Abstract

ASL fMRI data provides a quantitative measure of blood perfusion, that can be correlated to neuronal activation. In contrast to BOLD fMRI, it is a direct and closer to neuronal activity measure. However, ASL data has a lower SNR and resolution. We aim at using both signals advantages to improve the estimation of the response functions.

Model

In a given parcel \( P \), the generative model for ASL time series, with \( M \) experimental conditions, reads \( y_j \in \mathbb{C}^P \), with \( |P| = J \):

\[
y_j = \sum_{m=1}^{M} \alpha_m \omega_j + \beta_j
\]

where \( \alpha_m \) is the perfusion component and \( \beta_j \) is the BOLD component. The perfusion component is defined as:

\[
PRL = \sum_{m=1}^{M} \alpha_m \omega_j + \beta_j
\]

Physiological link between BOLD and ASL signals

The system of ordinary differential equations is linearized, as Khalidov et al. did in [6], to obtain a physiologically-inspired linear operator that links the BOLD or Hemodynamic Response Function (BRF or HRF) to the Perfusion Response Function (PRF).

\[
\mathbf{h}(t) = \mathbf{B}(t) \mathbf{g}(t)
\]

Model estimation and first results

Step M1: Hemodynamics estimation, by filtering out the perfusion component (i.e. \( \mathbf{C} = 0 \)). The ASL signal and the residuals \( r \) read:

\[
y_j = \omega_j \sum_{m=1}^{M} \alpha_m \omega_j + \beta_j
\]

Step M2: From \( r \), the perfusion component is extracted by using the HRF estimated previously in step 1 (i.e. \( \mathbf{B} = \omega_j \sum_{m=1}^{M} \alpha_m \omega_j + \beta_j \)).

Conclusion

ASL fMRI data analysis has been performed by considering a physiological link between the CBF and BOLD components embedded in the ASL signal, which allows to retrieve more physiologically plausible PRF and HRF shapes.

Perspectives

- Deeper analysis of the validity of the link between PRF/HRF.
- Quantification of ASL fMRI data.
- Larger validation (on whole brain analysis), and BOLD/ASL comparison on the same experimental paradigm and the same individuals.

References