

Elimination of Patient-Motion Artefacts in *In Vivo* MR Spectroscopy

Johannes Slotboom¹, Dirk van Ormondt²

Neuroradiology/DRNN, Inselspital, Bern, CH ¹, Applied Physics, TU Delft, NL ².

Johannes.Slotboom@insel.ch, D.vanOrmondt@tudelft.nl

27th September 2006

Abstract—In order to obtain a clinically acceptable signal-to-noise ratio (SNR), *in vivo* Magnetic Resonance Spectroscopy (MRS) entails addition of M consecutive identical measurements ('signal-averaging'). In practice, M equals *e.g.* 20, yielding an SNR improvement by a factor of $\sqrt{20}$. Typically, the total measurement time is about four minutes. During this time slot, a patient may well move, causing strong perturbation of several of the 20 consecutive measurements. The signal-average is affected by this phenomenon. The present work introduces median filtering as an alternative to signal-averaging, thus strongly reducing effects of patient-motion.

Keywords—MR Spectroscopy, patient motion, median filtering, rank-order filtering

I. INTRODUCTION

In order to obtain a clinically acceptable signal-to-noise ratio (SNR), *in vivo* Magnetic Resonance Spectroscopy (MRS) requires addition of M consecutive identical measurements ('signal-averaging'). In practice, M equals *e.g.* 20, yielding an SNR improvement by a factor of $\sqrt{20}$. Typically, the total measurement time is about four minutes. During this time slot, a patient may well move, causing strong perturbation of several of the 20 consecutive measurements. The signal-average is affected by this phenomenon. The present work introduces median-filtering as an alternative to signal-averaging. This method is capable of strongly reducing the effects of patient-motion. [1, 2] Median-filtering is a special case of the more general method of 'order statistics' [3–7].

The organisation of this paper can be gleaned from the Contents list and Figures list at the end.

II. MATERIALS AND METHODS

A. Measurements

For the present study, we measured 'single-voxel' proton MRS of the tibialis anterior muscle of a leg of a human volunteer. On request, this person could lie motionless or move his leg.

The data contain contributions from metabolites such as

creatine, tri-methyl ammonium (TMA), acetyl carnitine, intra- and extra-myocellular lipids. Those from creatine and acetyl carnitine can be used to study human muscle metabolism, before, during, and after muscle exercise [8]. The data were produced by a 3T Siemens MR-scanner equipped with a standard Siemens extremity coil (3 Tesla MRS scanner – Trio, Siemens Erlangen, Germany – adjusted to PRESS, with TE=135 ms, bandwidth 2.0 kHz, 8-step EXOR cycle, and voxel-size $40 \times 20 \times 20$ mm³. As mentioned in the Introduction, 20 consecutive data-sets were recorded and saved individually.

MRS data are complex-valued and are obtained in the time domain. The Figures in this paper show the real parts of the FFT's of the time-domain data, *i.e.*, the real parts of the spectra.

B. Arithmetic-Mean Filtering/Averaging

Ideally, the pdf of noise present in MRS signals is Gaussian. As indicated in the Introduction, the SNR is low. Presently, the universally accepted method (in the MRS community) to improve the SNR is to repeat the measurement M times and to then average all samples taken at the same point of time in these consecutive measurements. In the present study, $M = 20$. Note that ideally, and apart from noise, all M samples to be averaged should have the same value (level). When averaging (Arithmetic-Mean Filtering, AMF) M samples, the reduction of the standard deviation of the noise is given by the well-known relation

$$\sigma_{\text{out}}^2 = \frac{\sigma_{\text{in}}^2}{M}, \quad (1)$$

where σ_{in} is the standard deviation before averaging and σ_{out} that thereafter. AMF is a linear technique.

C. Rank-Order Filtering

Linear filtering techniques have serious limitations when dealing with signals that have been created or processed by a system exhibiting some degree of non-linearity [6]. Among the signals that linear filters perform poorly

on are those with changing levels (e.g. due to patient motion) and corrupting noise that is either heavy tailed (which means that the signal contain outliers), or signal dependent.

Image processing is the field where non-linear filter techniques have first shown clear superiority over linear filters [7]. The design of non-linear filters can follow many approaches since there is no single underlying theory on non-linear filtering [4]. One non-linear filtering approach that has received considerable attention, and for which much theoretical study has been conducted, is that of so-called Rank-Order Filtering, a method whose filtering effect is obtained by rank-ordering the input data. Rank-order filtering is also known as Order-Statistics Filtering.

