

Decomposition of dynamic MR images with low-rank and sparse matrix separationB. Trémouh ac¹, P. G. Batchelor², A. Menys³ and D. Atkinson³¹Centre for Medical Image Computing, University College London, ²Imaging Sciences and Biomedical Engineering, King's College London, ³Centre for Medical Imaging, UCL Division of Medicine

Background. A recent mathematical optimisation problem investigates the topic of decomposing a given matrix into its low-rank and sparse components [1, 2, 3]. While these papers mostly focus on theoretical aspects – in particular, whether it is possible to exactly recover the unobserved low-rank and sparse components from the observed matrix – Cand es *et al.* [3] have shown practical use of the decomposition in video surveillance and face recognition. In medical imaging, Gao *et al.* [4] have recently incorporated this separation model into the conventional inverse problem in Computed Tomography and were able to reconstruct better images with fewer measurements than state of the art techniques.

Objectives. We investigate the potential usefulness of this separation process in dynamic Magnetic Resonance Imaging (MRI). More specifically, motivated by experiments on real data, we are interested to know if this method (a) could separate the global (or respiratory) motion from the local motion, and (b) could detect local changes of intensity.

Methods. Mathematically, the decomposition process can be posed as the following convex optimisation problem, $\min_{L,S} \|L\|_* + \lambda \|S\|_1$ subject to $X=L+S$, where $\|L\|_*$ and $\|S\|_1$ denote respectively the nuclear norm of L (the sum of the singular values) and the l_1 norm of S defined as the sum of the absolute values of all entries (i.e. l_1 norm of S viewed as a vector). λ is a trade-off parameter between low-rank and sparse components. X is the observed data matrix, $X=[x_1 \dots x_M]$, $X \in \mathbb{R}^{N \times M}$, with temporal image i of the M -sequence as its column vectors x_i . Minimisation of the problem can be performed by various optimisation techniques but the Alternating Direction Method (ADM) appears to be the best choice, especially when it comes to large-scale problems. ADM, an improvement of the Augmented Lagrangian method, exploits the favorable structure appearing in both the objective function and the constraint [2, 3]. Both MATLAB implementations of the algorithm in [2, 3] have been made available online at perception.csl.uiuc.edu/matrix-rank/. Although λ is set to $\max(N,M)^{-1/2}$ in [3], justified by a theoretical analysis and a no tuning parameter approach, it is in our case a parameter we tune by visual inspection. Based on the Shepp-Logan phantom, we generate a 20 frames sequence with time varying intensity and a mixture of global and local motion (figure 1) to understand how the separation works in this context.



Fig.1: Global (respiratory) motion is simulated by slightly and slowly changing size of the main ellipse. Local motion is simulated by three small ellipses at the bottom. Intensity change from 0 to 1 is visible on the right side ellipse. (Left) y - t profile of the generated sequence. (Right) Extracted frames from the whole sequence at time $\{1, 4, 7, 12, 16, 20\}$.

Results. We show in figure 2 the resulting decomposition of the entire Shepp-Logan phantom sequence for a chosen value of the trade-off parameter equal to $2 \cdot \max(N,M)^{-1/2}$. We first note that local motion is clearly reflected in every sparse frame yielding a straight forward segmentation of the moving local ellipses. We also remark the respiratory-like motion appears only in the low-rank frames, although edges of the outer ellipse do appear in the sparse frames. Perhaps more interestingly is the intensity varying ellipse which is distinctly represented in the sparse matrix in the last few frames of the whole sequence. This could yield applications in Dynamic Contrast Enhanced MRI since this method gives a direct segmentation of the varying local intensity change. Figure 3 shows the sensitivity of the method to isolating peristalsing small bowel motion in a healthy individual undergoing small bowel enterography. (A cine MRI sequence of 20 frames with both large-scale respiratory motion and local motion of the small bowel.) This could be useful for clinicians since motion detection is becoming an increasingly useful diagnostic parameter for assessing disease status non-invasively. Finally, we think it is also important to notice that processing the Shepp-Logan sequence or the real data (both of size $512 \times 512 \times 20$) takes only a few seconds on a simple desktop computer using algorithms [2] or [3] thanks to the use of the ADM approach.

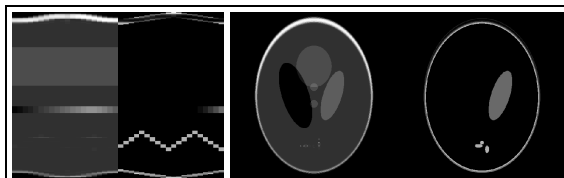


Fig.2: Low-rank and sparse components resulting from the decomposition. (Left) y - t profile of the whole sequence (Right) Frame 20.



Fig.3: Decomposition on small bowel MR data. Respiratory motion appears largely in the low-rank time frames whereas peristaltic motion appears in the sparse frames. (Left) Data (Middle) Low-rank component. (Right) Sparse component.

Conclusions. We have proposed to apply the low-rank and sparse separation problem to dynamic MRI sequences as an image post-processing method. Using a simple simulation and a specific value of the trade-off parameter, we have shown this method can detect local motion and local intensity changes in the sparse frames, as well as isolating the respiratory motion in the low-rank frames. Through application to real data, we hope to have convinced the reader that this method could lead to a better understanding and/or interpretation of the images from a clinical perspective.

References. [1] V. Chandrasekaran *et al.* Rank-sparsity incoherence for matrix decomposition. *SIAM J. Optim.* (to appear), 2009. [2] X. Yuan and J. Yang. Sparse and low-rank matrix decomposition via alternating direction methods. *Pac. J. Optim.* (to appear), 2009. [3] E. Cand es *et al.* Robust principal component analysis? *J. ACM* 58, 2011. [4] H. Gao *et al.* Robust principal component analysis-based four-dimensional computed tomography. *Phys. Med. Biol.* 56, 2011.