MR Phase-Contrast Imaging with Automatic Inline Flow Quantification and Visualization

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Introduction: Typically, MRI flow measurements require loading acquired 2D CINE phase-contrast (PC) data into a post-processing application to perform flow analysis. We present an automatic inline flow processing method for analysis of 2D PC MRI directly at the scanner. Our method has a simplified workflow which processes reconstructed flow images at the scanner for background phase correction, dynamic vessel segmentation, flow quantification and visualization, and produces final results as DICOM outputs for viewing. Our proposed method substantially reduces the complexity and time required for flow analysis and brings accuracy improvements to the scanner.

Materials and Methods: ***1) Acquisition:*** Data were acquired at 1.5 and 3T (MAGNETOM Aera & Skyra, Siemens, Erlangen, Germany) in 9 adult volunteers and 4 pediatric aged patients using a standard ECG-triggered 2D PC sequence. The 2D PC acquisition plane was defined to be perpendicular to the target vessel and the table position was adjusted to have the target vessel at isocenter. In order to maximize the static tissue to be used in the background phase correction, the FOV was defined to avoid wrap-around artifacts. The operator also provided a seed point to indicate the target vessel. ***2) Inline processing****:* The inline flow processing prototype was integrated in the MR scanner's image computing environment (ICE) platform and executed at the end of image reconstruction. It was fully automatic and included static tissue detection, first-order background phase correction, dynamic vessel segmentation, comprehensive flow quantification, velocity color overlay and vector rendering. Final quantification and visualization results were produced as several DICOM series. The background phase error was corrected by first determining static tissue pixels in the image based on adaptive thresholding of the temporal variance of magnitude, PC and PC angio components of flow data and then fitting a plane to static tissue velocities using orthogonal regression. The single seeded vessel segmentation builds on a previous work [1] based on finding minimum cost cycle in a graph using mean-shift edge responses. While the technique in [1] is robust with sub-voxel accuracy and efficient runtime, its sensitiveness to the input seed point location impacts its reproducibility. In this work a local refinement step using banded graph-cuts optimization to compute an image specific vessel seed point was incorporated. Specifically, an initial boundary of vessel was first obtained using [1] at input seed point (Fig 1a). Then a banded 4-connected grid graph around this initial boundary with edge weights from local image gradients was constructed and the minimum cut via a max-flow algorithm [2] computed (Fig 1b). The final boundary was extracted by running the same method [1] but using the center of the minimum cut as a seed point (Fig 1c). The vessel was segmented at a reference time frame corresponding to peak contrast around input seed point and then propagated across the entire time sequence using a deformable registration [3]. The flow visualization included color coded signed velocity and velocity magnitude images as well as vector rendering of the velocity. The comprehensive flow quantification included peak velocity, average velocity, average flow, flow volume (forward, backward, net), and area (average, minimum, maximum).

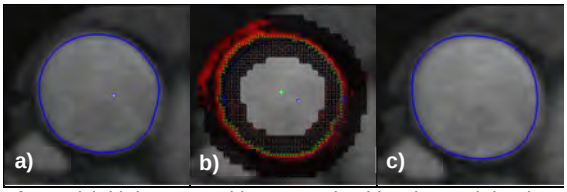

Fig. 1 a) initial contour, b) our graph with edge weights in color (black-red: high-low), minimum cut (green points) and its center (green-white point), c) final contour

Results: The technique was successfully evaluated in all subjects for a total of 36 vessels. The automatic static tissue detection and background phase correction were successful in 34/36 vessels. The automatic segmentation was successful in 30/36 vessels. Inline PC correction, segmentation, visualization and quantification images are given for one representative vessel in a pediatric patient in Fig. 2.

Discussion: An inline flow processing method that allows automatic quantification and visualization of 2D PC-MRI datasets was presented. By defining the target vessel location prior to the acquisition, it is possible to 1) bring the acquired vessel to the isocenter and 2) perform an automatic segmentation of the target vessel. In addition, our method provides an effective way to review the flow analysis results immediately after the acquisition, enabling the user to repeat the acquisition while the patient is still in the scanner in case of inconsistency. Overall, vessel auto-segmentation was highly successful (in 83% of vessels studied), and in rare cases of misregistration, retrospective correction of contours is possible by loading the data into a standard post-processing application. Advanced visualization including velocity color overlays and vector rendering may be useful to identify complex flow pattern such as retrograde flow regions. While further work is needed to evaluate the accuracy of the technique, inline flow processing could contribute to making application of 2D PC in the clinical setting easier and faster. Additionally, the improved first-order background phase correction may result in superior quantification accuracy.

References: 1. Gulsun et. al., MICCAI Workshop 2006 2. Goldberg, et. al., JACM 1988; 35(4):921–940 3. Guetter et. al., ISBI, 2011

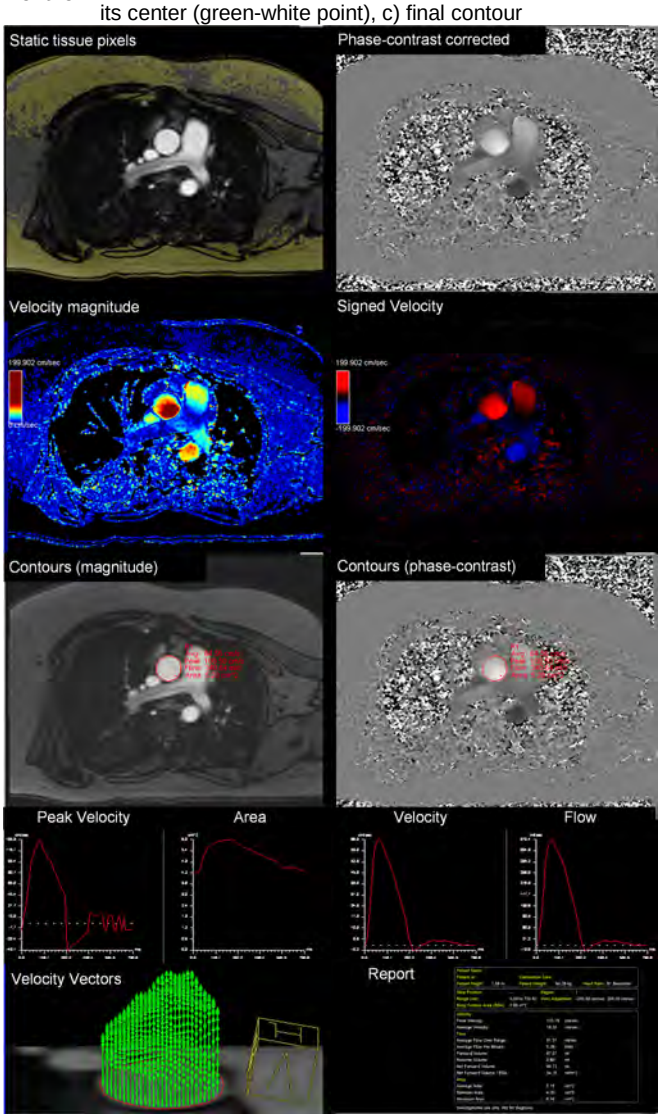

Fig. 2: Additional series produced by the automatic inline flow processing in the ascending aorta of a pediatric patient.