Note that in MRS context ‘rank’ stands for the value (size) of the sample. Sample values perturbed by patient motion will be shifted to far beyond the noise. Rank-order filtering will therefore push such samples toward outer regions of the output, far from the median value.

Much attention has been paid to rank-order filters since the ‘running-median filter’ was first applied to the smoothing of time series by Tukey in 1974 [9]. Rank-ordering of samples enables the design of filter structures that are (a) robust in environments where the assumed statistics deviate from Gaussian (which is the case in patient movement during data acquisition) and are possibly contaminated with outliers, and (b) track signal discontinuities without introducing transient or blurring artifacts as linear filters do.

D. Median Filtering

When using only the *median* value, instead of all ordered M values, one speaks of Median Filtering. The statistical properties of median filters can be examined through the derivation of output pdf’s and statistical conditions on the optimality of median estimates. This analysis generally assumes that the input to a filter is a constant signal with additive white noise. Concretely, the statistical analysis of the median filter enables the computation of the output mean and variance for a random input noise signal with a given input mean and variance. For Gaussian noise, the variance of the output noise of the M -size median filter is given by [4]

$$\sigma_{\text{out}}^2 = \frac{\pi\sigma_{\text{in}}^2}{2M}, \quad (2)$$

which is only a factor of $\pi/2$ higher than the averaging result of Eq. 1.

III. RESULTS AND DISCUSSION

Fig. 1 shows the real parts of the spectra of $M = 20$ consecutive measurements, some of which are perturbed

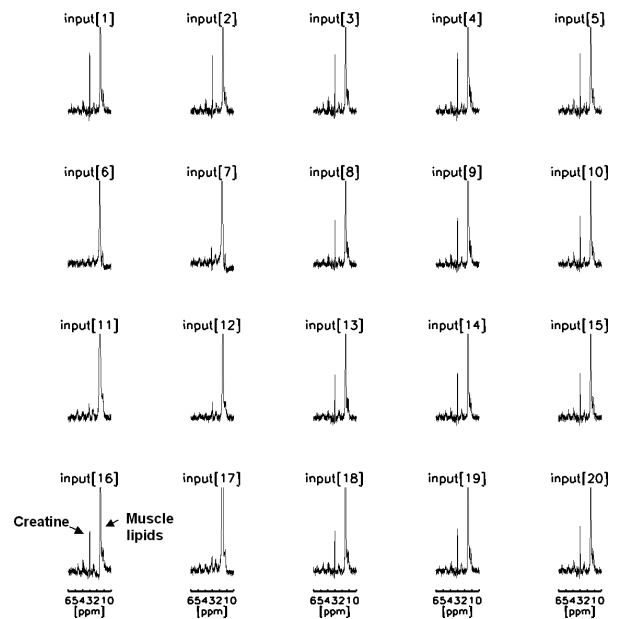


Fig. 1

Real part of the FFT (spectrum) of $M = 20$ consecutive *in vivo* MRS signals. #16, bottom left, indicates the main metabolites. Some spectra are perturbed by patient-motion; see, e.g., #2 and #17. The frequency unit along the horizontal axis is ‘parts per million’ (ppm).

by motion of the volunteer. The large resonances on the right of the spectra stem from lipids (from muscle, or subcutaneous lipids, or bone marrow). The small peaks on the left of the spectra stem from creatine and other metabolites. These metabolites are primarily present in the muscle, and, in much lower concentration, in bone marrow and subcutaneous fat.

Motion artifacts are manifested as variation of the heights and phases of the MRS spectral peaks. For instance, in spectrum #6 only lipid peaks are visible and none of other metabolites: apparently, the volunteer moved his leg such that the voxel selected by the scanner is moved from the muscle into bone marrow or subcutaneous fat.

Note that, apart from regular Gaussian scanner noise, some spectra are perturbed by outliers due to leg motion. These perturbations can be regarded as a second noise source. The distribution of this second type of noise is not Gaussian but ‘heavily tailed’. We are thus dealing with two independent noise sources.

After applying rank ordering to our data, we obtain 20 output signals (or spectra). Fig. 2 shows the results. As for the Gaussian noise, the SNR of all output spectra has improved with respect to that of the input spectra. In addition, the baselines of the output spectra are shifted, except that of the median spectrum. This shift has been estimated

