Examining the relationship between cerebral blood flow 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:

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\text{Full Model : } CBF \sim \beta_1 \ast \text{Prob(gray matter)} + \beta_2 \ast \text{Prob(white matter)} + \beta_3 \ast \text{Thickness} + \beta_4 \ast \text{FA} + \beta_5 \ast \text{MD}
\]

Additionally, we examine how each measure relates to 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 higher 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 | References
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1) GM | 0.0415 +/- 0.0572 | 1. Jain, et. al. Radiology. 263(2)
2) GM + WM | 0.0798 +/- 0.0809 | 2. http://www.picsl.upenn.edu/ants
3) WM + WM + Thickness | 0.1004 +/- 0.0859 | 3. Shattuck, et. al. NeuroImage 39(3)
4) WM + WM + Thickness + FA | 0.1213 +/- 0.0904 | 4. http://www.nirep.org
5) WM + WM + Thickness + FA + MD | 0.1403 +/- 0.0925 | 5. Das, et.al. NeuroImage 45(3)

Figure 1. R-Squared map for model 5