Factor Analysis in Segmentation of 4D DCE-MRI Renal Studies

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Introduction

Segmentation is mandatory to obtain quantitative physiological information from 4D dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) of the renal system. We have previously reported results from cluster analysis and factor analysis[1] (FA). Here we show that FA alone can perform all the necessary segmentations yielding 3D volumes of renal cortex, medulla, pelvis, ureters, liver, spleen, arteries, veins and if present, ventricles, lungs etc. We compare a FA approach similar to previously published methods[2,3] (PFA), a particular modification of PFA (VBFA) and independent component analysis[4] (ICA) on two very different clinical datasets and on images obtained in a porcine model of renal disease.

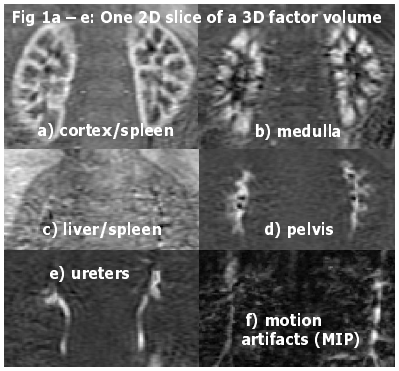
Methods and Materials

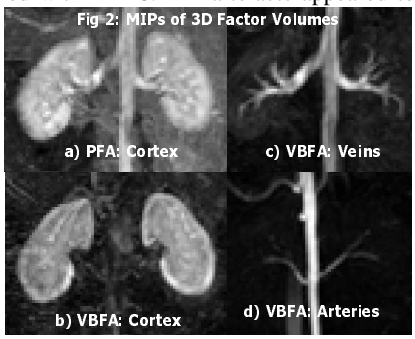
FA decomposes a matrix of dynamic image data $\boldsymbol{D}$ into a matrix $\boldsymbol{F}$ (physiology) of K factor intensity curves (FIC) and a matrix $\boldsymbol{A}$ (anatomy) of K factor images. A principal components analysis (PCA) is followed by an iterative adjustment under certain constraints to set the K orthogonal PCA curves obliquely. Several difficulties have been reported[3]: lack of convergence, susceptibility to noise and $K \leq 3$. In our VBFA algorithm we introduced a simple modification to PFA: a binary $\boldsymbol{A}$-matrix during the oblique rotation generated by a user adjustable threshold (s) in the range 0 – 1 (PFA: $s = 0$), below/above which elements of $\mathbf{A}$ are set to 0/1 respectively. ICA was implemented via the FastICA algorithm[5]. All analyses were performed in MATLAB 7.1 (MathWorks, Natick, MA), running on a Xeon processor (2GHz; 2GB RAM).

Clinical dataset 1: Ten 4D DCE-MRI datasets were selected (corrected for kidney motion with a cross correlation method) representing a wide range of renal function[1]. Acquisition details in brief: study time: 16 - 31min; 1 - 6 pre-contrast volumes; 3D volumes: 24 – 44 of 10 - 18 2D coronal images (2DCI), acquisition period (TA) ≈17s. Porcine datasets (8 animals: normal: 3; outflow obstruction: 5; 3D volumes: 120 of 6 - 9 2DCI collected for ≈4min post injection of Gd-DTPA) had two main features: 1) minimal respiratory movement so motion correction was not required and 2) TA ≈2.3s - 2.8s, ensuring negligible MR motion artefacts and good temporal resolution during the first pass of the contrast agent. Scanner parameters were: FA: 18°; TR: 3.6ms; TE: 1.7ms; FoV: 256×192mm; matrix:128×96; voxel dimensions: 2×2×6mm. Clinical dataset 2: 4D DCE-MRI obtained from 5 subjects with normal function acquired during free breathing with a range of respiratory motion[6]. FoV included chest and abdomen. Acquisition details in brief: study time: ≈5.7min; 3D volumes: 138 of 18 2DCI; 3.1×3.1×7.5mm; TA ≈2.5s.

Results and Discussion

Processing time was 5s – 2 min (all FA methods) depending on the size of the matrix $\boldsymbol{D}$, number of factors to be extracted (K: 2 – 32) and s. Clinical dataset 1: VBFA and ICA converged even when extracting greatly in excess of the number of physiologically relevant factors (approximately 8). All methods generated negative elements in $\boldsymbol{A}$ but amplitudes were least in ICA and VBFA with $s \geq 0.95$. Elements of $\boldsymbol{A}$ were more closely confined to the range 0 – 1, a fundamental tenet of FA, using VBFA with $s \geq 0.95$. FICs were always positive when produced by PFA and VBFA. FICs from ICA contained physiologically inappropriate negative values. PFA could not generally converge for $K > 5$. Factor images produced by VBFA and ICA contained similar anatomical features: liver, renal cortex, medulla, pelvis and motion artefacts (Fig 1; $K = 28$). Renal cortex was always associated with spleen and was connected to veins. Using low K (2 – 3) with $s = 0.95$ produced renal parenchyma that could be used to isolate cortex from the spleen in results obtained with $K \geq 8$. MR artefacts appeared to increase K required to achieve an acceptable decomposition.





Porcine datasets: In these almost perfect datasets, PFA could not converge to a solution within 500 iterations, was still unstable at $s = 0.3$, but although unexpectedly convergence did occur at $s = 0.95$ ($K \leq 24$), cortex was connected to veins and arteries (Fig 2a). By contrast and contrary to a previous speculation[1], VBFA and ICA produced excellent isolation of the renal cortex from spleen, arteries and veins for $K = 16 – 32$ (Fig 2b, c, d; $K = 24$). The increased cortical contrast (Fig 2b) made segmentation possible in the presence of confounding intense gut signal in the raw data (not shown). Medullary collecting system and ureters were also isolated and able to be segmented into 3D volumes, but not in obstructed pigs.

Clinical dataset 2: When respiratory motion had maximum displacement (MD) of 3 - 9mm, VBFA isolated cortex alone and all other renal and abdominal structures at $K = 24$. On greater respiratory excursions (MD: 15 - 24 mm) cortex and medulla began to break up into two or more factors and cortex could be attached to spleen. Segmentation of structures within the chest (lung, ventricles) was also readily achieved in these datasets.

FICs obtained by VBFA for each anatomical structure in all datasets were physiologically plausible, although subtle differences could be masked between left and right compartments when isolated as one. Diseased cortex was isolated with medulla in the contra-lateral kidney in some studies. Relative cortical volumes and transit times through renal compartments were readily assessed from FA segmentations.

Conclusions

VBFA is a stable platform for complete segmentation of 4D DCE-MRI renal studies with a performance similar to ICA. ICA did not always produce physiologically plausible FICs. Motion correction to within 9mm and 3D volume acquisition times of <3s are required for best segmentation results.

References

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