Accuracy of assuming uniform temporal sampling in the analysis of cardiac perfusion MRI datasets

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Introduction: Myocardial perfusion studies acquire images of multiple slices in each heart beat. It is typically assumed that the bolus tracking images are uniformly sampled in time. This is often not an accurate assumption, since ECG (or vectorcardiography) triggers can be missed, arrhythmias can occur, and heart rate can change. It is not known to what degree the inaccuracy of the uniform sampling assumption affects semi-quantitative or quantitative estimates of perfusion.

Methods: Time stamps were obtained from cardiac dynamic MRI perfusion studies on a Siemens 3T Trio system. The scanner provides a time stamp for each readout line (k-space line) in the raw measurement data. Alternatively, similar time information for each image can often be found in the DICOM image header. If heart rate changes during the scan or if an ECG trigger is missed, then the standard assumption that the images are spaced uniformly in time is not accurate. Figure 1 shows a complex example of a (saturated) arterial input function (AIF) from a volunteer whose heart rate slowed dramatically shortly after the start of their breathold (the "diving response") but then the sequence missed triggers as the rate returned to baseline.

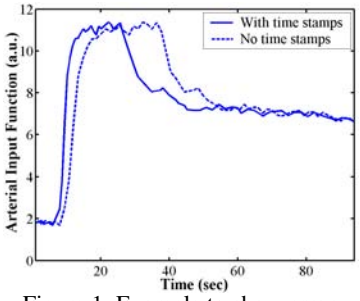

Figure 1: Example to show error that can arise in time curves due to heart rate changes during the dynamic scan.

To determine the impact of changing sampling rate on perfusion estimates, one slice in 4 subjects was processed with and without the time stamp information. The perfusion data were acquired with a turboFLASH sequence with saturation recovery magnetization preparation (TR/TE ~ 2/1msec, TI~100msec, flip=12, 8mm thick slices). The data were registered manually to compensate for respiratory motion and contours were drawn on the endocardial and epicardial borders. The slice was divided into 6 equiangular transmural regions and the signal difference (scaled so that all of the regions matched each other pre-contrast to account for coil sensitivity non-uniformities) was computed. The signal difference curves were then processed with standard methods for maximum normalized upslope measurement [1] and with a two compartment model (one tissue compartment) [2]. The time stamps were used with spline interpolation to convert the non-uniformly sampled signal difference curves to uniform samples of the same sampling rate used in the processing without time stamps which was the average heart rate for that patient. Since the sampling rate was typically not radically different, interpolation was used rather than fitting the non-uniformly space data which requires a different form of convolution [3].

Additionally, a dual bolus dataset was acquired during adenosine stress in which the scaled AIF from the first acquisition was used to provide an accurate non-saturated AIF for the tissue curves from the second bolus. The doses were 0.022 mmol/kg and 0.088 mmol/kg. The low dose was given 2.5 minutes after the start of the adenosine infusion and the high dose 105 seconds later so that imaging was complete prior to the end of the 6 minute adenosine infusion. The scaled AIF and the high dose tissue curves were interpolated based on their respective set of time stamp data to the same uniform sampling rate and then fit to a two compartment model. This was compared to assuming all of the curves were acquired at the same uniformly sampled rate.

Results and Discussion: Of 4 subjects analyzed, the largest difference in perfusion parameter estimates was an increase of 18% in a single region, and 9% average increase in a slice using a two compartment model. For the same slice analyzed with the maximum normalized upslope method, the greatest regional change was a decrease of 21% and the average upslope value in the slice decreased 16%. More typical changes were on the order of 5%. Since the sampling rate changes both the arterial input function and the tissue signal curves, this may reduce the impact of the error in timing when using a model that uses all of the input function data, such as the compartment model. In contrast, the upslope model uses only a portion of the data which can make it more sensitive to sampling rate changes if those changes occur near the maximum upslopes.

Potentially, larger errors will be found when pre-bolus studies are done to obtain a correct arterial input function from a small bolus and use it to correct a larger bolus. At pharmacological vasodilation, if the heart rate is slowly changing this could significantly change the AIF and the perfusion estimates. Fig. 2 shows the differences in sampling rate for one study performed in this fashion; resampling the curves according to the time stamp information resulted in an average 29% increase in flows in the six regions in one slice.

Note that arrhythmias and significant changes in heart rate can cause slices to be acquired in a different spatial location than in other frames such that they provide signal from a different tissue. This is particularly true in the base of the heart that moves over 1cm in systole. Such frames should be discarded rather than resampled. If a subject does have large heartrate changes when holding their breath, it may be better to acquire without a breathhold, during shallow breathing. Also, sampling non-uniformities later in the acquisition, where the regional signals are changing slowly, have little effect.

Since heart rate changes are likely to be different at stress and rest, the effect of non-uniform temporal sampling is not expected to cancel out as some artifacts do when perfusion reserve is estimated.

Semi-quantitative and quantitative perfusion estimates can be significantly changed by variations in sampling rate. Perfusion estimates can be improved by incorporating the time that each sample acquisition is measured into the processing algorithm.

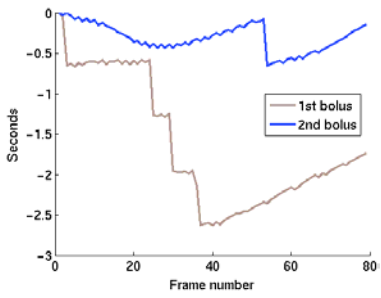

Figure 2: Cumulative time stamp differences from nominal time between samples (0.68 sec, heartrate= 88) during adenosine stress for two separate acquisitions. If the time stamps occurred every 0.68 seconds this would give a flat line at 0. The sudden jumps reflect missed ECG triggers.

References

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2. Vallee, Lazeyras et al., *JMRI 9:197-203, 1999.*
3. Riabkov and DiBella, *Phys Med Biol 49:639-664, 2004.*