

ASL-MRICloud: Towards a comprehensive online tool for ASL data analysis

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Introduction:

To accommodate a surging interest in ASL in research and clinical community, we launched a cloud-based tool for ASL data analysis under the infrastructure of MRICloud.org[1-3]. Compared with other existing ASL toolboxes[4-9], which are based on local computing, ASL-MRICloud relies on a web interface for uploading data and downloading results, providing a fully automated interface to end users. The availability of the T1-based brain segmentation tool in MRICloud platform also allows region-specific quantitative reports of ASL-

derived parameters. This abstract provides a summary of its current functionalities, main algorithms underlying the pipeline, and representative results.

Methods:

Data upload: Raw ASL data can be uploaded on our website (Fig. 1a, Ref. 10) using any mainstream browsers. At present, ANALYZE files are the accepted format. DICOM and other PHI-containing files must be converted and de-identified due to HIPAA regulations. Our website provides a downloadable software for DICOM-to-ANALYZE conversion.

ASL processing: The ASL-MRICloud accepted Continuous/pseudo-continuous and Pulsed ASL datasets. The user is asked to select or type in the following imaging parameters that are relevant for perfusion kinetic modeling: labeling scheme, control/label order, acquisition scheme, labeling duration, post-labeling delay, background suppression, etc. Then the user can click the "submit" button and the job will be placed in a processing queue on the cloud server. CBF quantification follows models described in the ASL white paper[11].

M0 in CBF quantification: There is an optional button to upload an M0 image, which provides a voxel-by-voxel M0 map for CBF quantification. If an M0 image is not uploaded or the dimension of the M0 image does not match that of ASL data, then a global M0 is obtained from averaging all voxels in the ASL image or the M0 image and used for all voxels in the brain.

Spatial registration/normalization: To allow registration of the CBF image to T1-anatomic image and MNI-space, an optional button is available to upload a composite file generated from the T1-based brain segmentation tool in MRICloud platform. ASL images will then be automatically registered to individual T1 and normalized to MNI space.

Outcomes include absolute and relative CBF maps in each of the following spaces: ASL space, T1-MPRAGE space, and MNI space. ROI values will also be obtained from T1-atlas. Three sets of ROIs values can be obtained depending on how fine one wishes to divide the brain.

Quality control (QC): Two QC indices are included as part of the downloadable outcomes. One is a single number indicating the general SNR of the data, from 1 (Excellent) to 4 (Poor), that is based on standard error of the voxel-wise CBF map across measurements. The second index is a voxel-wise mask indicating potential hyper- and hypo-perfusion regions. In establishing what is normal and what is hyper(hypo)-perfusion, we used a large CBF database consisting of 309 healthy volunteers ranging from 20-89 years old[12]. A Z-score was calculated for each voxel, and a p-threshold of 0.005 was used to delineate voxels with abnormal CBF.

Results:

Figure 1b shows voxel-wise CBF maps generated by the ASL-MRICloud. In Figure 1c, three levels of parcellation and their corresponding regional CBF values are presented. We validated QC index 1 by comparing it to a manual rating conducted by an experienced ASL researcher (Fig. 2a left panel). A strong correlation ($r=0.82$) was observed. Figure 2a right panel shows representative image for each of the 4 QC categories. Figure 2b shows an example of abnormality detection in a patient with Moyamoya disease, in whom both hypoperfusion (due to ischemia) and apparent hyperperfusion (due to delayed bolus clearance) are present.

Conclusions:

ASL-MRICloud may be a useful tool for ASL-MRI data analysis in clinical and research settings.

