Fully automatic visualization of 4D Flow data

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Introduction: While the assessment of complex blood flow patterns using 4D Flow MRI is gaining attention, its clinical application remains limited by its long acquisition times and complex post-processing [1]. During data analysis and visualization, the 3D or 4D segmentation of 4D Flow data often requires manual interaction and can be tedious. The visualization of 4D flow data can be realized based on the representation of particle traces for which one particle emitter plane must be defined [2]. The positioning of this emitter plane can be tricky as it can have a strong impact on the visualization. In order to overcome the complexity of the processing of 4D Flow data, we suggest a fully automatic approach for visualization of 4D Flow data. We developed a simple technique based on data clustering in three regions (for air/lungs, static tissues, vessels) and particle traces with volume seeding.

Materials and Methods: 7 Datasets of volunteers and patients from 5 different centres acquired at 1.5T and 3T were used for evaluation of the algorithm. The dataset collection included data of the Aorta, pulmonary arteries, ventricles and carotid. Data pre-processing integrated automatic correction for Maxwell terms and eddy currents. Each dataset was temporally registered to correct for motion occurring during the cardiac-cycle. The phase-contrast angiography, velocity magnitude and the temporal standard deviation of the spatial velocity gradient were computed as features which were normalized on a logarithmic scale (Fig. 1-2). A clustering algorithm was then executed using these features to separate all the 4D Flow voxels into 3 regions. This is based on the assumption that any 4D Flow volume can be separated into 3 regions corresponding to 1) low-signal background (air/lungs) 2) static body tissues 3) vessels/ventricles. The clustering algorithm was based on a maximum-likelihood estimation of the Gaussian mixture model by expectation maximization (EM clustering [3]). Seed points for the particle traces were automatically generated with a pseudo-random distribution everywhere within the volume of the mask of the vessels/ventricles region. The path of the particles in the 4D Flow velocity field was then integrated over time and their trajectory was restricted to the boundaries of the time-resolved vascular model. Data pre-processing and visualization were performed using Siemens 4D Flow prototype V2.2. The computations of the different contrasts and the clustering were performed using Mathworks Matlab R2010b. The data was visually inspected and the average of the total running angle per particle trace was used as an estimator of the traces tortuosity and hence of their quality. The implementation was compared to a manual threshold segmentation using PCMRA contrast and to the creation of seeds everywhere in the volume (without any masking). In all cases, volume particle traces seeding with an identical total number of particles was used.

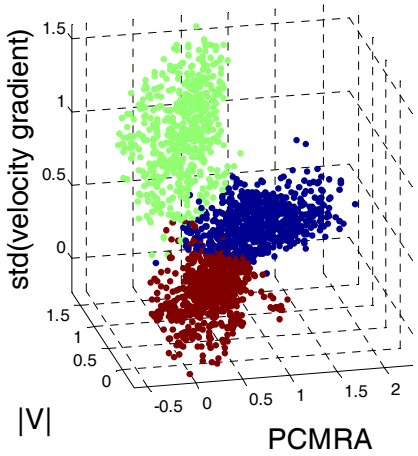

Fig. 1 Scatter plot of 4D flow voxels within the feature domain used by the clustering algorithm. The colors of the points are defined according to the identified clusters.

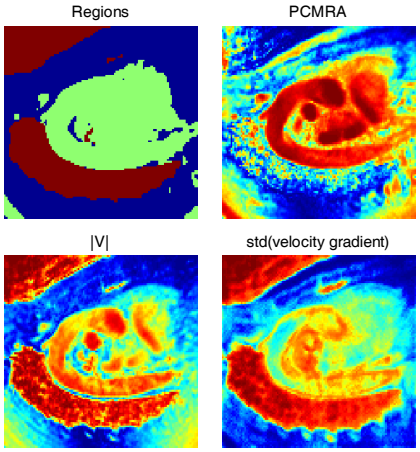

Fig. 2 mid-volume slice representing the identified clusters as well as the feature-contrasts (after histogram normalization).

