Numerical methods and software for functional Magnetic Resonance images reconstruction

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Some Magnetic Resonance Imaging (MRI) applications require a time series of imaging to monitor a dynamic process. MRI is usually a Fourier transform based technique: the data are acquired in the Fourier space and then inverse Fourier transformed to get the desired image. Hence, for such an imaging technique, the number of available data points is fundamental for the image quality. In dynamic imaging applications, in order to improve the temporal resolution, a reduced number of samples is acquired in the Fourier space for all the images of the sequence, except one or two (*reference images*). The problem is then to reconstruct images of good quality from undersampled data in the Fourier space. The keyhole method, currently implemented on commercial systems, produce Gibbs artifacts and loss of resolution that degrade the quality of the reconstructed images. We followed a different approach, the Reduced–encodins Imaging by Generalized Series Renconstruction (RIGR), proposed by Liang et Lauterbur [2] based on the Generalized Series model. The image functions are represented as

$$I_{GS}(x) = C(x) \sum_n c_n \phi_n(x)$$

where $\phi_n(x)$ are complex exponential basis functions, $C(x)$ is a contsraint function that contains *a priori* informations from the reference images. We analysed the RIGR method by using both one and two reference images.The coefficients c_n are obtained by minimizing a cross–entropy measure, that finally consists in solving a large number of small size linear systems, each with semipositive definite Toeplitz matrix. The systems can be ill conditioned. The regularization methods for problems with positive semidefinite matrix are not extensively treated in literature, hence our work concerned also the analysis of suitable methods for this kind of problems. We considered the Truncated Singular Value Decomposition, the Lavrentiev method and some conjugate gradients type methods, with different criteria for the choice of the regularization parameter in each case. We tested these methods both on simulated and real data acquired on the MRI system at theDepartment of Clinical Pathophysiology of the University of Florence. In order to make the methods tested available to the physicians we produced a software, conceived as a Matlab Toolbox, with a graphical interface that allows to test the methods without knowing anything of the underlying mathematics.

References

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