signal and subtract it from the original signals as it has been introduced in section 1. In next section the basic morphological operation will be illustrated.

3 WATER SIGNAL SUPPRESSION

In order to perform water removal, many algorithms have been proposed since 1990 in the time and frequency domain (Vanhamme, Sundin, Hecke and Huffel, (2001); Poullet, Sima and Huffel, (2008)), but nowadays only some of them are really used in multivoxel spectroscopy imaging. Ideally, the FID signal obtained with the MRS machine is noiseless and results from the addition of K exponentially damped sinusoids which are characterized by frequencies f_k, amplitudes A_k in *arbitrary units (a.u.)*, phases φ_k, damping factors α_k, length of the FID N, i the square root of -1 and Δt the sampling interval, as:

$$X_n = \sum_{k=1}^{K} A_K e^{i\varphi_k} e^{(-\alpha_k+2\pi i f_k)n\Delta t} \qquad n=0,\ldots,N-1. \qquad (2)$$

In order to remove the water signal, the exponentially damped sinusoids whose frequencies appear in the water region are estimated and subtracted from the original FID. For example, Hankel Lanczos Singular Value Decomposition (HLSVD-PRO) algorithm (Laudadio, Mastronardi, Vanhamme, Van Hecke and Van Huffel, 2002), estimates the whole set of model parameters making full use of mathematical model functions, reconstructing the water signal and subtracting it from the original signals.

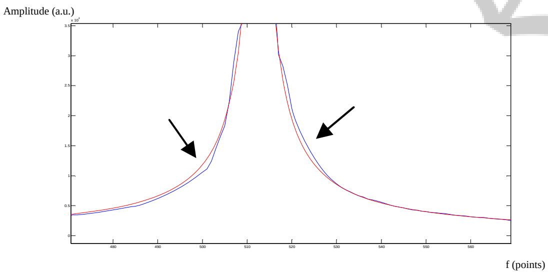

Figure 3: Imperfect reconstruction of water contribution to subtract it from the original signal. In blue and in red the original and the reconstructed signal respectively.

The main problem of this method lies in the accurate reconstruction of the water contribution to subtract it from the original signal (Figure 3); sometimes the water peak is not well reconstructed, other times the base of a signal has imperfections and it is so difficult to fit the parameters. For this reason, the method proposed in this work uses the geodesic reconstruction by means of a delta centred on the maximum value of the original signal as marker, and the original signal as reference signal, allowing us to perform the water reconstruction accurately in frequency domain without affecting other signals. In figures 4, 5, and 6, the full process of water suppression is illustrated.

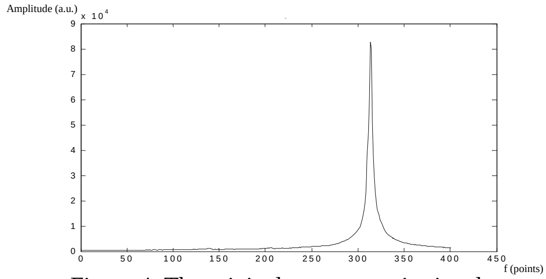

Figure 4: The original spectroscopic signal.

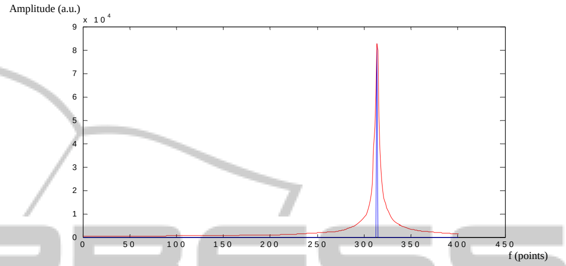

Figure 5: In blue, the delta used as marker. In red, the reconstructed signal after using geodesic reconstruction.

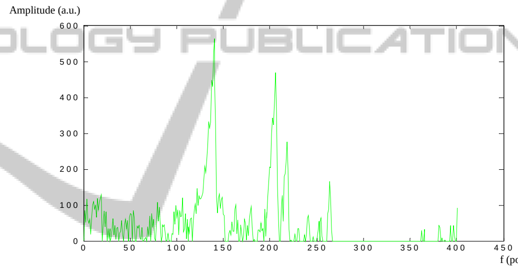

Figure 6: Residue after performing the process.

4 EXPERIMENTS AND RESULTS

As it was told in section 2, the introduction of mathematical morphology for 1D signal processing could help us when we want to suppress water signal or calculate metabolite quantitation. In Figure 7 the original spectroscopic signal in black and the water reconstruction in red using the geodesic reconstruction are observed together. Then, the red signal is subtracted from the original one in time domain, eliminating the large amount of the water.

