Performance Analysis of the Inline Quantitative Cerebral Perfusion Measurements with MR

A. Sen[1], S. Maheshwari[1], J. J. Mouannes[2], C. Eddleman[3], S. Zuehlsdorff[4], S. Shah[4], and T. J. Carroll[1,2]

[1]Radiology, Northwestern University, Chicago, IL, United States, [2]Biomedical Engineering, Northwestern University, Chicago, IL, United States, [3]Neurological Surgery, Northwestern University, [4]CMR Research and Development, Siemens Healthcare, Chicago, IL, United States

Introduction

The American Heart Association has deemed the quantification of cerebral perfusion in stroke to be of paramount importance. Fast, accurate and automated determination of perfusion image maps is essential for analyzing tissue at risk after an ischemic stroke event [1,2]. The need for offline post-processing of Dynamic Susceptibility Contrast (DSC) images can delay the availability of time critical information (i.e. the extent of the perfusion diffusion mismatch predicts the response to intra venous thrombolysis in ischemic stroke). Therefore we have developed an inline protocol to eliminate the offline, time-consuming generation of perfusion maps.

Currently, offline post-processing of DSC images requires specially trained personnel, additional workstations and introduces an unwanted delay in the generation of critical images. A reproducible, reliable and accurate method for producing quantitative values of cerebral perfusion using the parenchymal T1 changes has been developed [3-8] and validated [6]. Under normal circumstances, offline MR perfusion post-processing takes on average over >60min to generate quantitative cerebral blood flow (qCBF), quantitative cerebral blood volume (qCBV), and mean transit time (MTT) maps. In response, we developed and validated an inline software tool that has eliminated the offline post-processing steps and the associated latency between MR data acquisition and generation of quantified perfusion maps. Colormaps of qCBF, qCBV, and MTT are generated without additional personnel or workstations. Furthermore, this inline protocol reduces the inter- and the intra-operator variability. Time efficiency has been quantified by comparing our inline protocol with the clinical standard methods in a routine setting. The short 3 to 4.5 hour therapeutic window for administration of IV thrombolytic agents in the treatment of ischemic stroke underscores the need for a fast, reliable and reproducible post-processing system.
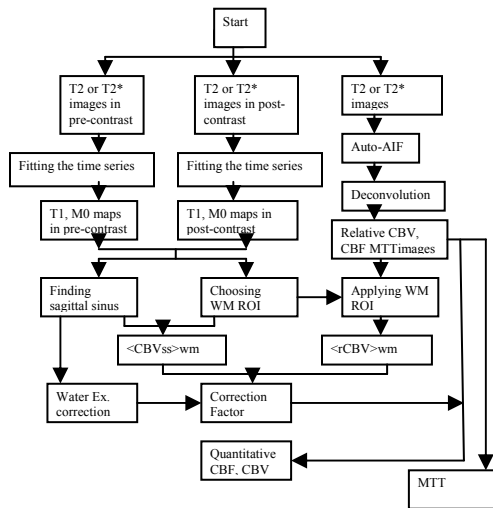

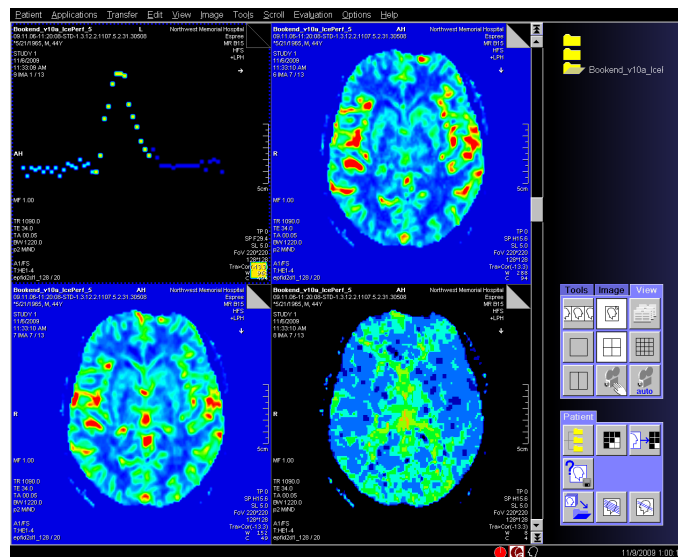Figure 1. Post-processing flowchart to determine the perfusion parameters.

