Perfusion indices such as Cerebral Blood Volume (CBV), Cerebral Blood Flow (CBF), and Mean Transit Time (MTT) are calculated based on the temporal response of the MR signal to the administered contrast agent. Since the temporal response is altered in the case of brain pathology, CBV, CBF, and MTT are good indicators of compromised regions.

Segmentation of perfusion images allows CBV, CBF, and MTT to be evaluated per tissue type.

Independent Component Analysis (ICA) applied to perfusion data, differentiates tissue types based on their temporal response: GM, WM, and CSF responses are distinct. Hence ICA can serve as a segmentation technique. ICA can also independently identify pathology since the analysis is based on the temporal response.

**MATERIALS & METHODS**

**Imaging:** Acquisition during pre and post Gd-DTPA injection using EPI on a 1.5 T MRI system.

**Perfusion analysis** was conducted using the MEDx Perfusion module (Sensor Systems).

**Signal time courses** i.e. susceptibility curves were converted into concentration curves. Concentration curves were fitted to gamma variates and evaluated for arterial contribution.

**The arterial input function (AIF)** was deconvolved from the concentration curve using SVD to determine the residue function, the maximum amplitude of which is CBF (1). Area under the concentration curve was normalized by AIF to determine CBV (2). MTT=CBV/CBF.

**ICA** (3, 4) was conducted with the MELODIC ICA tool (5) using a latent variables model of the time courses:

\[ x(0) = \sum a(k) s(k) + e(0) \]

\[ X = AS + e \]

For the number of ICA components, in general Bayesian model selection was applied to a probabilistic PCA model (6). PCA can express high-dimensional data in terms of lower dimensional data + noise. The latent variables model was viewed as a maximum-likelihood estimation PCA model (6, 7). The eigenvalues of the covariance matrix \( C = AA' + C_n \) were then calculated to obtain posterior probability of the data to form MAP estimates of the rank of A. Other criteria used were Bayesian information and minimum description length.

**RESULTS**

ICA conducted on perfusion concentration data was capable of identifying subtextures within the region of stroke.

In normal brains, ICA segmented WM and GM. The thresholded ICA segmentation results could then be used for masking to obtain average regional perfusion parameter values.

**DISCUSSION**

The information provided by ICA is uniquely determined by the number of ICA components. After extracting the essential information with a few dominant components, mostly Gaussian noise remains. From then on, extraction of non-Gaussian ICs in a Gaussian environment makes the results dependent on initial conditions. Thus spurious maximum likelihood solutions may arise due to the under-determined nature of the problem. The total number of components was most reliably estimated via Minka’s method.

In the presence of gross anomalies of the brain, ICA was not successful as a segmentation technique. However, it could detect gradations within such regions. In the stroke case, the extent of the stroke could be much better appreciated with ICA analysis compared to perfusion results. The component with a timecourse resembling a concentration curve further identified viable regions within the stroke while pointing to regions of similar signal intensity at the back of the brain.

In conclusion, ICA conducted on perfusion susceptibility or concentration data, can provide additional information, especially in brains with clinical anomalies. The existence of a segmentation component only exists in normal cases.

**REFERENCES**

5. FSL - FMRIB’s Software Library