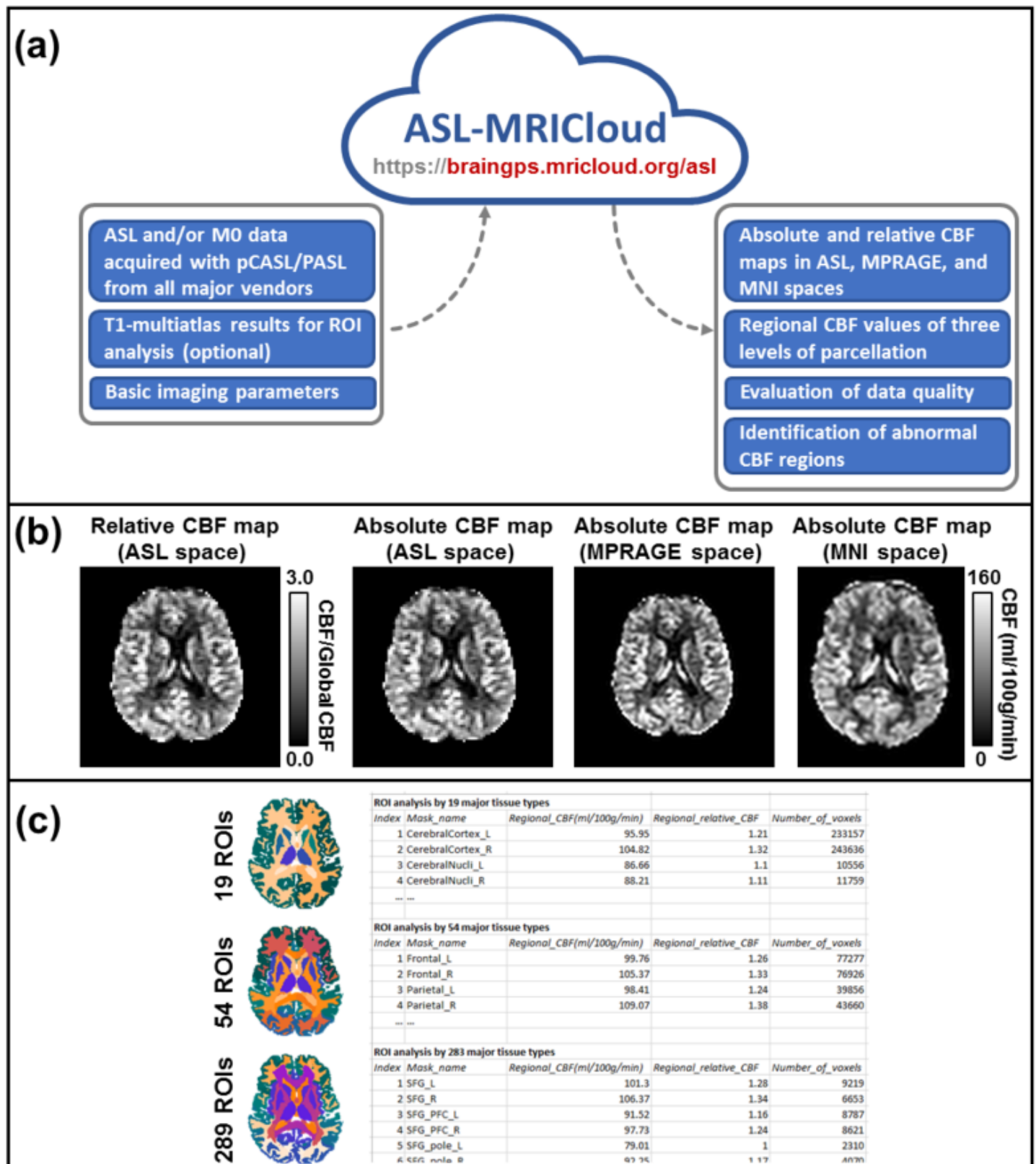


Fig. 1. (a) Illustration of the workflow of ASL-MRCloud. ASL and/or M0 data, along with T1-based segmentation results are uploaded to the cloud server. The ASL-MRCloud generates a comprehensive analysis results in minutes, and then a file package is ready for download. **(b)** CBF maps in multiple spaces generated by the ASL-MRCloud from one representative subject. **(c)** Three levels of brain parcellations and their corresponding ROI-specific CBF values. Number of voxels within each parcellation are also included in the results.

