Automated Principal Component Analysis (PCA) filtering for denoising DCE-MRI data

B. Daniel[1], N. Kachenoura[2], I. Thomassin[1], R. Thiam[1], L. Fournier[1,3], Y. Rozenholc[4], and C. A. Cuenod[1,3]

[1]LRI EA 4062, Université Paris Descartes, Paris, France, [2]UMR_S 678, Université Pierre et Marie Curie, Paris, France, [3]Service de Radiologie, Hôpital Européen Georges Pompidou, Paris, France, [4]MAP5 - UMR CNRS 8145, Université Paris Descartes, Paris, France

Introduction

Dynamic Contrast Enhanced MRI (DCE-MRI) is recognized as an efficient diagnosis and prognostics tool in several lesions such as in solid cancers. However, the improvement of its quantification remains crucial. Among other questions, the signal to noise ratio (SNR) is known to be poor in DCE-MRI, yielding a low efficiency of the DCE-MRI to detect and characterize small o heterogeneous lesions. Conventional spatial or time low pass filters induce losses in spatial or time resolution providing possible quantification errors. Here an adaptative Principal Component Analysis (PCA) filtering process is proposed to avoid these limitations. The originality of the process consists in selecting automatically the number of PCA factors for a maximal denoising efficiency, which is acceptable for a minimal loss of physiological information.

PCA filtering

In data analysis, the PCA is a well known method used to compress large volumes of redundant data. It has been used as a signal filtering technique in medical applications such as for MEG signal denoising [1]. For PCA time analysis, the n_p pixels contrast enhancements of a zone of interest are interpreted as vectors in an n_t dimensional space, where n_t is the number of time points of the signals. PCA changes the current basis so that the energy of the dataset on the first components (factors) subspace is maximal. The energy is the sum of the amplitude of the signals. Thus, for the pixel p and a rank k: $\mathbf{s_p}(t) = \sum_{i=1}^{k} a_{ip} \cdot \mathbf{f_k}(t) + \mathbf{r_{kp}}(t)$, where $\mathbf{s_p}$ is the pixel enhancement, $\mathbf{f_k}$ the k^{th} factor, a_{ip} the $\mathbf{s_p}$ projection on $\mathbf{f_k}$ and $\mathbf{r_{kp}}$ the residual of the partial PCA. For a more detailed description, see for example [2].

Fraction of Residual Information

To know how many factors are required to limit losses of time information, the Fraction of Residual Information (FRI) was used [3]. Assuming that the filtering residual is the sum of a non-random component ($\mathbf{i_{kp}}$) bearing information and of a random noise ($\mathbf{b_{kp}}$), the FRI is defined by $FRI^2 = \|i_{kp}\|^2 / \|r_{kp}\|^2 = \|i_{kp}\|^2 / \|i_{kp} + b_{kp}\|^2$. In practice $\|i_{kp}\|^2$ was assessed, as in [3], by fitting the autocorrelation function of the residual by a polynomial function for positive lags and prolonging it to zero. The range of lags was [1 5] and the polynomial fitting limited to a linear regression.

Selection of PCA factors

PCA filtering was tested by increasing the factors number. The test consisted to evaluate the pixels fraction (α) which had an FRI upper than a specified limit (FRI_{95}). FRI_{95} corresponded with the 95th percentile of an FRI set of values provided from a generated normal random noise with the same dimensions than the dataset. Information losses were detected in the residuals for $\alpha > 5\%$. A tolerance factor was used to accept possible local losses of information, such as losses in without interest organ bounds impaired by specific motions. Thus, the PCA filter was accepted for $\alpha \leq 7\%$. The results were controlled by producing an FRI map and a film of original series, filtered series and residual series.

Set of Data Test

The algorithm was tested on DCE-MRI series acquired during a clinical ovarian tumor study for which ethics committee approval were obtained, on a 1.5 T Unit (Siemens), with an injection of a 0.1 mmol/kg gadolinium chelate contrast agent (Dotarem) [4-5]. The temporal series lasted for 130s with a temporal resolution of 2.4s

Results

The typical efficiency of the filtering on the images is illustrated on the top of fig 1. There was no visible loss of tissue structures and no visible information losses in the contrast enhancements, except locally, as shown on the residual image. There is a striking improvement in the enhancement curves found in individual pixels of vessels and tissues as shown in fig 1, with the original enhancements (left), the filtered enhancements (center) and the residual (right).

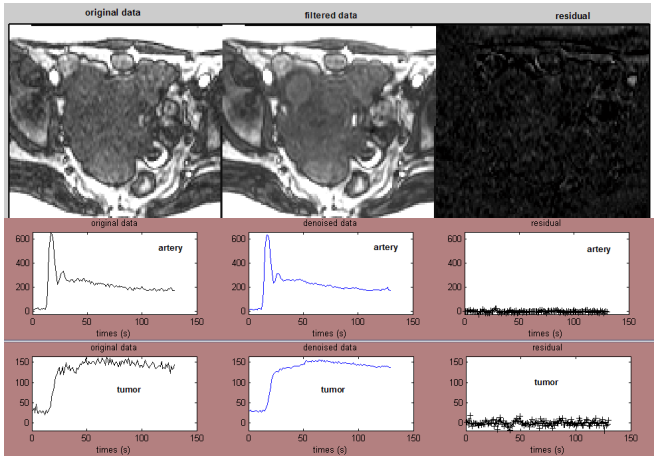

figure 1: image and signal filtering with adapted PCA filtering

Conclusion

Adapted PCA filtering provides promising results, with large denoising effects on the images and on the dynamic enhancement curves. It could help the user to draw regions of interest in improve quantitative pharmacokinetic regional analysis and improve the efficiency of pharmacokinetic modeling, specially in pixel by pixel analysis.

References

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