# Independent component analysis of dynamic contrast-enhanced magnetic resonance images of prostate tumours

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## Introduction:

Independent component analysis (ICA) is a data-driven statistical technique that has been successfully applied for exploratory analysis of functional MRI (fMRI) data to extract spatially independent patterns or functional maps of task-related activation sources in the brain (Mckeown et al 1998). Analogous to an fMRI dataset, various regions on dynamic contrast-enhanced (DCE) MR images that are enhanced differently by the arrival of contrast medium can be regarded as 'source locations' with 'activation' time profiles depicted by the corresponding contrast enhancement behaviour. DCE MRI studies have shown that the prostate cancer typically enhances more rapidly than the peripheral zone and commonly exhibits a 'washout' enhancement behaviour.

#### Aim'

To extract tumour component maps from prostate DCE MRI datasets corresponding to a washout enhancement behaviour for comparison with histology.

## Materials and Methods:

Five prostate DCE MRI cases with histology comparison were processed with ICA. DCE MRI was performed on a 1.5T MR unit (Philips Intera R9.0) with 4 channel body array coil using an axial fast three-dimensional Spoiled Gradient-Recalled echo (3D SPGR) sequence planned on the prostate. Scan parameters were: TE = 1.31ms, TR = 3.9 ms, flip angle = 10°, 8 slices per slab, 150 post-contrast acquisitions at temporal resolution of 4 s. Gadodiamide was injected at a dose of 0.3 mmol/kg, using an automatic injector and at a rate of 5 ml/s. Only the central 6 slices were processed. Following DCE-MRI imaging a prostatectomy was performed within 1 week on the imaging study. At prostatectomy the gland was sectioned transversely and both fresh slices and stained whole-mounts (latter with histologically-defined tumour outines) were photographed.

A spatial ICA approach similar to those applied on fMRI images (Mckeown et al 1998) was implemented on the DCE MR images. For a series of T (=150) dynamic MR images, a T-by-M matrix X is constructed, where M (=256×256) is the number of voxels in each image, such that each row in X contains the spatial (image) information sampled at a particular time point. Assuming that X can be expressed as a linear generative model X = AC, where the mixing matrix A (T-by-M) and the component matrix C (N-by-M) are unknown, the spatial ICA approach attempts to arrive at solutions for C = WX, by appropriately selecting the unmixing matrix W such that the components (rows) in C are mutually (statistically) independent of each other. The FastICA algorithm which implements a fast fixed-point iteration scheme (Hyvärinen 1999) was used. Each independent component (IC) in C can be expressed as a linear generative model C can be reverted back to a spatial image or IC map, and the columns in C (or C is the time courses of activation for the IC maps. The usual ICA preprocessing steps of centering (i.e subtracting the dataset C by its mean) and whitening (a linear transformation of C such that the resulting components have unit variance and are uncorrelated) were applied before performing FastICA.

### Results and Discussion:

ICA extracts spatial component maps corresponding to a few consistent enhancement profiles within the prostate DCE MRI datasets: (i) gradual enhancement with/without plateau, (ii) rapid enhancement with washout, and (iii) accumulation of tracer in the bladder. The other ICs generally pertain to noise and movement artifacts. Previous studies have indicated that the washout signal-time profile could be highly associative with malignant tumours while the plateau signal-time profile could be associative with benign hyperplasia or normal glandular kinetics, although there were occurrences of