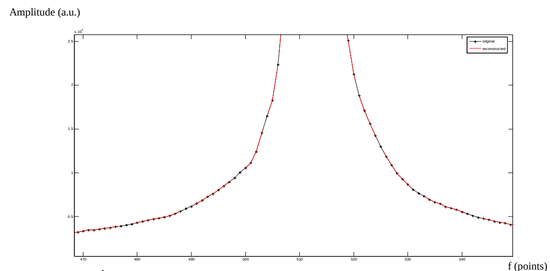

Figure 7: ^{1}H MR original spectroscopy (black) and water reconstruction (red) signals.

Other processing algorithms as phase correction, apodize funtions or SNR improvement can be applied. Figure 8 shows the result after signal filtering, SNR improvement and HLSVD quantitation for several spectroscopic signals.

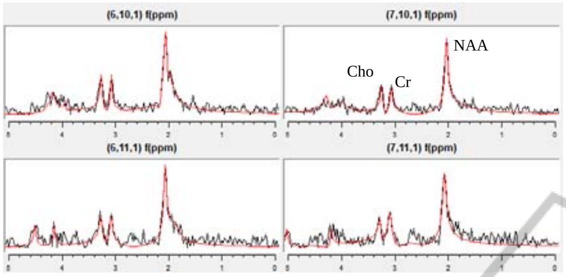

Figure 8: Signal processing for metabolite quantitation.

5 CONCLUSIONS AND FUTURE WORK

In this paper, we have introduced the use of 1D mathematical morphology in a software tool to help surgeons detect brain cancer through the use of the magnetic resonance spectroscopy. This method is appropriate for water removal when the metabolite signals are not overlapped with the water contribution; otherwise, methods as HLSVD are recommended in order to avoid a bad suppression. However, a depth study about the use of morphological methods in overlapped signals must be done since an appropriate family of filters can obtain the desired signal. Coming soon experiments are focused on the comparison of the proposed algorithm with other filtering methods to verify its efficiency and in the study of new quantification methods based on non-linear filters (1D mathematical morphology) for its use in MRS.

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REFERENCES

Coron, A., Vanhamme, L., Antoine, J. P., Hecke, P. V. and Van Huffel, S. (2001). The filtering approach to solvent peak suppression. *Journal of Magnetic Resonance*. 152(1):26-40.

De Beer, R. and Van Ormondt, D. (1992). Analysis of NMR data using time domain fitting procedures. *NMR Basic Principles and Progress.* 26:202-48.

Günther, U. L., Ludwig, C. H., and Rüterjans, H. (2002). *WAVEWAT-improved solvent suppression in NMR spectra employing wavelet transforms. Journal of Magnetic Resonance*. 156(1):19-25.

Laudadio, T., Mastronardi, N., Vanhamme, L., Van Hecke, P. and Van Huffel, S. (2002). Improved Lanczos algorithms for blackbox MRS data quantitation. *Journal of Magnetic Resonance*. 157:292-297.

Pijnappel, W. W. F., Van den Boogaart, A., De Beer, R., and Van Ormondt, D. (1992). SVD-based quantiffication of magnetic resonance signals. *Journal of Magnetic Resonance.* 97(1):122-134.

Poullet, J. B, Sima, D. M., and Van Huffel, S. (2008). MRS signal quantitaion: a review of time- and frewuency-domain methods. *Journal of Magnetic Resonance*. 195(2):134-144.

Serra, J. (1982). Image Analysis and Mathematical Morphology, volume I. Ac. Press, London.

Simonetti, A. W., Poullet, J-B., Sima, D. M., De Neuter, B., Vanhamme, L., Lemmerling, P., and Van Huffel S. (2006). An open source short echo time MR quantitation software solution: AQSES.

Stefan, D., Di Cesare, F., Andrasescu, A., Popa, E., Lazariev, A., Vescovo, E., Strbak, O., Williams, S., Starcuk, Z., Cabanas, M., Van Ormondt, D., and Graveron-Demilly, D. (2009). Quantitation of magnetic resonance spectroscopy signals: the jMRUI software package. *Measurement Science and Technology*, volume 20.

Sundin, T., Vanhamme, L., Van Hecke, P., Dologlou, I., and Van Huffel, S. (1999). Accurate quantification of 1H spectra: From infinite impulse response filter design for solvent suppression to parameter estimation. *Journal of Magnetic Resonance*. 139(2):189-204.

Van Huffel, S., Chen, H., Decanniere, C., and Van Hecke, P. (1994) Algorithm for time-domain NMR data fitting based on total least squares. *Journal of Magnetic Resonance*. 110:228-237.

Vanhamme, L., Sundin, T., Hecke, P. V., and Huffel, S. V. (2001). MR Spectroscopic Quantitation: a Review of Time-Domain Methods. *NMR in Biomedicine*. 14:233-246.