On-Line Spatio-Temporal Independent Component Analysis for Motion Correction in Renal DCE-MRI

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Abstract—Dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) renography, in common with other medical imaging techniques, is influenced by respiratory motion. As a result, data quantification may be inaccurate. This work presents a novel on-line approach for motion correction by implementing a spatio-temporal independent component analysis method (STICA). This methodology firstly results in removal of motion artefacts and secondly provides independent components that have physiological characteristics. The STICA was applied to 10 healthy volunteers' renal DCE-MRI data. The results were evaluated using independent component curve gradients (ICGs) from different regions of interest and by comparing them with the Rutland-Patlak (RP) analysis. The r^2 values for the ICGs were significantly higher compared to the RP curves. The standard deviations of the IC curve gradients also showed less dispersion with comparison to the RP curve gradients across all the ten volunteers' renal data.

I. INTRODUCTION

THE application of DCE-MRI renography to provide accurate quantification of single kidney perfusion, glomerular filtration rate (GFR) and filtration fraction is fraught with difficulty due to various confounding factors including movement of the kidneys. DCE-MRI renography starts with the acquisition of abdominal dynamic MR images [1], that may undergo several post processing steps including movement correction [2], [3], partial volume correction [4], segmentation [2], [5] and a final stage of quantification using a tracer-kinetic method [6], [7], [8], [9]. Renal DCE-MRI data suffer from respiratory motion artefacts, partial volume contamination and have relatively low signal-to-noise ratio (SNR). These cause inaccuracy in the kidney assessment. [2], [4], [5], [10].

Several authors have proposed movement correction methods for DCE-MRI renography based on rigid and non-rigid registrations [2], [3], [11]. A method of movement correction and segmentation based on a two-step registration coupled with a k-means clustering was also proposed in [2]. A method of segmentation based on an independent component analysis (ICA) was proposed in [12]. While these methods may improve the post processing of DCE-MRI renography further, they do not provide a complete solution. These are not fully data driven methods and have to be performed off-line (after the images are acquired), since they rely on

an operator to provide regions of interest (ROIs). The ROIs are usually derived manually or semi-automatically which is a time-consuming process and is subjected to contrast and observer variation [13], [14].

The motion correction approach proposed in this paper is a fully data-driven approach based on a blind source separation (BSS) technique which exploits the distribution properties of the spatial data, incrementally, in the direction of the time axis. Conventional BSS methods such as temporal or spatial independent component analysis (TICA, SICA) are based on the assumption of temporal and spatial independence respectively. The role of the related ICA technique is therefore to find an optimal filter that maximizes the statistical independence of the observed signals. The approach here is based on combining both TICA and SICA to provide a spatio-temporal (STICA) method which aims to estimate an optimal filter that maximize the statistical independence of the observed signals over space and time simultaneously (see Fig.1).

The movement artefacts are mainly the result of respiration which can be regarded as an independent process having a quasi-sinusoidal effect on the physiological processes (although no assumptions are made about this behaviour). The main assumptions are statistical independence and non-Gaussianity of the underlying source signals. The plausibility of the assumptions lies in the fact that in a dynamic imaging technique such as DCE-MRI different regions or tissues respond differently, over time, to the stimulus i.e. contrast agent. Therefore the DCE signals emanated from these tissues are assumed to be independent of each other at each sampling time (spatial independence) as well as over the entire time of acquisition (temporal independence). Similar assumptions have lead to many useful BSS techniques in biomedical signal processing [15]. An spatio-temporal ICA method was also developed and applied to the event-related fMRI data [16].

II. MATERIALS AND METHODS

A. Dynamic Image Data Acquisition

Healthy volunteers' data were acquired at baseline and after injection of 0.05 mmol/kg of Gd-DTPA (Magnevist), on a 1.5T Siemens Avanto MRI scanner, using a TIM 32 channel body phased array coil and a 3D spoiled gradient echo sequence with TR=1.6ms, TE=0.6ms and FA=17°. The data consist of 12 contiguous 7.5mm slices with in-plane resolution of 3.1×3.1mm and temporal resolution of 1.5s collected for 180s.

