Automatic analysis of hepatic DCE-MRI data

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Purpose:

The blood supply to the liver is derived jointly from the hepatic arteries and the portal venous system. The influence of breathing, the large number of pharmacokinetic parameters and the fast variations in contrast concentration in the first moments after product injection reduce the efficiency of traditional approaches. Non-linear sampling seems to optimise the measured points in dynamic contrast enhanced (DCE) MR imaging. In this communication, we present a tool for easy and automatic analysis of liver DCE-MRI data.

Methods and Materials:

Subjects:

A complete protocol of DCE-MR with parametric pharmacokinetic analysis was applied to 25 subjects. Contrast agent concentrations and bolus injection rates were selected randomly between 0.2-0.3 ml/Kg and 4-5 ml/s respectively

Pulse sequence program:

Thirteen dynamic acquisitions of a MR images set (24 slices covering the whole liver) were acquired during 210 seconds using variable delays between acquisitions, according to perfusion theoretical curves. The pulse sequence used included two blocks of 4 consecutive acquisitions during a breath hold, between 20 and 60 seconds after injection. The remaining 5 acquisitions were distributed along the whole duration of the experiment from the moment previous to bolus injection (pre-contrast series) to the final point at steady-state.

Co-registration of images:

4D (XYZ + time) co-registration of MRI images was achieved by iterative application of built-in routines of the ITK (package. Images were 4D (XYZ+time) co-registered in a GRID environment

Pharmacokinetic model:

A one-compartment two-input model was used for the pharmacokinetic characterization of hepatic perfusion (Figure 1). Parameters for optimisation in this pharmacokinetic model included kpi, kai and klo. Curves-representation, area-integrations, Levemburg-Marcquard least-squares and parametric imaging were obtained using a internal MATLAB 6.5.1. (The Mathworks, Natick, MA, USA) computer software for automatic analysis of DCE-MRI data, developed for this purpose.

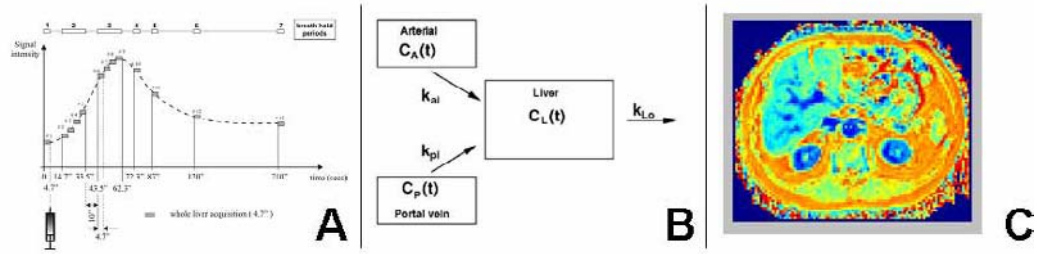

Figure 1. A) Diagram showing the adjustment of the dynamic acquisition to the theoretical perfusion curve, B) the pharmacokinetic dual-input one-compartment model for the liver perfusion, C) parametric image of kho for a patient.

Results:

Liver DCE-MRI data were measured, co-registered and analyzed for 25 patients. Good 4D (XYZ + time) co-registration was critical for apply pharmacokinetic models to DCE-MRI data. Concentration/time curves obtained by non-linear sampling allowed the capture of contrast concentration peaks, improving the accuracy of parametric images and the correlation of the data to the pharmacokinetic models. The software allowed the analysis of concentration/time curves and correlation between the data and different pharmacokinetic models (Figure 2). Parametric images of TTP, rBV and several pharmacokinetic constants were also created (Figure 3).

Discussion

The approach presented here for the study of liver perfusion allows the interpretation of the data in terms of a pharmacokinetic model and provides radiological information for the whole liver. The use of variable delays between acquisitions, according to perfusion theoretical curves, allows better capture of contrast concentration peaks. The software developed allowed the automatic semi-empirical or pharmacokinetic analysis of liver DCE-MRI data. This software may also help in the diagnosis of liver diffuse diseases.

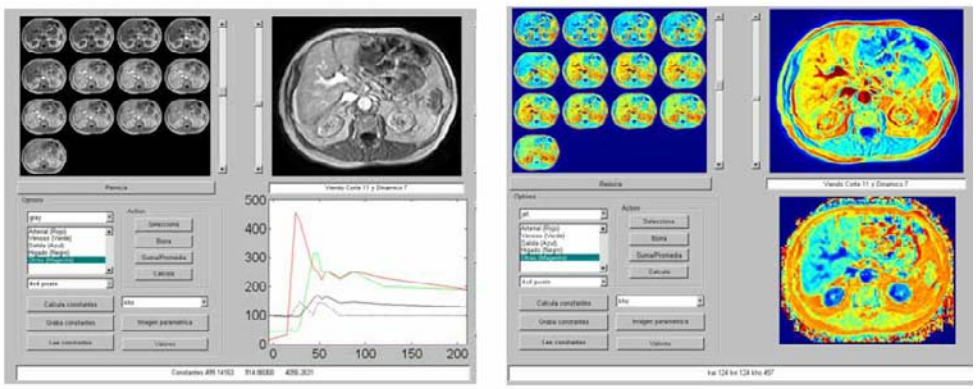

Figure 2. Two snapshots of the MATLAB software developed for the analysis of the DCE-MRI abdominal data showing the different dynamic acquisitions and the contrast concentration vs time curves (left) and some parametric images(right).