A flexible software phantom for generating realistic dynamic contrast-enhanced MR images of abdominal tumours.

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Introduction. Physiological motion, in particular breathing, can change the position and orientation of a tumour located in the abdomen whilst a time series of dynamic contrast-enhanced (DCE) MR images is being acquired. The accuracy and precision of any tracer kinetic model parameters estimated from these data will depend on the degree to which the tissue-to-voxel mapping changes between the images of the time series. A registration algorithm can be used to align the images before the tracer kinetic model is fitted to the derived time course data. However, the benefits of registration are hard to quantify from *in-vivo* data as ground truth for the tracer kinetic model parameters is not known. In this work we present a software phantom that can be adapted to the specific imaging scenario for which the registration algorithm is required, for example DCE-MR of liver tumours. Synthetic data can then be produced for a wide range of cases within that scenario, for example by varying the degree of motion and the tracer kinetic parameter values. The accuracy, precision and robustness of a registration technique can then be assessed.

Software phantom design. The three main packages of the design (Physiology, Signal Generation and Image Generation) are shown in Fig. 1. The Physiology package generates the contrast agent concentration, c_t, for each tissue at each time point. Various tracer kinetic models and arterial input functions (AIFs) can be implemented to give the required ground truth. The Signal Generation package uses the value of c_t to calculate the signal intensity for each tissue at each time point. It is possible to provide Signal Generation packages for imaging modalities other than MR, such as computed tomography. For an MR module the pulse sequence and its parameters can be altered to match the required imaging scenario. Neither the Physiology nor the Signal Generation package have any knowledge of the anatomy being emulated and calculate their outputs on a per tissue type basis only. The anatomical definition is the responsibility of the Image Generation package which maps the signal intensities for each tissue into the image volume whilst remaining blind to the mechanism by which the signal intensity values were generated. The anatomical representation is determined by masks for each tissue or by tracer kinetic parameter maps and can account for partial volume effects. Noise and time dependent motion can be added to the images and their descriptions can easily be changed to generate synthetic images for a wide range of simulated experimental cases. The design was implemented in C++ for Linux.

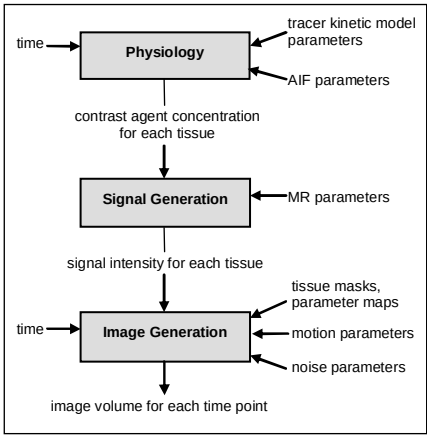

Figure 1. Output and input of the three main packages of the software phantom: Physiology, Signal Generation and Image Generation.

Synthetic images. Example images are shown in Figs 2, 3 and 4. These were simulated using a T1 weighted spoiled gradient echo pulse sequence equation with a TR of 4ms and a flip angle of 30°; the extended Kety tracer kinetic model[1]; and a parameterised form of a high temporal resolution population AIF[2]. Pre-contrast $T1$, M_0, K_{trans} (the volume transfer coefficient between the intravascular space and the extravascular-extracellular space (EES)), v_p (the fractional volume of the blood plasma), and v_e (the fractional volume of the EES) values were selected to be characteristic of each tissue type. A dynamic series with 75 time points, approximately 5 s apart and contrast agent (Gd-DTPA) administration at the 7th image was simulated. Image volumes consisted of a 128x128x25 matrix with a voxel size of 3x3x8 mm. Zero mean Gaussian noise with a SNR of 10 was added to the signal intensity values. No motion was added. Images that correspond to a pre-contrast time point and a series from approximately 5 s to 20 s post contrast agent injection are shown in Fig. 4. The position of the outer layer of fat, liver and aorta seen on Figs 2 and 4 were determined from binary masks defined manually on an acquired data set. The tumour core and rim (see Fig. 3) were defined by K^{trans} parameter maps generated by an existing software program that, for both tissue types, draws values from a simple statistical model that is trained on patient data. Constant values of pre-contrast T_1, M_0, v_p, and v_e that are characteristic of each tissue type were applied to the tumour core and rim.

Figure 2. Coronal slice (left) and sagittal slice (right) at the 9th time point.

Figure 3. The tumour region of an image generated from K^{trans} parameter maps.

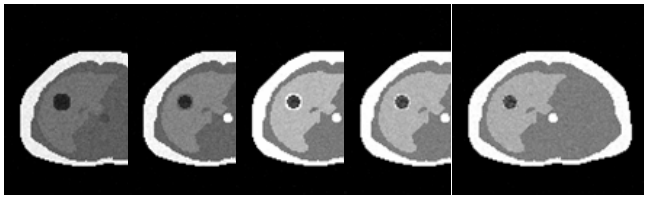

Figure 4. Images from a time series produced by the software phantom.

Conclusion. The software phantom is capable of producing DCE-MR images based on realistic anatomical definitions from acquired data sets and generated parameter maps. The component based design gives the software phantom flexibility allowing data sets to be generated with the spatial and time dependent features that are characteristic of the DCE-MR images. Synthetic data sets that match the context for which a registration algorithm is required can therefore be generated and used for validation. A wide range of ground truth values and motion descriptions can be provided allowing the accuracy, precision and robustness of the algorithms to be tested. Validation has particular relevance within clinical trial work where tracer kinetic model parameters are used to evaluate the efficacy of anti-vascular and anti-angiogenic agents. Firstly, there are specific quality standards that must be met by any registration and model fitting software used to analyse clinical trial data. Secondly, establishing and increasing the accuracy and precision to which the tracer kinetic model parameters can be estimated allows the presence of true drug effects to be determined.

References 1. Tofts, P.S., J. Magn. Reson. Imag., 1997. 7(1): p. 91-101. **2.** Parker, G., et al., Magn. Reson. in Med., 2006. 56(5): p. 993-1000.
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