B. Transformation of 2-D Spatial Data to 1-D Signals

The central slice of each subject's image data that include a large portion of each kidney was chosen (see Fig.1). The im-

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Fig. 1: Main steps of the STICA method are illustrated in this flow chart. Images are taken from a subject's central kidney slice and two of the estimated ICs for the same slice. m , n and t represent the number of rows, columns and sampling time respectively.

ages were then transformed to one-dimensional (1-D) vectors by concatenating the rows of voxels:

$$x(t)^{2D} = x(t)^{m \times n} \rightarrow x(t)^{1D} = x(t)^{1 \times mn} \quad (1)$$

$$i = 1, 2, \dots, m \quad j = 1, 2, \dots, n \quad t = 1, 2, \dots, k$$

Where i, j and t denote row, column and time indices respectively. The transformation of an image from 2-D to 1-D does not change the structure of the data. It only repositions the voxels to form a vector (denoted as a random variable), so that all the information within the image can be considered at once.

C. Principal Component Analysis

PCA is a linear transformation of a multivariate variable in order to produce a set principal components (PCs). These PCs represent data variation along a particular projection in space. In the case of renal data here, variation is due the underlying tissues responding differently to the contrast agent.

Fig. 2: The image above is taken from a subject's central slice at the contrast peak enhancement. Three ROIs: large rectangle, cortical and single voxel on both right and left kidneys, were used to evaluate the estimated ICs for 10 subjects. (a) Time-Intensity curve of a whole kidney rectangular ROI of central kidney slice. The fluctuations on the curve are mainly due to respiratory motion artefacts. (b, c & d) Time-Intensity curves of three ICs for the same slice: (b) represents filtration similar to $K(t)$ in the Patlak method [8], and (c) represents perfusion similar to aortic input curve. Motion correction is evident from the smoothness of both curves. (d) represents characteristics such as motion artefacts but may also contain other components such as noise.

These variations are reflected in the MR signals with varied intensities at each sampling time. The PCA method, used here, is based on the eigenvalue decomposition of the samples' covariance matrices e.g. $\hat{\Sigma}_t$ or just Σ_t , where all the variables

Fig. 3: An exemplar of Patlak curves (left figures) and IC Curves (right figures). The Patlak data are from three ROIs on the subject one's left kidney. The IC curves are from the three ROIs on the subject one's left kidney independent component. The gradients of the fitted line is proportional to renal filtration.

are centred before estimation of the covariance matrices i.e. $E[X] = 0$.

The covariance matrix is symmetric and positive semi-definite which means that for a non-zero vector v , $v^T \Sigma v \geq 0$. Therefore it is transformed to a matrix of orthogonal eigenvectors V with corresponding eigenvalues Λ :

$$\Sigma_{X_t} = E[X_t X_t^T] = v_t \lambda_t v_t^T = V \Lambda V^T \quad (2)$$

Here t is incremented $t + \tau$, to update the eigenvectors at each step i.e. $\Sigma_{X_{t+\tau}}$ $t = 0, 1, 2, \dots, k$. The spatial data are hence orthogonalized at each $t + \tau$ step with the eigenvectors representing the direction of variations in the data space. The significance of the eigenvectors in a multidimensional random vector is reflected by their magnitudes and hence the smaller magnitudes represent less significant eigenvectors. A very small threshold of 10^{-4} was chosen in order to

allow the estimation of most eigenvectors ($\approx 99.9\%$) while eliminating most insignificant ones at the end of the spectrum. The eigenvectors and eigenvalues form the bases for the whitening transformation W that transform the input signals X_t to uncorrelated vectors of unit dispersion:

$$W = V \Lambda^{-\frac{1}{2}} V^T \quad Z_t = W_t X_t \quad (3)$$

This is a very useful transformation as a preprocessing step, in the sense that it decreases estimation complexity of the ICA, which is based on higher-order statistics. The whitening transformation is defined as: The transformed vector Z has orthogonal variables with unit variance along all dimensions. The decorrelation of the variables is a weaker form of independence since decorrelation does not necessarily imply independence. The whitening is therefore an unmixing transformation based on the principal components given by

Fig. 4: Standard deviations for Patlak K1s and independent components gradients ICGs were evaluated for the ten subjects' left kidneys (left figure) and right kidneys (right figure). As it is evident from the figures the standard deviations for the three ROIs; large rectangle (ROI1), cortical (ROI2) and single voxel (ROI3) (see an exemplar in Fig.2), do not vary significantly for the ICGs. This suggests that the ROI size and shape become insignificant when the estimated IC is a representative of the renal filtration function.

