Assessment of Renal Function from Motion-Corrected 3D DCE-MRI using Clustering and Independant Componant Analysis

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Introduction

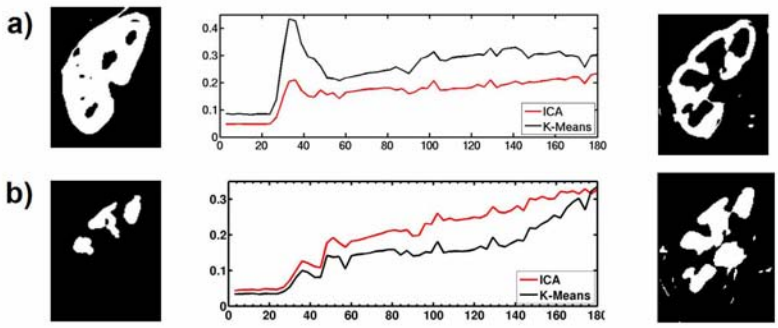
Diagnosis of renal dysfunction is today based on blood tests and urine sampling. These indirect measures are rather imperfect, e.g. a significant change in creatinine level is only detectable until a 60% function loss has occurred. Furthermore, no split function between left and right kidney, or functional localization is achieved. To overcome these limitations dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) is an emerging technique for a more accurate assessment of local renal function [1]. Analysis of DCE-MRI time series is typically based on manual or semi-automated delineation of regions of interest in the recorded images (e.g. [2]). However, such procedures are time consuming, expensive and error prone [3], and subject to intra- and interobserver variations. Automated pattern recognition techniques can help overcome these limitations and provide more objective and reproducible results. In functional imaging of the brain, unsupervised data-driven approaches, such as k-means clustering and independent component analysis (ICA), have been reported to give good results in both perfusion imaging studies [4] and BOLD fMRI [5]. In this work we compare the performance of k-means clustering and ICA in the assessment of motion-corrected DCE-MRI data from the human kidneys. In a situation with proper motion-correction of the voxel time-courses (e.g. [6]) these methods, which optimizes quite different objective functions and statistical characteristics in the data, will partition the time-courses according to their enhancement patterns and the functional similarities of the corresponding voxels. Such automated partitioning could thus eliminate the need of manual interaction for (i) the separation and segmentation of left and right kidney (split function), and for (ii) delineation of functional compartments (normal or abnormal) within the kidney.

Methods

In our comparison study we applied k-means and ICA to four normal DCE-MRI time series of different length, temporal and spatial resolution, recorded on a 1.5T Siemens Symphony and a 3T GE scanner. Prior to data-driven time series analysis, all voxel time-courses were motion-corrected using multimodal, non-rigid 3D registration techniques as described in [6]. K-means clustering was performed according to [7]. For ICA analysis we applied the fastICA algorithm [8]. The comparison was carried out by visual inspection of the resulting clusters and independent components (ICs) and their mean time-courses, and by calculating the correlation between k-means and ICA derived mean time-intensity curves of the renal cortex and renal medulla.

Results

Figure 1 depicts k-means and ICA mean time-intensity curves for the renal cortex (a) and the renal medulla (b) for slice 22/44 in one of the 3T datasets. The upper left panel is a cortical ROI obtained from ICA, the upper right panel is cortical ROI from k-means. Cross-correlation between their mean time-intensity curves were 0.9. Similarly, the lower left and right panels are medullar ROIs yielding a cross-correlation coefficient of 0.95 between the ICA-derived and k-means derived mean time-intensity curves. We also see that k-means in this case gave a cluster within the cortex, evenly distributed around the kidney, with voxels characterized by very fast and strong enhancement as well as fast wash-out. The IC in Fig. 1(a) was a superset, consisting of voxels with also minor enhancements. Similar results were obtained for the other datasets, and in all cases left and right kidney could easily be separated accurately and automatically. The time-intensity curves also give information about the quality of the registration. Small peaks in all time-series around 60, 100, 130, and 175 sec from start of DCE-MRI represent periods with breathing, yielding corrupted 3D image frames that could not be properly registered.



Discussion

The results indicate that both k-means and ICA are able to segment functional compartments such as renal medulla and renal cortex, with very similar mean time-intensity curves. Since the two methods build on quite different statistical principles: minimizing intra-cluster and maximizing between-cluster spread between time-courses in k-means, and maximizing statistical independence of components in ICA, yielding a kind of blind source separation, both methods should be applied as tools to explore diagnostically important information distributed in time and space of the recorded DCE-MRI data. A next step will be to extract time-course features such as time-to-peak, slope of enhancement, as well as model-based pharmacokinetic parameters (e.g. GFR) from the segmented regions and thereby produce potentially useful parametric images for clinical interpretation.

References

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