Examining the relationship between cerebral blood flood and grey matter structure in typically developing children

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Purpose

We will use pseudo-continuous arterial spin labeled (pCASL) MRI to measure cerebral blood flow (CBF) and identify the amount of CBF variance explained, both voxel-wise and globally, by tissue microstructure as measured by structural MRI.

Methods

Images were acquired for 61 normally developing children aged 7-17 years. For each subject, pCASL images were acquired [1] along with T1-weighted and diffusion tensor images (DTI). A subset of the data (n=30) was used to create a population specific templates for each of the modalities using ANTs [2]. The pCASL and DTI templates were then aligned to the T1-template to create a single multi-modality reference space. The T1 template then served as the basis for multi-atlas labeling using publicly available data sets of whole brain [3] as well as three tissue segmentation [4]. Each image for each subject was then aligned to the corresponding component of the multi-modal template for brain masking. Intra-subject registration is then used to align all of the brain-masked images for a given subject to the T1 image.

Each subject's T1 image was used to obtain a probabilistic three tissue segmentation using Atropos [2] and a voxel-wise measure of cortical thickness [5]. The DTI images were used to calculate fractional anisotropy (FA) and mean diffusion (MD), while the pCASL data was used to calculate CBF. Finally, the intra-subject warps were composed with the T1 subject-to-template warps to align all images into the common template space. In order to examine the extent to which structural MR measures influence cerebral blood flow as measured by pCASL, **R** was used to perform voxel-wise linear regression for all voxels in the gray matter according to:

Full Model : CBF ~ $\beta 1 * \text{Prob(gray matter)} + \beta 2 * \text{Prob(white matter)} + \beta 3 * \text{Thickness} + \beta 4 * \text{FA} + \beta 5 * \text{MD}$

Additionally, we examine how each measure relates the CBF variability by initially limiting the model to the probability of gray matter and then adding each factor to the model in a step-wise manner.

Results

The average r-squared values for each model are listed in table 1. To visualize the performance of each model, the R-squared value for the linear regression at each voxel was used was created an image as illustrated in Figure 1.

Conclusions

In all models, the highest R-squared values were found along the gray-white border and superior cortical regions tended to have hihger R-squared values than more inferior regions. The addition of metrics derived from DTI improved the fit over models 1-3 that relied upon metrics derived from T1 images only, however there remains a great deal of variance in the CBF signal that does not appear to be directly determined structural properties of the tissue.

Model	*Mean R-Squared*
1) GM	0.0415 +/- 0.0572
2) GM + WM	0.0798 +/- 0.0809
3) WM + WM + Thickness	0.1004 +/- 0.0859
4) WM + WM + Thickness + FA	0.1213 +/- 0.0904
5) WM + WM + Thickness + FA + MD	0.1403 +/- 0.0925

References

1. Jain, et. al. Radiology. 263(2)
2. http://www.picsl.upenn.edu/ants
3. Shattuck, et. al. NeuroImage 39(3)
4. http://www.nirep.org
5. Das, et.al. NeuroImage 45(3)

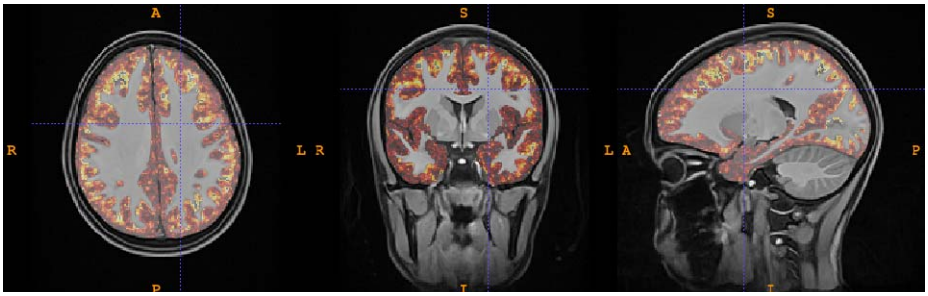

Figure 1. R-Squared map for model 5