Patlak (K1) VS IC curve gradient (ICG) for ROI1 (large rectangle), ROI2 (cortical) and ROI3 (single voxel).
Left Kidney

Subjects	(x10 ³)	ROI1	r ²	ROI2	r ²	ROI3	r ²	Min - Max
1	K1	3.0	0.29	2.7	0.16	3.7	0.12	2.7 - 3.7
	ICG	4.0	0.99	4.2	0.96	4.5	0.90	4.0 - 4.5
2	K1	3.0	0.31	3.4	0.30	7.0	0.50	3.0 - 7.0
	ICG	4.7	0.66	4.3	0.81	4.5	0.62	4.3 - 4.7
3	K1	7.1	0.08	3.8	0.42	0.5	0.08	0.5 - 7.1
	ICG	4.4	0.75	3.8	0.78	3.8	0.82	3.8 - 4.4
4	K1	4.0	0.56	2.4	0.37	0.8	0.04	0.8 - 4.0
	ICG	4.7	0.75	4.5	0.79	4.7	0.75	4.5 - 4.7
5	K1	2.5	0.31	2.8	0.23	4.7	0.24	2.5 - 4.7
	ICG	4.3	0.75	4.2	0.80	4.5	0.93	4.2 - 4.5
6	K1	2.1	0.30	1.2	0.10	0.1	0.07	0.1 - 2.1
	ICG	4.2	0.85	4.4	0.79	3.8	0.61	3.8 - 4.4
7	K1	3.3	0.50	5.8	0.66	4.1	0.32	3.3 - 5.8
	ICG	4.3	0.67	4.3	0.80	4.5	0.67	4.3 - 4.5
8	K1	3.1	0.31	0.3	0.02	2.0	0.10	0.3 - 3.1
	ICG	3.7	0.94	3.3	0.70	3.4	0.79	3.3 - 3.7
9	K1	1.0	0.10	2.8	0.20	2.3	0.10	1.0 - 2.8
	ICG	3.3	0.70	3.6	0.95	3.4	0.84	3.3 - 3.6
10	K1	3.9	0.30	0.2	0.12	5.1	0.51	0.2 - 5.1
	ICG	4.5	0.87	4.1	0.77	3.9	0.92	3.9 - 4.5

Patlak (K1) VS IC curve gradient (ICG) for ROI1 (large rectangle), ROI2 (cortical) and ROI3 (single voxel).
Right Kidney

Subjects	(x10 ³)	ROI1	r ²	ROI2	r ²	ROI3	r ²	Min - Max
1	K1	2.8	0.27	3.3	0.26	4.9	0.17	2.8 - 4.9
	ICG	4.7	0.98	4.2	0.97	4.9	0.99	4.2 - 4.9
2	K1	5.3	0.41	3.7	0.42	3.1	0.05	3.1 - 5.3
	ICG	4.3	0.65	4.6	0.96	4.5	0.66	4.3 - 4.6
3	K1	3.0	0.41	3.2	0.46	0.2	0.10	0.2 - 3.2
	ICG	4.4	0.65	3.6	0.63	3.8	0.60	3.6 - 4.4
4	K1	4.4	0.69	2.6	0.32	1.8	0.11	1.8 - 4.4
	ICG	4.6	0.75	4.3	0.64	4.1	0.64	4.1 - 4.6
5	K1	3.6	0.51	1.6	0.10	0.7	0.04	0.7 - 3.6
	ICG	4.1	0.95	4.2	0.73	4.2	0.90	4.1 - 4.2
6	K1	3.5	0.70	2.8	0.50	2.1	0.04	2.1 - 3.5
	ICG	4.0	0.96	4.3	0.87	4.2	0.82	4.0 - 4.3
7	K1	4.4	0.58	5.2	0.68	4.6	0.23	4.4 - 5.2
	ICG	4.4	0.64	4.3	0.77	4.2	0.70	4.2 - 4.4
8	K1	3.6	0.33	1.9	0.05	1.2	0.20	1.2 - 3.6
	ICG	3.8	0.96	3.6	0.60	3.6	0.82	3.6 - 3.8
9	K1	1.4	0.04	3.6	0.38	2.6	0.08	1.4 - 3.6
	ICG	2.9	0.85	2.9	0.93	3.3	0.94	2.9 - 3.3
10	K1	2.7	0.45	1.8	0.07	3.8	0.27	1.8 - 3.8
	ICG	3.2	0.93	3.6	0.66	3.4	0.85	3.2 - 3.6

TABLE I: Patlak K1s and independent component gradients (ICGs) are shown for the ten subjects' left and right kidneys (left and right tables respectively). The higher r^2 values for the IC curves suggest a better curve fitting with less error compared to the Patlak curves. Also the minimum and maximum values of K1s and ICGs, as shown in the last columns, represent a smaller range of variation for ICGs

the PCA.