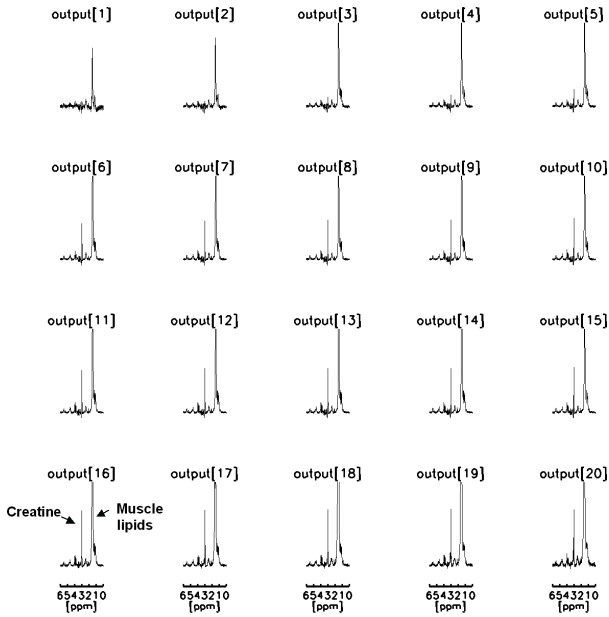


Fig. 2

Seize-ordered – by individual frequency-sample – versions of the spectra shown in Fig. 1. The top row is Creatine-deficient. The bottom row has oversized Lipids. The frequency unit along the horizontal axis is ‘parts per million’ (ppm).

and subsequently subtracted.

As for the second type of noise, all high values turn up in the maximum-value output channels (bottom row in Fig. 2) of the rank-order filter. The contributions originate mostly from muscle (large creatine peak) and subcutaneous lipids (large lipid peak).

On the other hand, the minimum-value output channels (top row in Fig. 2) contain only some contribution from lipids but not from metabolites. The latter spectra stem from signal combinations recorded when the voxel selected by the scanner was located in bone and bone marrow.

The spectra around the median (middle rows in Fig. 2) are related to time slots during which the leg was predominantly in its intended position: the bulk of the contribution stems from muscle.

Fig. 3 shows the mean spectrum (conventional average of all inputs), the median spectrum, and the difference between the average and the median spectrum.

It turns out that the lipid peaks in the median spectrum are narrower than those in the averaged spectrum. This can be explained by the fact that peaks are shifted during motion. Addition (averaging) of all peaks then results in peak-broadening. On the other hand, motion-effects are eliminated from the median spectrum, and therefore peak-broadening does not occur.

Note too that the difference is negative for creatine and positive for lipids. The median possesses a cleaner muscle spectrum which contains relative less lipid (positive in difference) and more creatine (negative difference). Together with the fact that the peak-widths of lipid contributions are much smaller, we conclude that median filtering is successful in filtering out motion-related signal contributions, normally referred to as artifacts.

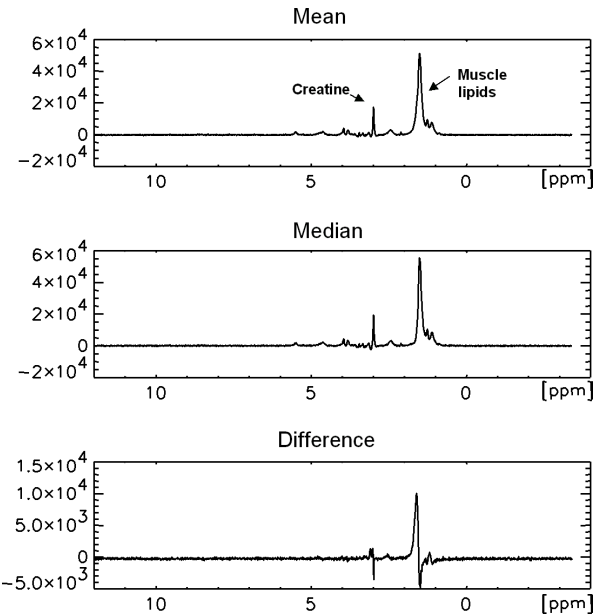


Fig. 3

Top: Mean (average) spectrum. Middle: median spectrum – by individual sample. Bottom: Difference of the mean and median spectra. The median spectrum is the better one. The frequency unit along the horizontal axis is ‘parts per million’ (ppm).

Fig. 4 shows three enlarged spectra from Fig. 2, namely the minimum-, maximum-, and median-value spectra. Note the enormous variation in peaks that should be equal in absence of motion and scanner drift.

