Extraction of the Contribution of the First Bolus Passage to the Signal in Dynamic Perfusion Measurements

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Introduction

Dynamic perfusion measurements are based on the tracer dilution theory as presented in [1]. The theory proposes a method for the extraction of blood flow and volume from the dynamic measurement of a concentration time course, which can be achieved in the human body by a contrast agent injection. In a closed circuit such an injection bolus will recirculate. Depending on the circulation speed and dispersion as well as the injection time, two subsequent recirculation boli may partially overlap. The human heart connects more such circuits redistributing each input in every circuit, leading to a fast mixing process of the tracer within the blood. Under conditions of a typical MRI dynamic perfusion measurement, the first bolus will be followed by a partially overlapping second bolus. A third bolus passage is hardly visible in the signal of the well mixed state. During the measurement time of approximately two minutes, the washout of the tracer is negligible. As noted by Zierler [1], the tracer dilution theory has to be extended to include recirculation or the methods have to be applied to the extracted first bolus passage signal only. In many studies an extraction of this contribution using a gamma variate function fit to the measured signal is applied [2],[3],[4]. In this work, we present an alternative, data driven method based on the reduction of the measured signal to the signal of a δ-functional injection.

Method

A simple closed circuit can be modelled as a dispersive circular flow of a liquid inside. An injected marker will appear more and more dispersed after each recirculation, until the marker is equally distributed over the liquid. The relation between two subsequent bolus passages c_i and c_{i+1} can be written as the convolution $c_{i+1} = h^* c_i$, where h is the transport function of the system. The well mixed state will occur faster with increasing injection time and the number of detectable recirculations decreases. The narrowest recirculation bolus shapes in this system can be obtained by a δ-functional injection. In practice, such an injection is not available, the bolus passages created by the desired injection function however can be found by deconvolution of the measured bolus with the real injection function. Easily accessible parameters of a real injection function are set by the total tracer volume and the (constant) injection flow. The shape of this injection bolus is strongly dispersed in the lungs. Despite this fact and considering the low sampling rate (e.g. 5 measurements during the first bolus passage), at the input to the heart only the zeroth, first and second moment of the injection function (approximation by a Gaussian function) are considered in this model. The deconvolution of the measured signal with such a Gaussian injection function yields a decreased overlap of the first two boli, which allows an easier separation. Technically, the "δ-input" boli can be separated by a minimum search followed by an exponential extrapolation of the function down to zero. The convolution of the so found function with the above injection function yields the first bolus passage contribution in the measured signal.

Results

For a comparison of the proposed method to the commonly used gamma variate fit approach, a synthetic tracer time course at an SNR 20 with varying delay (5 to 15 TR) and varying second bolus amplitude (0% to 66% of the first bolus) was used for rCBV computation (Fig. 1 and Fig. 2). The initial rCBV was set to one for all time courses. The enlarged plateau at the level of one in Fig. 1 in comparison to Fig. 2 illustrates the increased stability of the method. A variation of the SNR (data not shown) yielded a better accuracy of the proposed method compared with the gamma variate fit approach at higher SNR. At low SNR the methods yield approximately the same results. The two methods were also compared using patient data acquired on a TRIO 3T scanner with a multiecho EPI (64x64x16x40) sequence. In Fig. 3 a histogram of the computed rCBV values for both methods (fb and gam) from a ROI drawn in healthy tissue is presented, whereas in Fig. 4 the histogram from a ROI drawn on solid tumor. The total CBV was normalized to 6% for both methods. The insert in Fig. 3 shows a typical, the insert in Fig. 4 an extreme time course (dash dotted line) with extraction results (fb - solid line, gam - dashed) .

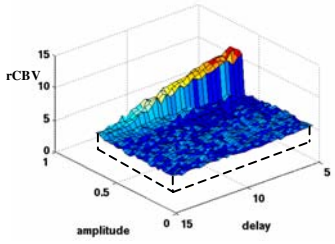

Fig. 1: First pass extraction

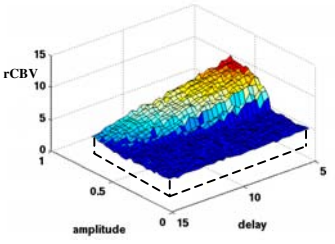

Fig. 2: Gamma variate

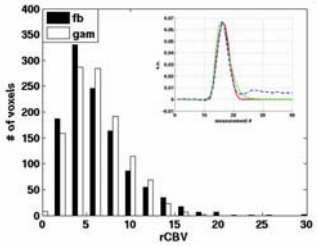

Fig. 3: Healthy brain tissue

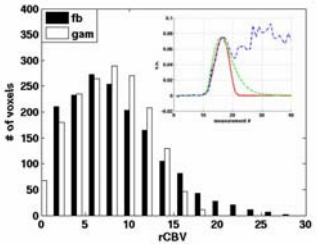

Fig. 4: Solid tumor

Discussion

The input function assumed above is based on the injection parameters and takes into account the broadening effect of the lungs and the mixing in the heart. Expansion of the input function only up to a Gaussian function is an expression of the low sampling rate within the time frame of the first passage. As the separation of the first passage contribution is performed on the transport function, the convolution still reproduces a fairly accurate shape of the first bolus. The measured bolus shape information is contained in the shape of the transport function. The trade off within the proposed method lies in the choice of the width of the injection function, which on one hand limits the number of points available to store the real shape parameters in the transport function but, on the other hand, sets the accuracy of the separation. The proposed extraction method shows an increased stability in comparison to the gamma variate fit approach (compare Fig. 1 and Fig. 2). Real data experiments show a tendency to smaller rCBV values as well as a sharper change in their distribution between healthy and solid tumor tissue (compare fb to gam in Fig. 3 and Fig. 4).

References

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