D. Source Separation via Maximization of Negentropy

This is a BSS technique since the source signals and mixing system are unknown. It based on optimization of a negentropy cost function (FastICA) [17]. Statistical independence and non-Gaussianity of the source signals are the only assumptions used here.

Approximation of negentropy is given by

$$J(y) \propto [E\{G(y)\} - E\{G(\nu)\}]^2 \quad (4)$$

Where y G denotes a loss or cost function and ν is a normalized Gaussian variable with zero mean and unit variance. The loss function used here is defined as:

$$G(y) = \frac{1}{\alpha} \log(\cosh(\alpha y)) \quad (5)$$

That is regarded as a robust loss function in the sense that it does not grow too fast and reduces the effect of outliers [18]. The cost function is optimized via a constrained Newton's method based on second order derivatives. The maxima given by the optimization of $J(y)$ are set of weights that transform the random variables to be as non-Gaussian as possible. It is evident that $J(y)$ reaches its maximum when $J(y) = E\{G(y)\}$. Therefore the optimization is defined as:

$$L(x) = \begin{cases} \text{Maximize : } J(y) = J(w^T x) \propto [E\{G(w^T x)\}] \\ \text{Subject to : } E\{(w^T x)^2\} = \|w\|^2 = 1 \end{cases} \quad (6)$$

This is now a constrained optimization problem where the method of Lagrange multipliers can be applied to find the optimal weight vectors w :

$$\nabla E\{G(w^T x)\} - \lambda \nabla E\{(w^T x)^2\} = 0 \quad (7)$$

Where λ is the Lagrange multiplier and ∇ is the gradient operator. The above constrained problem (after some algebraic manipulation) is reduced to:

$$\begin{aligned} w^+ &= E\{xg(w^T x)\} - E\{g'w^T x\}w \\ w &= \frac{w^+}{\|w^+\|} \end{aligned} \quad (8)$$

That is iterated in a fixed number of iterations or until it converges to an optimal solution. The w^+ is the new weight vector estimated after each iteration. g and g' are the first and second order derivative functions of the cost function G .

E. Sequential Extraction of Components

The optimization of the cost function, depending on the number of independent components, results in a number of unmixing coefficients or weight vectors. The vectors are estimated sequentially and each one is orthogonalized with the previous ones using the Gram-Schmidt orthogonalization method. The sequential extraction of the weight vectors is based on the vector rejection technique that is also referred to as *deflation* and is defined as:

$$w_n^\perp = w_n - \text{proj}_{w_1}(w_n) - \text{proj}_{w_2}(w_n) - \dots - \text{proj}_{w_{n-1}}(w_n) \quad (9)$$

$w_n^\perp$ is an orthogonal vector rejected from the previous vectors where $\text{proj}_{w_{n-1}}(w_n)$ is the projection of w_n onto a line spanned by w_{n-1} .

F. Components Ordering

The unmixing coefficients are a set of orthonormal vectors in a multi-dimensional space that transform the mixed signals into some signals that are expected to be maximally independent. The estimation process of the source signals, however, does not indicate the sign, scale or order of the actual source signals. This will generally lead to an ordering and scaling problem in cases such as here where the signals

are partially estimated at each $t + \tau$. At each step, a number of components need to be correctly linked to the former ones. In order to address the ordering and scaling issues, the correlations (*Pearson correlation* [19]) between mixing coefficients were evaluated at each $t + \tau$ step and at the end the extracted components were normalized globally. The correlation coefficients of the mixing weights were evaluated as follows:

$$r_{A_{t-\tau}, A_t} = \frac{E[(A_{t-\tau} - \bar{A}_{t-\tau})(A_t - \bar{A}_t)^T]}{\sqrt{E[A_{t-\tau}]^2} \sqrt{E[A_t]^2}} \quad (10)$$

$r \in \mathbb{R} : -1 \leq r \leq 1$

The r values are compared at each step where the largest positive value indicates stronger correlation. The mixing weights that have the strongest correlation with the preceding weights are chosen to form the final mixing vector. The negative r values, however, mean anti-correlation and in the cases that the largest values between the current and the previous weights are negative the current mixing weights are inverted so that their relationship can be described in terms of correlation rather than anti-correlation.