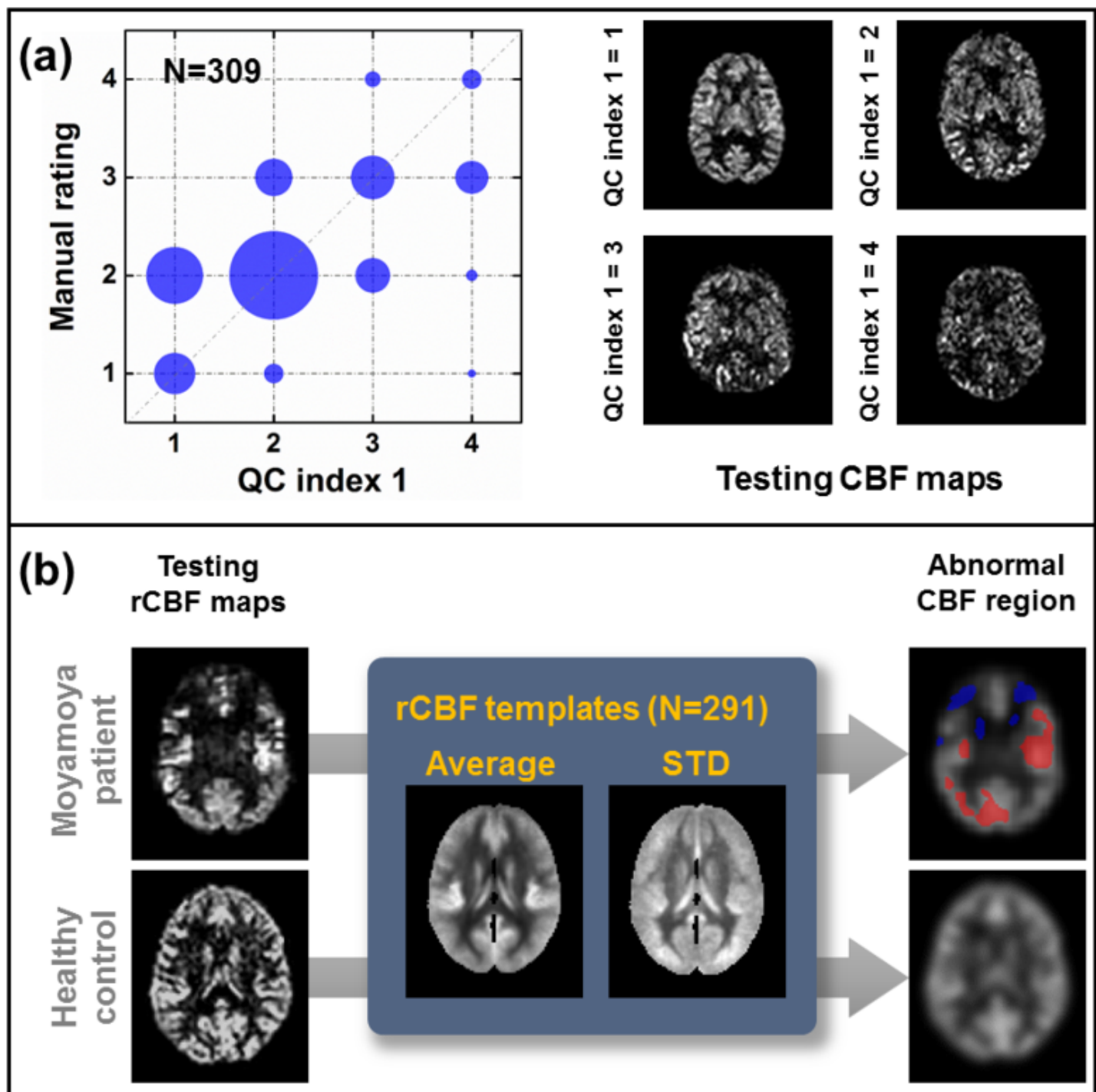


Fig. 2. (a) Left panel, Scatter plot of manual ratings and quality control (QC) index 1 on 309 ASL datasets (circle area is proportional to the number of datasets). QC index 1 was generated based on standard error of the voxel-wise CBF map across measurements. **Right panel**, Four testing CBF maps with their corresponding QC index 1. **(b)** Identification of abnormal CBF regions. Middle panel shows the mean and STD images of the 291 out of 309 relative CBF (rCBF) maps (that have manual rating < 4) from the database. After the rCBF map is generated from uploaded ASL data, its Z-score map is calculated based on these templates. The voxels with extra high/low Z-scores are detected, labeled as red/blue respectively. Here two rCBF maps are shown for example, one is from a patient of Moyamoya disease, and the other is from a healthy control.

Informatics:

Brain Atlases ²

Physiology, Metabolism and Neurotransmission :

Cerebral Metabolism and Hemodynamics ¹

Keywords:

Cerebral Blood Flow
Data analysis
FUNCTIONAL MRI

¹²Indicates the priority used for review

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