A Realistic Digital Phantom for Perfusion C-arm CT based on MRI Data

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Abstract—CTP is an important imaging modality for diagnosis of ischemic stroke, which is computed from of a series of consecutive CT-scans during the injection of contrast agent. Contrast flow at any point in space can be tracked as minor changes in intensity over a period of about 40 seconds to one minute, represented as a time-attenuation curve (TAC) for every voxel. This work presents an isotropic, dense, physiologically realistic and dynamic brain phantom for CT perfusion. The phantom is based on MRI scans of a volunteer and is freely available for download.

I. INTRODUCTION

In a 3D+t brain perfusion scan, a voxel represents a time-attenuation curve (TAC). Perfusion parameter maps can be calculated from TACs which represent quantities such as cerebral blood flow (CBF), cerebral blood volume (CBV) or time-to-peak (TTP). They provide information about the location and extent of the affected tissue. The difficulty of perfusion imaging is time-resolved 3D imaging at a low contrast-to-noise ratio. As radiation exposure is minimized, projection data is corrupted by high levels of noise, while minor changes of attenuation in a range of just 5-30HU must be observable. Artifacts dominate these low-contrast variations and both CTP and FD-CTP must rely on strong filtering to extract the desired information. The most practical reconstruction and filtering algorithm for CTP and FD-CTP is therefore the one which is most resilient to noise and artifacts and still detects minor variations in tissue.

This work discusses a realistic digital 4D brain phantom for the repeatable evaluation of Perfusion CT (CTP) and Flat Detector Perfusion CT (FD-CTP) using C-Arms reconstruction algorithms. It is an extension to the work by Riordan et al. [6] and freely available for download [1]. For a repeatable evaluation, we develop a realistic brain model based on physiological data, while avoiding sparsity by continuously varying perfusion parameters and anatomical structures using MR data. The Digital Brain Perfusion Phantom package [1] provides data and Matlab tools to create a 3D-time-series of CT volumes, which can be forward projected for arbitrary protocols. The phantom is flexible with respect to the amount

of noise, the location and severity of the simulated stroke, as well as the introduction of patient motion to simulate streak artifacts. See Figure 1 (left) for an example slice of the phantom with segmented white and gray matter and annotated infarct core (red) and penumbra (yellow), a ground truth CBF map (center), as well as simulated streaks on a slice near the base of the skull (right) on a CBF map reconstructed from forward projections such as Figure 2 (left).
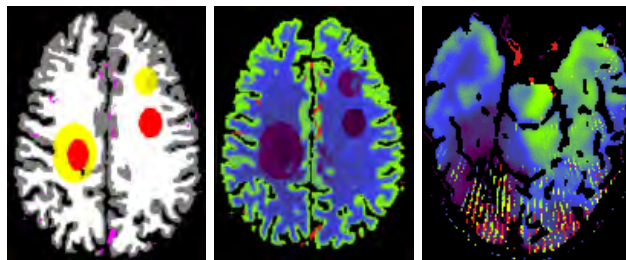

Figure 1. left: annotated regions for infarct core and penumbra, center: ground truth CBF, right: a slice of a CBF map from the base of the skull (reconstructed using FDK-JBF algorithm [4]) which is corrupted by realistic streak artifacts)

II. METHODS

A. Overview

Classical digital CT phantoms consist of homogeneous structures and have sparse representations in transformations such as total variation or wavelets. This in turn favors iterative reconstruction techniques in an evaluation, when a strong regularization of the output enforces homogeneity. An essential step in most algorithms is the subtraction of a base-line scan. Ideally, this subtraction removes most, of the typical reconstruction artifacts, since they affect any one of the scans identically. Misalignments due to motion of the patient or inaccuracies of scanner rotation, however, prevent a perfect subtraction and lead to streak artifacts. This particularly impacts the quality of FD-CTP, where a relatively slow C-Arm rotation and low angular sampling make patient motion more likely and streaks more severe. A realistic phantom should be capable of modeling these artifacts.