G. 1-D Independent Components to 2-D spatial Data Transformation

The final stage of the STICA is to transform back the identified 1-D ICs to their original 2-D spatial domain. This is achieved by forming columns and rows from the elements of the components. That is inverting the process in II-B:

$$x(t)^{1D} = x(t)^{1 \times mn} \rightarrow x(t)^{2D} = x(t)^{m \times n} \quad (11)$$

III. IDENTIFIABILITY AND SEPARABILITY

It is assumed that the original physiological signals are linearly mixed. This instantaneous mixing process is defined as $X^n = A^{n \times m} S^m$, where X denotes the observation vector, S is a vector of latent variables (i.e. unmixed source signals) and A is a full column rank matrix defining the instantaneous mixing process. n and m : ($n \geq m$) denote the number of observation and source signals respectively. Both S and A are unknown, however, they belong to an identification space $(A, S) \in \mathbb{I}$ [20], that has some unique properties such as particular waveforms e.g. quasi-sinusoidal breathing waveform or mixing channel characteristics e.g. device noise. The estimated components however, may not be exactly the same as original components as described by the identification space $\mathbb{I}$ in the sense that they satisfy certain properties of $\mathbb{I}$ under the relationship, $\mathbb{R}$, while may also have some ambiguities, for instance, column permutation or scale factor of $A^{n \times m}$. This relationship between the identified space and the original space is defined as $\{(\hat{A}, \hat{S}) \in \hat{\mathbb{I}}\} \mathbb{R}\{(A, S) \in \mathbb{I}\} \rightarrow (\hat{\mathbb{I}} \cap \mathbb{I})$. Here in order to minimize the permutation ambiguities and to reduce the effect of noise on the mixing model the data space dimensionality was further reduced from $\approx 99.9\%$ to $\approx 98\%$ which included the five largest eigenvalues and was possible to estimate up to five ICs.

IV. REGIONAL ANALYSIS

Regional analysis was performed using number of ROIs for the estimated components (see Fig.2 as an exemplar). From all the estimated components there were at least three ICs for every volunteer that appear to have distinct physiological characteristics such as breathing, renal perfusion and filtration (similar to $K(t)$ derived in the Patlak method [8]). The smoothness of the derived curves, representing perfusion and filtration, indicates that there is no detectable movement. To compare the the results of STICA with the original spatial data, the IC curves resembling renal filtration were quantified using the Rutland-Patlak method [8], [21] defined as:

$$\frac{k(t1)}{b(t1)} = K1 \frac{\int_0^{t1} b(t)dt}{b(t1)} + K2 \quad (12)$$

Where $k(t)$ and $b(t)$ represent the renal ROI curve and arterial input curve respectively. $K1$ denotes the gradient of the regression line which is proportional to renal filtration and $K2$ denotes the regression offset which is proportional to the size of compartment one (blood vessels). The estimated $K1$ from the Patlak method were compared with the gradient of the IC curves (ICG) for three different ROIs (see Fig.3) The higher r^2 values in ICGs suggested a more accurate curve fitting across all subjects left and right kidney. The standard deviations evaluated for $K1$ s and ICGs for all ten subjects showed less dispersions (see Fig.4) which suggests that the ROI selection does not affect the filtration quantification in comparison an analytical method such as Patlak.

V. DISCUSSION AND CONCLUSIONS

A novel approach to motion artefacts correction in renal DCE-MRI, using a spatio-temporal ICA method, is presented. The STICA was applied to 10 healthy volunteers' DCE data to remove the motion artefacts as an independent process as well as separating out other independent processes. The estimated components are maximally independent and represent the major components of the original signals. This is based on the main assumptions of statistical independence and non-Gaussianity. Quantitative assessment using ROI analysis showed virtually no movement in either the first IC (Fig.2 b) that resembles filtration, or the second IC (Fig.2 c) that resembles perfusion. The third IC (Fig.2 d) shows the respiratory movement but may well contain other components such as noise. The gradient of the first IC curve was evaluated and compared with the Patlak method for all volunteers using three different ROIs (see table I). The standard deviations (Fig.4) and r^2 values for both Patlak $K1$ s and ICGs showed a more accurate and reliable evaluation of filtration when using IC curves. The application of STICA in renal DCEMRI is useful as it can be applied to a large number of datasets without a priori knowledge, to remove the movement artefacts and may represent significant proportions of single kidney perfusion and filtration.

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