Figure 2. The screen shot from a workstation which show the typical perfusion parameter maps after inline post processing. The top left and right screen images show the AIF time series and the qCBF parameter map, respectively. The bottom left and right screen image represents the qCBV and the MTT parameter maps, respectively.

Materials and Methods

The inline production and evaluation of perfusion images was fully integrated into the Siemens Image Calculation Environment (ICE) of both clinical 1.5 and 3T scanners (MAGNETOM Espree and Trio, Siemens AG Healthcare Sector, Erlangen, Germany). Figure 1 flowcharts the algorithm used to automatically calculate qCBF, qCBV, and MTT maps. A standard DSC gradient echo EPI scan was modified to include both T1 and T2* contrast weighting [9]. The inline post-processing involves three ICE functor modules, which are inserted in succession to the reconstruction of magnitude images. The post-processing steps closely follow the standard offline method as outlined in Figure 1. The unsupervised algorithm integrates automated selection of the arterial input function (AIF) [3] and performs a voxel by voxel deconvolution analysis [4], followed by T1 mapping, and water exchange correction before the perfusion maps are generated and stored as standard DICOM images in the database. A representative result is shown in Figure 2. The differences between the inline and offline protocol are in the implementation of the deconvolution and the fitting algorithms. Accuracy of this inline protocol was evaluated by comparing the images of qCBF and qCBV with the standard offline method. A series of images acquired in 19 subjects were compared under Siemens simulation environment to show the similarity of the inline results with the offline, for this IRB approved study. Offline post-processed images calculated using MATLAB (The Mathworks, Inc., Nantick, PA) served as a reference standard. Every image is divided into a grid with boxes of size 8x8 pixels. The mean value for each square box of an inline image within the volume of the head is matched to the corresponding value from the offline processed image. Thus the inline protocol results of qCBF and qCBV were verified by correlating with the standard offline protocol results.

To quantify time efficiency, duration was compared between the automatic map calculation and the conventional clinical workflow of typical patients for imaging. The conventional clinical workflow involves offline downloading of patient's data, followed by offline processing and generation of the maps, before uploading them to the PACS workstation for viewing. In a retrospective analysis, we quantified the time efficiency in a consecutive series of 56 patients, scanned as part of the standard care at our institution. The delay between image acquisition and PACS deposition served as an estimate of image availability latency (IAL). The data for IAL was retrospectively collected over a span of 6 months, by monitoring patients who were treated using the standard supervised offline post processing, at our treatment care facility in CAMRI.

Results:

In all cases, reconstruction time for inline quantified perfusion map generation was less than 60 sec after the completion of image acquisition (IAL < 1 minute). In comparison, we found the standard of care post-processing protocol resulted in an IAL of 118 ± 253 minutes. The results of perfusion maps are automatically displayed in color after the processing is complete (Figure 2). After comparing the two methods, the average slope with correlation was 1.04 ± 0.12, r=0.98 for qCBF and 0.9 ± 0.05, r= 0.93 for qCBV. The average was obtained over 19 data sets.

Discussion

The results indicated that quantitative inline image reconstruction protocol maps are as reliable and accurate as the offline system. Further, the inline protocol also eliminated the IAL inherent in the current paradigm for the stroke imaging. This inline perfusion processing protocol can significantly reduce the time required for treatment decisions in stroke patients, which has been shown to improve patient outcomes by eliminating the post-processing delay.

References

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