Riordan et al. [6] present a phantom with a similar complexity as a human brain which uses MRI data to simulate residue functions for different tissue types and takes special care to simulate noise in the CT projections. We use this idea to create a dense physiological model by continuously varying perfusion parameters based on MR data as discussed in Section II-B. In addition, we estimate dense bony structures from MRI

Figure 2. Forward Projected Brain Phantom (left: with skull; middle: without skull; right: without skull but with poisson noise)

Figure 3. Pseudo-CT estimation from a volunteer acquisition. (left: First Echo: UTE-TE1, center: Second Echo: UTE-TE2 right: MR-predicted CT)

and introduce a small artificial motion into the time-series. Applying a differing amount of 2D rotation to the z-slices of the 3D volumes from the time-series simulates a tilting of the head. Our phantom thus allows for a more realistic evaluation by providing a dense brain model based on real physiological data complemented by realistic skull bone and a small head motion, as it would be typical in clinical practice.

B. Definition of time-dependent parameters

The phantom was created by segmenting brain MRI scans from a human volunteer into white and gray matter, cerebrospinal fluid (CSF), skull and arteries. White/gray matter and CSF segmentation was done from T1 weighted MRI data using the Freesurfer software [2]. Arteries were segmented from a time-of-flight acquisition by thresholding and manual post-processing. The estimation of the skull bone from MRI is discussed in more detail in Section II-C. To reduce the sparsity of the brain phantom, the MRI data is used to vary the perfusion parameters assigned to the tissue voxels by the annotation. Therefore each tissue voxel is associated with a normalized value of its T1 weighted MR value. The MR values are normalized to the unit interval $[-1, 1]$ in each slice by first computing the mean and the standard deviation σ of all MR values inside the slice associated to a segmented tissue voxel. Then the mean is subtracted from the MR values and the values are clamped to $[-2\sigma, +2\sigma]$. The perfusion parameters of each tissue voxel are varied by $PV(x) = P(x) + NMR(x) \cdot DP(x)$, where $PV(x)$ denotes the varied perfusion parameter of voxel x (CBF or MTT, CBV is defined as CBF·MTT), $P(x)$ the default perfusion parameter of voxel x according to annotation, $NMR(x)$ the normalized MR value and $DP(x)$ the maximal deviation of the perfusion parameter. The HU values of the anatomic structures are varied in a similar way to further reduce sparsity. For an overview of computational methods to calculate perfusion parameters from TACs see [3].

C. Skull estimation from MRI sequences

Detecting cortical bone from conventional MR sequences is inherently difficult due to the similarity between air and bone intensities. Navalpakkam et al. [5] present a method to estimate the cortical bone based on dedicated MR-sequences. We use Ultrashort Echo Time (UTE) echoes TE1 (0.07ms) and TE2 (2.46ms). Cortical bone and other tissues with short T2* appear on UTE-TE1 but are absent on UTE-TE2, thus enabling their detection. This can be seen from Figure 3. Data from 5
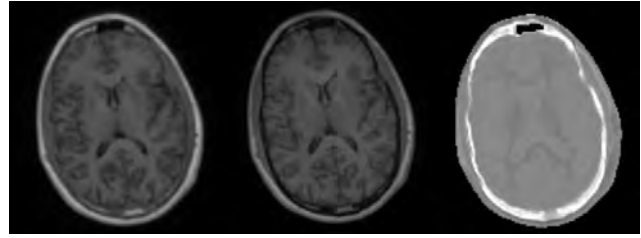
patients that were scanned on a PET/CT Siemens Biograph 64 (Siemens AG, Healthcare Sector, Erlangen, Germany) and PET/MR Siemens Biograph mMR (Siemens AG, Healthcare Sector, Erlangen, Germany) was used for model training. A UTE and a 3D Dixon-VIBE (Volume-Interpolated Breath-Hold Examination) scan was performed for each of the 5 patients. Features such as mean, median, maximum, minimum and variance were extracted from them and a pattern recognition algorithm (epsilon-insensitive Support Vector Regression with Radial Basis Functions) was trained to learn the mapping between the extracted features and the patient CT [7]. Fat ($-300 \leq HU < 0$), water ($0 \leq HU < 300$) and cortical bone ($HU \geq 300$) classes were included for training. The estimated CT-intensities are then added to the time curves described in the previous section.

III. CONCLUSION

We have presented a digital 4D brain perfusion phantom for evaluation of reconstruction algorithms, particularly those using non-linear regularization for perfusion CT and perfusion C-arm CT. It relies on real MRI data to create a dense physiological model based on indicator-dilution theory, complemented by cortical bone. The realism of this phantom is reflected in its ability to mimic streak artifacts in its reconstructions. This enables a more realistic evaluation of reconstruction algorithms than with previously published phantoms. MATLAB scripts to create the phantom are freely available for download[1], which allows researchers to create their own projection data for arbitrary protocols and hardware.

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