IV. CONCLUDING REMARKS

We are the first to show that median filtering can supersede conventional averaging in single-voxel *in vivo* MRS. Without affecting the width of the spectral components, median filtering efficiently filters out all motion-related signal artifacts (heavily-tailed noise contributions). Like averaging, median filtering does not require any user interaction. By comparing the median-filtered with the averaged signal, conclusions can be drawn about the quality of the measurement: If there is a large difference, measurement conditions were not stationary, and the median must be taken to process further. If the difference is small, the average is preferable, since its SNR is 3dB better. Statis-

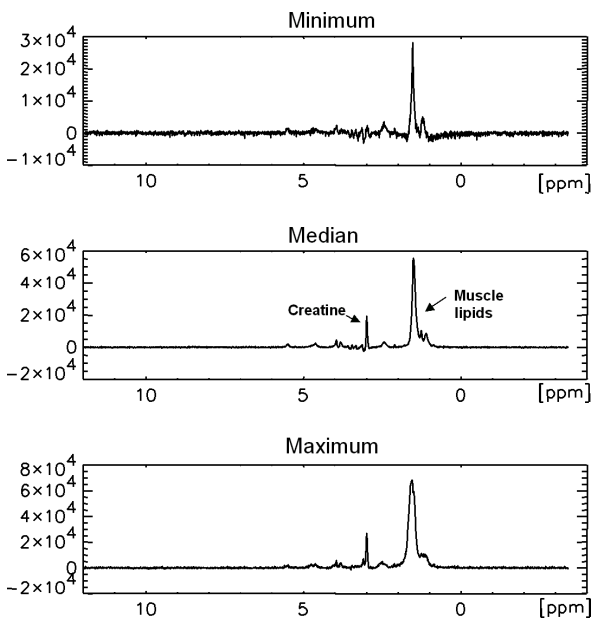


Fig. 4

Top: #1 of Fig. 2. Middle: mean of #10 and #11 of Fig. 2. Bottom: #20 of Fig. 2. Note the differences between the vertical scales. The frequency unit along the horizontal axis is ‘parts per million’ (ppm).

tical tests, enabling an automatic and optimal choice between median filtering and averaging, are now being developed.

ACKNOWLEDGMENTS

This work is supported by the Swiss National Foundation 3200B0-107499/1. The authors would like to thank Mrs. M. Mordasini and Mrs. C. Stuker for their help in the data acquisition, and R. de Beer for critically reading this manuscript.

REFERENCES

[1] J. Slotboom, D. van Ormondt, C. Brekenfeld, A. Nirikko, and G. Schroth, “The usage of Median-Filtering for the Elimination Patient Motion related signal artifacts in single voxel spectroscopy,” in *Proc. ESMRMB*, 2006.

[2] J. Slotboom and D. van Ormondt, “The application of All-Ranks Selection Order Statistic-filtering (ARSOS) in Single Voxel in vivo MR-Spectroscopy,” in *Proc. ESMRMB*, 2006.

[3] G.R. Arce, Y.-T. Kim, and K.E. Barner, “Order-statistic filtering and smoothing of time-series: Part I,” in *Handbook of Statistics*, N. Balakrishnan and C.R. Rao, Eds., vol. 17, pp. 525–554. Elsevier, 1998.

[4] K.E. Barner and G.R. Arce, “Order-statistic filtering and smoothing of time-series: Part II,” in *Handbook of Statistics*, N. Balakrishnan and C.R. Rao, Eds. Elsevier, 1998.

[5] M. Gabbouj, E.J. Coyle, and N.C.J. Callagher, “An Overview of Median and Stack Filtering,” *Systems and Signal Processing, Special issue on Median and Morphological Filtering*, vol. 11, pp. 7–45, 1992.

[6] M. Gabbouj and J. Astola, “Nonlinear order statistic filter design: Methodologies and challenges,” in *Proceedings of Eusipco*, Tampere, Finland, September 2000, pp. 377–384.

[7] P. Kuosmanen J. Astola J., *Fundamentals of Nonlinear Digital Filtering*, CRC Press, 1997.

[8] A.C. Nirikko, K.M. Rosler, and J. Slotboom, “Muscle Metabolites: Functional MR Spectroscopy during Exercise Imposed by Tetanic Electrical Nerve Stimulation,” *Radiology*, vol. 241, pp. 235–242, 2006.

[9] J.W. Tukey, “Non-linear (non-super-imposable) methods for smoothing data,” in *Conf. Rec (Eascon)*, 1974.

CONTENTS

I	Introduction	1
II	Materials and Methods	1
II-A	Measurements	1
II-B	Arithmetic-Mean Filtering/Averaging	1
II-C	Rank-Order Filtering	1
II-D	Median Filtering	2
III	Results and Discussion	2
IV	Concluding Remarks	3

LIST OF FIGURES

1	Spectra of 20 Consecutive MRS signals	2
2	Seize-ordered Versions of the Spectra	3
3	Median-filtered Spectra	3
4	Minimum-Median-Maximum Filter Outputs	4