CBF-based Modular Architecture Derived from ASL MRI

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Introduction

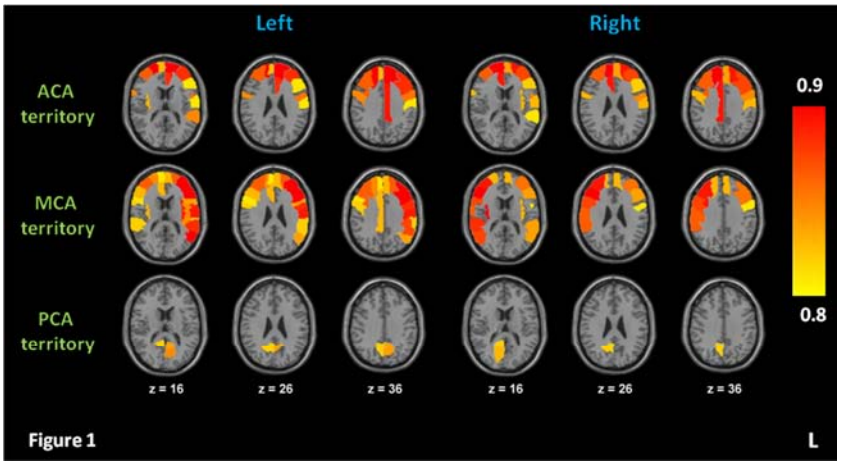
The connectional architecture of the human brain, referred to as the "connectome", is fundamentally important in cognitive neuroscience and neuropsychology [1]. Most studies have focused on investigating the hemodynamic consequences of neural activity using blood oxygenation level dependent functional MRI during stimulation or resting state. Arterial spin-labeling (ASL) MRI is a non-invasive method of perfusion imaging, characterized by cerebral blood flow (CBF), and could be used to map neural activation during task condition [2] and resting [3]. Recently, the structure-based modular architecture derived from cortical thickness measurement could demonstrate the large-scale anatomical connection patterns in the brain [4,5]. Based on the previous study, this study aimed to investigate the CBF-based modular architecture derived from ASL MRI for the bilateral anterior, middle, and posterior cerebral artery (ACA, MCA, and PCA) territories, and default mode network (DMN).

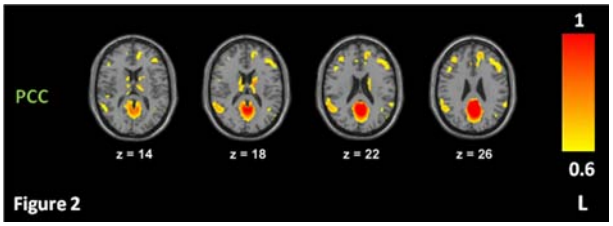
Methods

A total of 116 healthy subjects (33 females, age ranged 19-59 yrs, 36.9 ± 11.2 yrs) participated in this study, where were taken from the CBFBIRN Database. Whole-brain CBF maps were acquired at a 3T whole body imaging system using a standardized 2D single shot FAIR protocol with presaturation pulses and QUIPSS II post-inversion saturation pulses (TR/TE = 4000ms/3 ms for GE (spiral readout) or 12ms for Siemens (partial Fourier EPI readout), TI1/TI2 = 600ms/1600ms, FOV = 220mm x 220mm, slice thickness = 5mm, 24 axial slices, 104 volumes) [6]. The raw image data from all subjects were uploaded to the CBFBIRN Database & Analysis Pipeline, which was used to generate the individual CBF maps in physiological units of mL blood/100g tissue-min [6]. For the ROI-based analysis, the individual CBF map within the entire cerebral cortex was extracted based on the subject-specific gray matter mask and then parcellated into 90 regions using the automated anatomical labeling (AAL) template [7]. Individual CBF maps from all subjects were concatenated to from a 4D file, which was used to compute the correlation coefficients (r) between each area in the AAL template and the seed region such as bilateral ACA, MCA, and PCA territories. For the seed-based correlation analysis, the native CBF maps were normalized to MNI space, smoothed with a 6mm Gaussian kernel using SPM8, and detrended using REST (http://resting-fmri.sourceforge.net). The preprocessed CBF maps from all subjects were concatenated. A spherical seed ((2, -51, 27); radius = 4 mm) within the posterior cingulate cortex (PCC) region was defined based on a previous study [8]. The resultant r map was acquired by correlating the seed region and every other voxels in the brain and then transformed to approximate Gaussian distribution using Fisher's z transformation.

Results

Figure 1 shows the CBF modular architecture for the bilateral ACA, MCA, and PCA territories from the concatenated subjects' CBF map. The CBF modules for the unilateral ACA territories have better short-range connections with the bilateral ACA regions and better long-range connections with several bilateral MCA regions, especially in the contralateral insula. The CBF modules for the unilateral MCA territories have better short-range connections with the ipsilateral MCA regions and better long-range connections with bilateral ACA and several contralateral MCA regions. The CBF modules for the unilateral PCA territories have less short- and long-range connections with other regions and more intra-regional variation within the PCA regions. In addition, the symmetric connections between bilateral brain regions are: ACA > MCA > PCA. Figure 2 shows the CBF modular architecture for the PCC region from the concatenated subjects' CBF map. The CBF module for the PCC region has better short-range connections with the PCC and precuneus regions and better long-range connections with the medial prefrontal cortex and bilateral inferior parietal lobules.





Conclusion

This study found the patterns of CBF variations in the bilateral ACA, MCA, and PCA territories, and DMN among 116 subjects. This is probably due to the characteristics of blood vessels, such as neurovascular coupling, autoregulation and vasoreactivity. This study provides a preliminary result of intrinsic CBF modularity of the human brain.

References

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