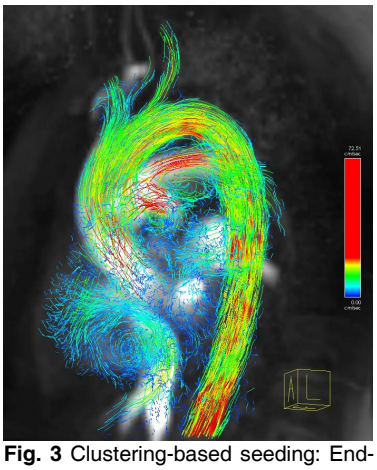

Fig. 3 Clustering-based seeding: End-systole particle traces visualization demonstrates flow in the entire aorta as well as swirling flow in the ventricles (3T dataset).

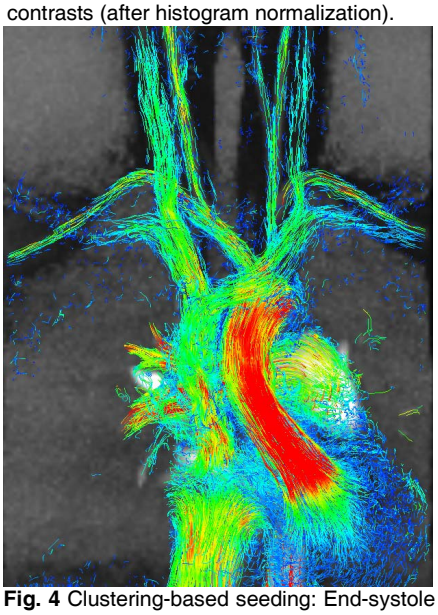

Fig. 4 Clustering-based seeding: End-systole particle traces visualization in a healthy volunteer (1.5T). Arterial and venous blood flow in the aortic root, vena cava subclavian, pulmonary, carotids and jugulars can be observed. Some noisy particle traces due to imperfect clustering are apparent.

Results: Automatic 4D flow clustering and visualization were successful for all datasets, as the clustering-based masking approach was able to capture the major blood vessels. The clustering-based approach and the manual threshold segmentation were able to capture as well most of the secondary vessels (Fig. 3-4). On lower SNR datasets (e.g. Fig. 4), some noisy particles can be observed. The clustering-based automatic visualization produced particle traces with similar tortuosity compared to data segmented with a manual threshold (Table 1), while seeding particles all over the volume without any segmentation produced the most tortuous particles.

Discussion: It was possible to perform fully automatic visualization of the particle traces of 4D Flow data. This automatic global visualization could potentially be used to identify specific regions where to quantify flow parameters or perform localized visualization (e.g. using seeding particles only at one plane to focus on a specific pattern). In this implementation, we used 3 feature-contrasts and identified 3 regions, but it could be possible to include additional feature-contrasts (e.g. CE-MRA) for the clustering algorithm or to identify more than 3 regions (e.g. differentiate venous from arterial circulation). While the clustering-based masking does not produce perfect segmentation (see isolated low velocity particles on Fig. 4), this impacts only slightly the visualization as noisy particle traces appear shorter and darker compared to particle traces belonging to vessels. While the current integration of the technique still requires some manual steps, it could become integrated as a zero-click solution. The output is fully reproducible as it does not depend on any manually adjusted value. In a context where phase-contrast MRI remains of marginal clinical use, faster acquisition techniques combined with the integration, automatization and streamlining of the post-processing are key factors to enhance the accuracy, reproducibility and time effectiveness of the technique and help bring it to clinical routine.

	Tortuosity
Seeding all over the volume	912 º ± 320 º
Threshold segmentation	367 º ± 243 º
Clustering-based seeding	371 º ± 119 º

Table 1 Estimation of particle traces tortuosity: average over all traces and patients of the total running angle per trace.

References: 1. Markl et al. JCMR 2011;13 2. Wigström et al. MRM 1999;41 3. Gupta el al. Found. & Trends in Sign. Proc. 2010; 4